GenCore version 5.1.6
Run on: February 24, 2005, 20:19:41 ; Search time 345.736 Seconds
(without alignments)
10941.049 Million cell updates/sec
Title: US-09-989-724-386_COPY_7_645
Perfect score: 639
Sequence: 1 atgttgtggctgctcttttt.....tattaatgatgccttcatga 639
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 4390206 seqs, 2959870667 residues
Total number of hits satisfying chosen parameters: 8780412
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries
Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No. Score Match Length DB ID Description

RESULT 1
ID AAZ65097 standard; cDNA; 1346 BP.
DE Membrane-bound protein PRO1312 encoding cDNA.
PN WO9963088-A2.
PD 09-DEC-1999.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 3; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 2
ID AAC58612 standard; cDNA; 1346 BP.
DE Human PRO1312 protein UNQ678 encoding cDNA SEQ ID NO:160.
PN WO200053758-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 3; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 3
ID AAA77680 standard; cDNA; 1346 BP.
DE Human PRO1312 cDNA sequence SEQ ID NO:213.
PN WO200032221-A2.
PD 08-JUN-2000.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 3; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 4
ID AAS21484 standard; cDNA; 1346 BP.
DE Human cDNA sequence encoding for PRO1312 polypeptide.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 4; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 5
ID AAF44243 standard; cDNA; 1346 BP.
DE Human PRO1312 (UNQ678) nucleotide sequence SEQ ID NO:386.
PN WO200073454-A1.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 5; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 6
ID ACA64416 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 8; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 7
ID ACA03843 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 8; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 8
ID ABX89381 standard; cDNA; 1346 BP.
DE DNA encoding novel secreted and transmembrane protein PRO1312.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 8; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 9
ID ABX80875 standard; cDNA; 1346 BP.
DE Human secreted/transmembrane protein cDNA, #157.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 639; DB 8; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 10
ID ACD44384 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO1312 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 8; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 11
ID ACD42035 standard; cDNA; 1346 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #241.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 8; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 12
ID ABX79555 standard; cDNA; 1346 BP.
DE Human sectreted/transmembrane protein cDNA, #157.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 8; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 13
ID ACA93576 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 639; DB 8; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 14
ID ABX81258 standard; DNA; 1346 BP.
DE Novel human secreted or transmembrane protein PRO1192 DNA.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 639; DB 8; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 15
ID ACA04264 standard; cDNA; 1346 BP.

DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 481.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 8; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 16
ID ACA93074 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 639; DB 8; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 17
ID ABX17158 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 8; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 18
ID ACA68013 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 19
ID ACA88462 standard; cDNA; 1346 BP.
DE Human secreted and transmembrane polypeptide PRO1312 cDNA.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 20
ID ACD81969 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO1312 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 21
ID ADA46000 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 22
ID ADA76431 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 23
ID ADA19081 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 24
ID ADA61704 standard; cDNA; 1346 BP.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 25
ID ADB19489 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 26
ID ADB28030 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 27
ID ADA86509 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 28
ID ADB16073 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 29
ID ADA37897 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1312.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 30
ID ADA47859 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 31
ID ADA21583 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO1312.
PN US2003054404-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 32
ID ADA10370 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1312.
PN US2003059831-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 33
ID ADA67654 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;

RESULT 34
ID ADB30661 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 35
ID ADA85957 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 36
ID ADA17914 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO1312 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 37
ID ADA97169 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 38
ID ADA79473 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 39
ID ADA87612 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 40
ID ADB16814 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 41
ID ADA28022 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1312.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 42
ID ADA91906 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 43
ID ADB14969 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 44
ID ADB18930 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 45
ID ADA94145 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 46
ID ADB20041 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 47
ID ADB13353 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 48
ID ACD98664 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 49
ID ADA94602 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1312.
PN US2003059832-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 50
ID ADA74607 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 51
ID ADB24840 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide SEQ ID NO 481.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 52
ID ADA82364 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003082701-A1.
PD 01-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 53
ID ADA75327 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 54
ID ADA85405 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 55
ID ADA84853 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 56
ID ADB30109 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 57
ID ADA80637 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 58
ID ADA75879 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 59
ID ADA38827 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1312.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 60
ID ADA47104 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 61
ID ADB25400 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide SEQ ID NO 481.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 62
ID ADA93576 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 63
ID ADB26926 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 64
ID ADB31213 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 65
ID ADA92948 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1312.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 66
ID ADA61141 standard; cDNA; 1346 BP.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 67
ID ADB24288 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide SEQ ID NO 481.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 68
ID ADA96617 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 69
ID ADA81189 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 70
ID ADA96065 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 71

ID ADB26374 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 72
ID ADB21859 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 73
ID ADA77638 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 74
ID ADB18378 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 75
ID ADA87061 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 76
ID ADA88164 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 77
ID ADA46552 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 78
ID ADB28582 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 79
ID ADB29134 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 80
ID ACH65530 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1312.
PN US2003044806-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 81
ID ADA77086 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 82
ID ADA22509 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO1312.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 83
ID ADA88716 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 84
ID ADA97721 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 85
ID ADB27478 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003022239-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 86
ID ADB22411 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087344-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 87
ID ACD39520 standard; cDNA; 1346 BP.
DE Human cDNA encoding PRO1192.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 88
ID ADA06675 standard; cDNA; 1346 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #121.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 89
ID ADA39368 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1312.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 90
ID ADA67102 standard; cDNA; 1346 BP.

DE Human PRO polynucleotide #241.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 91
ID ADB22963 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 92
ID ADB23736 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide SEQ ID NO 481.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 93
ID ADA92458 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 94
ID ADB15521 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 95
ID ADB38773 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 96
ID ADB96394 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2003054403-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 97
ID ADB38221 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 98
ID ADB66693 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 99
ID ADB89773 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 100
ID ADB90505 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 101
ID ADB39606 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 102
ID ADB47229 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 103
ID ADB86836 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 104
ID ADB77441 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 105
ID ADB34598 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide SEQ ID NO 481.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 106
ID ADB35702 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide SEQ ID NO 481.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 107
ID ADB34046 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide SEQ ID NO 481.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 108
ID ADB35150 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide SEQ ID NO 481.
PN US2003077718-A1.
PD 24-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 109
ID ADB36254 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide SEQ ID NO 481.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 110
ID ADB46649 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 111
ID ADC57866 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2003027754-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 112
ID ADC55230 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2003045463-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 113
ID ADC12097 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1312.
PN US2003049681-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 114
ID ADC56519 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2003064375-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 115
ID ADC07574 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1312.
PN US2003068647-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 116
ID ADC11564 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1312.
PN US2003069403-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 117
ID ADC50522 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 118
ID ADC72069 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 119
ID ADC60048 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 120
ID ADC53055 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID481.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 121
ID ADC57409 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID481.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 122
ID ADC60600 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 123
ID ADC51075 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 124
ID ADC65602 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 125
ID ADC54700 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID481.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 126
ID ADC53661 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID481.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 127
ID ADC59184 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID481.
PN US2003087359-A1.
PD 08-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 128
ID ADC56062 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID481.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 129
ID ADC58632 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID481.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 130
ID ADC14686 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 131
ID ADD08218 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 132
ID ADD03306 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 133
ID ADC90298 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 134
ID ADC82043 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 135
ID ADC69717 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 136
ID ADC48606 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 137
ID ADD10135 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 138
ID ADD07685 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 139
ID ADD04710 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 140
ID ADC82576 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 141
ID ADC80666 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 142
ID ADD11173 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 143
ID ADC48054 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 144
ID ADD08756 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 145
ID ADC80114 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 146
ID ADD07005 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2002193300-A1.

PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 147
ID ADD09583 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 148
ID ADC83252 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 149
ID ADD41296 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 150
ID ADD52435 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 151
ID ADD53175 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 152
ID ADD53727 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 153
ID ADD55359 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 154
ID ADD56317 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 155
ID ADD51883 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;

RESULT 156
ID ADD02682 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 157
ID ADD02116 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 158
ID ADD54298 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 159
ID ADD54755 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 160
ID ADD92615 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 161
ID ADD91511 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 162
ID ADE04125 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 163
ID ADE26909 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087304-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 164
ID ADE32422 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 165
ID ADE22354 standard; cDNA; 1346 BP.

DE cDNA encoding human PRO polypeptide #241.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 166
ID ADD79578 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 167
ID ADE42114 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 168
ID ADE17931 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 169
ID ADD92063 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 170
ID ADE33526 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 171
ID ADE34078 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 172
ID ADD80130 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 173
ID ADD93167 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 174
ID ADE19587 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 175
ID ADE19035 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 176
ID ADE43231 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 177
ID ADD96020 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 178
ID ADE22906 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 179
ID ADD79024 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 180
ID ADE26376 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 181
ID ADE32974 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 182
ID ADE42666 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 183
ID ADD80682 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003207418-A1.
PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 184
ID ADD89710 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 185
ID ADE40994 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 186
ID ADE04793 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 187
ID ADE92922 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 188
ID ADF67313 standard; cDNA; 1346 BP.
DE Human PRO1312 nucleotide sequence SEQ ID NO:386.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 189
ID ADG21631 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 190
ID ADG23272 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 191
ID ADF97607 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 192
ID ADG80671 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 193
ID ADG80119 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 194
ID ADH55411 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 195
ID ADH55963 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 196
ID ADI35567 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2003050457-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 197
ID ADI64182 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 198
ID ADI65131 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 199
ID ADI63630 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 200
ID ADH82044 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 201
ID ADI00060 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 202

ID ADH81492 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 203
ID ABX77959 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2003027163-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 204
ID ABX80371 standard; DNA; 1346 BP.
DE Novel human secreted or transmembrane protein PRO1192 DNA.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 205
ID ACA69277 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1312.
PN US2003032023-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 206
ID ACD24093 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 207
ID ABX90348 standard; cDNA; 1346 BP.
DE Human secreted/transmembrane protein cDNA, #157.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 208
ID ABX64194 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO1312 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 209
ID ACA67234 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 210
ID ADM82661 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 11; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 211
ID ADN16060 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 11; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 212
ID ADN16689 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 11; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 213
ID ADN15508 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 11; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 214
ID ADN14956 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 11; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 215
ID ADC81218 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 216
ID ADD76666 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 217
ID ADD88030 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 218
ID ADD86434 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 219
ID ADE75882 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 220
ID ADE23458 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003092108-A1.
PD 15-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 221
ID ADE24010 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 222
ID ADE24653 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 223
ID ADD87478 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 224
ID ADE89344 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 225
ID ADE18483 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 226
ID ADE88792 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 227
ID ADE94812 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 228
ID ADE91223 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 229
ID ADF35512 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO1312 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 230
ID ADE95364 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 231
ID ADE93474 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 232
ID ADF35055 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 233
ID ADE92370 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 234
ID ADE90671 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 235
ID ADE91818 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 236
ID ADG11762 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO1312 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 237
ID ADG02397 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 238
ID ADG22183 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;

RESULT 239
ID ADG20253 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 240
ID ADF98159 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 241
ID ADG24376 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 242
ID ADF98730 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 243
ID ADG03561 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 244
ID ADF99282 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 245
ID ADG16867 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 246
ID ADG05326 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 247
ID ADG19593 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 248
ID ADG13430 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 249
ID ADG08487 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 250
ID ADG15657 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 251
ID ADF97055 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 252
ID ADG06240 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 253
ID ADG23824 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 254
ID ADG04113 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 255
ID ADG25014 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 256
ID ADG07311 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 257
ID ADG07863 standard; cDNA; 1346 BP.

DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 258
ID ADG55358 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 259
ID ADG61022 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 260
ID ADG62126 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 261
ID ADG82327 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 262
ID ADG57566 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 263
ID ADG57014 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 264
ID ADG55910 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 265
ID ADG58670 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 266
ID ADG71036 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 267
ID ADG58118 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 268
ID ADG53702 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 269
ID ADG71588 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 270
ID ADG81775 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003207805-A1.
PD 06-NOV-2003.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 271
ID ADH19632 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1312.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 272
ID ADH30737 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 273
ID ADH12104 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 274
ID ADG52526 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 275
ID ADG54254 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207416-A1.
PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 276
ID ADG81223 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 277
ID ADG56462 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 278
ID ADH12728 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 279
ID ADH21125 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1312.
PN US2003224358-A1.
PD 04-DEC-2003.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 280
ID ADG61574 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 281
ID ADH20165 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1312.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 282
ID ADH28661 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 283
ID ADG54806 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 284
ID ADG59846 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 285
ID ADI81270 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 286
ID ADG10013 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 287
ID ADI15484 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 288
ID ADG09361 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 289
ID ADI14816 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 290
ID ADI18411 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 291
ID ADJ63692 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 292
ID ADJ77587 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 293
ID ADJ65709 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;

RESULT 294
ID ADM27845 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 295
ID ADM42569 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 296
ID ADM28431 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 297
ID ADI95913 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 13; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 298
ID ADI96465 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 13; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 299
ID ADT94383 standard; cDNA; 1346 BP.
DE Human PRO1312 cDNA sequence.
PN AU2003259607-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 639; DB 13; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.7e-185;
RESULT 300
ID AAF94460 standard; cDNA; 666 BP.
DE Human hydrophobic domain containing protein clone HP10720 cDNA #74.
PN WO200112660-A2.
PD 22-FEB-2001.
PA (SAGA) SAGAMI CHEM RES CENT.
PA (PROT-) PROTEGENE INC.
Query Match 98.3%; Score 628; DB 4; Length 666;
Best Local Similarity 99.8%; Pred. No. 1.3e-181;
RESULT 301
ID ADI02664 standard; cDNA; 1312 BP.
DE Human cDNA differentially expressed in the vascular endothelium #205.
PN US2003166903-A1.
PD 04-SEP-2003.
PA (ASTR/) ASTROMOFF A.
PA (BAND/) BANDMAN O.
PA (COCK/) COCKS B G.
Query Match 98.3%; Score 628; DB 10; Length 1312;
Best Local Similarity 99.8%; Pred. No. 1.8e-181;
RESULT 302
ID AAF94470 standard; cDNA; 1347 BP.
DE Human hydrophobic domain containing protein clone HP10720 cDNA #84.
PN WO200112660-A2.
PD 22-FEB-2001.
PA (SAGA) SAGAMI CHEM RES CENT.
PA (PROT-) PROTEGENE INC.
Query Match 98.3%; Score 628; DB 4; Length 1347;
Best Local Similarity 99.8%; Pred. No. 1.8e-181;
RESULT 303
ID ADA39900 standard; cDNA; 1432 BP.
DE Human secreted protein encoding cDNA.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 98.3%; Score 628; DB 8; Length 1432;
Best Local Similarity 99.8%; Pred. No. 1.9e-181;
RESULT 304
ID ADA11489 standard; DNA; 1432 BP.
DE Human cDNA encoding a novel secreted protein, SEQ ID NO 17.
PN US2003055236-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 98.3%; Score 628; DB 9; Length 1432;
Best Local Similarity 99.8%; Pred. No. 1.9e-181;
RESULT 305
ID ADD37613 standard; cDNA; 1432 BP.
DE Human secreted protein encoding sequence #95.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 98.3%; Score 628; DB 10; Length 1432;
Best Local Similarity 99.8%; Pred. No. 1.9e-181;
RESULT 306
ID ADA56090 standard; DNA; 1432 BP.
DE Gene encoding human secreted protein #269.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 98.3%; Score 628; DB 10; Length 1432;
Best Local Similarity 99.8%; Pred. No. 1.9e-181;
RESULT 307
ID AAZ65261 standard; DNA; 1447 BP.
DE Human secreted protein gene 12.
PN WO9958660-A1.
PD 18-NOV-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 98.2%; Score 627.6; DB 3; Length 1447;
Best Local Similarity 99.7%; Pred. No. 2.5e-181;
RESULT 308
ID ADE11650 standard; cDNA; 1447 BP.
DE Human secreted polypeptide cDNA #12.
PN US2003100051-A1.
PD 29-MAY-2003.
PA (RUBE/) RUBEN S M.
PA (FLOR/) FLORENCE K A.
PA (NIJJ/) NI J.
PA (ROSE/) ROSEN C A.
PA (CART/) CARTER K C.
PA (MOOR/) MOORE P A.
PA (OLSE/) OLSEN H S.
PA (SHIY/) SHI Y.
PA (YOUN/) YOUNG P E.
PA (WEIY/) WEI Y.
PA (BREW/) BREWER L A.
PA (SOPP/) SOPPET D R.
PA (LAFL/) LAFLEUR D W.
PA (ENDR/) ENDRESS G A.
PA (EBNE/) EBNER R.
PA (BIRS/) BIRSE C E.
Query Match 98.2%; Score 627.6; DB 10; Length 1447;
Best Local Similarity 99.7%; Pred. No. 2.5e-181;
RESULT 309
ID ABZ78127 standard; cDNA; 1345 BP.
DE Human cancer-related coding sequence, 156P1D4.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 98.0%; Score 626.4; DB 8; Length 1345;

Best Local Similarity 99.7%; Pred. No. 5.6e-181;
RESULT 310
ID AAV40540 standard; cDNA; 1401 BP.
DE Homo sapiens secreted protein clone AM42_3.
PN WO9832853-A2.
PD 30-JUL-1998.
PA (GEMY) GENETICS INST INC.
Query Match 98.0%; Score 626.4; DB 2; Length 1401;
Best Local Similarity 99.7%; Pred. No. 5.7e-181;
RESULT 311
ID AAX19983 standard; cDNA; 848 BP.
DE Human secreted protein 5' EST SEQ ID NO:27.
PN WO9906439-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 98.0%; Score 626; DB 2; Length 848;
Best Local Similarity 99.2%; Pred. No. 5.9e-181;
RESULT 312
ID AAX39430 standard; DNA; 848 BP.
DE Human secreted protein 5' EST SEQ ID NO: 27.
PN WO9906551-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 98.0%; Score 626; DB 2; Length 848;
Best Local Similarity 99.2%; Pred. No. 5.9e-181;
RESULT 313
ID AAX41369 standard; cDNA; 848 BP.
DE Extended cDNA obtained from 5' EST, SEQ ID NO: 27 from WO 9906553.
PN WO9906553-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 98.0%; Score 626; DB 2; Length 848;
Best Local Similarity 99.2%; Pred. No. 5.9e-181;
RESULT 314
ID AAX97564 standard; DNA; 848 BP.
DE Extended human secreted protein coding sequence, SEQ ID NO. 27.
PN WO9931236-A2.
PD 24-JUN-1999.
PA (GEST) GENSET.
Query Match 98.0%; Score 626; DB 2; Length 848;
Best Local Similarity 99.2%; Pred. No. 5.9e-181;
RESULT 315
ID AAZ40770 standard; DNA; 848 BP.
DE Secreted protein extended EST coding sequence #6.
PN WO9940189-A2.
PD 12-AUG-1999.
PA (GEST) GENSET.
Query Match 98.0%; Score 626; DB 2; Length 848;
Best Local Similarity 99.2%; Pred. No. 5.9e-181;
RESULT 316
ID AAX26672 standard; RNA; 848 BP.
DE Extended cDNA derived from a 5' EST encoding a secreted protien.
PN WO9906554-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 98.0%; Score 626; DB 2; Length 848;
Best Local Similarity 99.2%; Pred. No. 5.9e-181;
RESULT 317
ID AAX51777 standard; cDNA; 848 BP.
DE Human secreted protein 5' EST clone 58-35-2-F10-FL2.
PN WO9906552-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 98.0%; Score 626; DB 2; Length 848;
Best Local Similarity 99.2%; Pred. No. 5.9e-181;
RESULT 318
ID AAX51449 standard; DNA; 848 BP.
DE Human secreted protein 5' EST SEQ ID NO. 27.
PN WO9906549-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 98.0%; Score 626; DB 2; Length 848;
Best Local Similarity 99.2%; Pred. No. 5.9e-181;
RESULT 319
ID AAX40428 standard; cDNA; 848 BP.
DE Extended cDNA derived from 5' EST.
PN WO9906550-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 98.0%; Score 626; DB 2; Length 848;
Best Local Similarity 99.2%; Pred. No. 5.9e-181;
RESULT 320
ID AAZ42251 standard; cDNA; 848 BP.
DE Human full length cDNA 58-35-2-F10-FL2.
PN WO9953051-A2.
PD 21-OCT-1999.
PA (GEST) GENSET.
Query Match 98.0%; Score 626; DB 3; Length 848;
Best Local Similarity 99.2%; Pred. No. 5.9e-181;
RESULT 321
ID AAC00012 standard; cDNA; 848 BP.
DE Human secreted protein cDNA sequence #3.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 98.0%; Score 626; DB 3; Length 848;
Best Local Similarity 99.2%; Pred. No. 5.9e-181;
RESULT 322
ID ADJ45874 standard; cDNA; 848 BP.
DE Novel human secreted protein-related cDNA sequence SeqID27.
PN US2003144490-A1.
PD 31-JUL-2003.
PA (EDWA/) EDWARDS J D M.
PA (DUCL/) DUCLERT A.
PA (BOUG/) BOUGUELERET L.
Query Match 98.0%; Score 626; DB 10; Length 848;
Best Local Similarity 99.2%; Pred. No. 5.9e-181;
RESULT 323
ID ADM77746 standard; cDNA; 848 BP.
DE EST encoding signal sequence #6.
PN US2003162176-A1.
PD 28-AUG-2003.
PA (EDWA/) EDWARDS J D M.
PA (DUCL/) DUCLERT A.
PA (BOUG/) BOUGUELERET L.
Query Match 98.0%; Score 626; DB 11; Length 848;
Best Local Similarity 99.2%; Pred. No. 5.9e-181;
RESULT 324
ID AAX88191 standard; cDNA; 848 BP.
DE Human secreted protein 6 extended cDNA.
PN WO9925825-A2.
PD 27-MAY-1999.
PA (GEST) GENSET.
Query Match 97.9%; Score 625.4; DB 2; Length 848;
Best Local Similarity 99.2%; Pred. No. 9.1e-181;
RESULT 325
ID AAX30083 standard; cDNA; 847 BP.
DE Human secreted protein 5' EST SEQ ID NO:27.
PN WO9906548-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 97.7%; Score 624.4; DB 2; Length 847;
Best Local Similarity 99.1%; Pred. No. 1.8e-180;
RESULT 326
ID AAH98224 standard; cDNA; 1365 BP.
DE Human EST-derived coding sequence SEQ ID NO: 81.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 96.6%; Score 617; DB 4; Length 1365;
Best Local Similarity 99.7%; Pred. No. 4.2e-178;
RESULT 327
ID AAX97957 standard; DNA; 1356 BP.
DE Human secreted protein gene 42.
PN WO9931117-A1.
PD 24-JUN-1999.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 96.4%; Score 616; DB 2; Length 1356;
Best Local Similarity 99.7%; Pred. No. 8.6e-178;
RESULT 328
ID ADA40381 standard; cDNA; 1356 BP.
DE Human secreted protein encoding cDNA.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 96.4%; Score 616; DB 8; Length 1356;
Best Local Similarity 99.7%; Pred. No. 8.6e-178;
RESULT 329
ID ADA11594 standard; DNA; 1356 BP.
DE Human cDNA encoding a novel secreted protein, SEQ ID NO 122.
PN US2003055236-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 96.4%; Score 616; DB 9; Length 1356;
Best Local Similarity 99.7%; Pred. No. 8.6e-178;
RESULT 330
ID ADD37752 standard; cDNA; 1356 BP.
DE Human secreted protein encoding sequence #234.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 96.4%; Score 616; DB 10; Length 1356;
Best Local Similarity 99.7%; Pred. No. 8.6e-178;
RESULT 331
ID ADA56545 standard; DNA; 1356 BP.
DE Gene encoding human secreted protein #269.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 96.4%; Score 616; DB 10; Length 1356;
Best Local Similarity 99.7%; Pred. No. 8.6e-178;
RESULT 332
ID ADO07092 standard; cDNA; 774 BP.
DE Human protein modification and maintenance molecule 26 (PMMM-26) cDNA.
PN WO2004033636-A2.
PD 22-APR-2004.
PA (INCY-) INCYTE CORP.
Query Match 83.3%; Score 532; DB 12; Length 774;
Best Local Similarity 88.0%; Pred. No. 3.6e-152;
RESULT 333
ID ABT42042 standard; DNA; 1181 BP.
DE Toxicity modelling related rat gene SEQ ID No 1744.
PN WO200295000-A2.
PD 28-NOV-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 76.0%; Score 485.6; DB 10; Length 1181;
Best Local Similarity 85.9%; Pred. No. 7.2e-138;
RESULT 334
ID AAX40832 standard; cDNA; 439 BP.
DE Human secreted protein 5' EST SEQ ID NO: 44.
PN WO9906554-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 63.1%; Score 403.4; DB 2; Length 439;
Best Local Similarity 99.8%; Pred. No. 7e-113;
RESULT 335
ID AAV86301 standard; cDNA; 462 BP.
DE EST clone AM42.
PN WO9845435-A2.
PD 15-OCT-1998.
PA (GEMY) GENETICS INST INC.
Query Match 62.4%; Score 399; DB 2; Length 462;
Best Local Similarity 98.0%; Pred. No. 1.6e-111;
RESULT 336
ID ABS69507 standard; DNA; 532 BP.
DE Novel murine polynucleotide isolated using gene trap technology #570.
PN US2002102543-A1.
PD 01-AUG-2002.
PA (FRIE/) FRIEDRICH G.
PA (ZAMB/) ZAMBROWICZ B.
PA (SAND/) SANDS A T.
Query Match 48.6%; Score 310.6; DB 6; Length 532;
Best Local Similarity 84.7%; Pred. No. 2.1e-84;
RESULT 337
ID ABL78658 standard; cDNA; 355 BP.
DE Human ovarian cancer related cDNA clone SEQ ID NO:1636.
PN WO200192581-A2.
PD 06-DEC-2001.
PA (CORI-) CORIXA CORP.
Query Match 36.4%; Score 232.6; DB 6; Length 355;
Best Local Similarity 83.9%; Pred. No. 1.4e-60;
RESULT 338
ID ADN43035 standard; cDNA; 379 BP.
DE Human secreted protein SECP-21 cDNA.
PN WO2004037987-A2.
PD 06-MAY-2004.
PA (INCY-) INCYTE CORP.
Query Match 31.8%; Score 203.4; DB 12; Length 379;
Best Local Similarity 99.5%; Pred. No. 1.2e-51;
RESULT 339
ID ABA71751 standard; DNA; 213 BP.
DE Human foetal liver single exon nucleic acid probe #20056.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 30.9%; Score 197.4; DB 4; Length 213;
Best Local Similarity 99.5%; Pred. No. 6.5e-50;
RESULT 340
ID AAI52077 standard; DNA; 213 BP.
DE Probe #20763 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 30.9%; Score 197.4; DB 4; Length 213;
Best Local Similarity 99.5%; Pred. No. 6.5e-50;
RESULT 341
ID ABA37840 standard; DNA; 213 BP.
DE Probe #16306 for gene expression analysis in human heart cell sample.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 30.9%; Score 197.4; DB 4; Length 213;
Best Local Similarity 99.5%; Pred. No. 6.5e-50;
RESULT 342
ID AAK46169 standard; DNA; 213 BP.
DE Human bone marrow expressed single exon probe SEQ ID NO: 20726.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 30.9%; Score 197.4; DB 4; Length 213;
Best Local Similarity 99.5%; Pred. No. 6.5e-50;
RESULT 343
ID AAK20115 standard; DNA; 213 BP.
DE Human brain expressed single exon probe SEQ ID NO: 20106.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 30.9%; Score 197.4; DB 4; Length 213;
Best Local Similarity 99.5%; Pred. No. 6.5e-50;
RESULT 344
ID ABS45886 standard; DNA; 213 BP.
DE Human liver single exon probe, SEQ ID No 20876.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 30.9%; Score 197.4; DB 4; Length 213;
Best Local Similarity 99.5%; Pred. No. 6.5e-50;
RESULT 345
ID ABS20478 standard; DNA; 213 BP.
DE Human genome-derived single exon probe ORF from lung SEQ ID No 20469.
PN WO200186003-A2.
PD 15-NOV-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 30.9%; Score 197.4; DB 6; Length 213;
Best Local Similarity 99.5%; Pred. No. 6.5e-50;
RESULT 346
ID ABA59231 standard; DNA; 464 BP.
DE Human foetal liver single exon nucleic acid probe #7536.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 29.5%; Score 188.2; DB 4; Length 464;
Best Local Similarity 96.0%; Pred. No. 6.2e-47;
RESULT 347
ID AAI39012 standard; DNA; 464 BP.
DE Probe #7698 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 29.5%; Score 188.2; DB 4; Length 464;
Best Local Similarity 96.0%; Pred. No. 6.2e-47;
RESULT 348
ID ABA27979 standard; DNA; 464 BP.
DE Probe #6445 for gene expression analysis in human heart cell sample.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 29.5%; Score 188.2; DB 4; Length 464;
Best Local Similarity 96.0%; Pred. No. 6.2e-47;
RESULT 349
ID AAK33216 standard; DNA; 464 BP.
DE Human bone marrow expressed single exon probe SEQ ID NO: 7773.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 29.5%; Score 188.2; DB 4; Length 464;
Best Local Similarity 96.0%; Pred. No. 6.2e-47;
RESULT 350
ID AAK07438 standard; DNA; 464 BP.
DE Human brain expressed single exon probe SEQ ID NO: 7429.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 29.5%; Score 188.2; DB 4; Length 464;
Best Local Similarity 96.0%; Pred. No. 6.2e-47;
RESULT 351
ID ABS32964 standard; DNA; 464 BP.
DE Human liver single exon probe, SEQ ID No 7954.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 29.5%; Score 188.2; DB 4; Length 464;
Best Local Similarity 96.0%; Pred. No. 6.2e-47;
RESULT 352
ID ABS08046 standard; DNA; 464 BP.
DE Human genome-derived single exon probe from lung SEQ ID No 8037.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 29.5%; Score 188.2; DB 6; Length 464;
Best Local Similarity 96.0%; Pred. No. 6.2e-47;
RESULT 353
ID AAC66136 standard; DNA; 862 BP.
DE Human kidney disease associated gene SEQ ID 6.
PN WO200061622-A2.
PD 19-OCT-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 25.5%; Score 163; DB 3; Length 862;
Best Local Similarity 99.4%; Pred. No. 4.3e-39;
RESULT 354
ID AAC84367 standard; DNA; 2415 BP.
DE Human Zace2 protein encoding degenerate sequence.
PN WO200070032-A1.
PD 23-NOV-2000.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 22.6%; Score 144.2; DB 4; Length 2415;
Best Local Similarity 39.1%; Pred. No. 4e-33;
RESULT 355
ID ABX93334 standard; DNA; 2415 BP.
DE Degenerate DNA sequence encoding human zinc metallopeptidase Zace2.
PN US2002177211-A1.
PD 28-NOV-2002.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 22.6%; Score 144.2; DB 10; Length 2415;
Best Local Similarity 39.1%; Pred. No. 4e-33;
RESULT 356
ID AAC84369 standard; DNA; 2415 BP.
DE Mouse Zace2-5 protein encoding degenerate sequence.
PN WO200070032-A1.
PD 23-NOV-2000.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 19.7%; Score 125.6; DB 4; Length 2415;
Best Local Similarity 38.6%; Pred. No. 2e-27;
RESULT 357
ID ABX93336 standard; DNA; 2415 BP.
DE Degenerate DNA sequence encoding mouse zinc metallopeptidase mZace-5.
PN US2002177211-A1.
PD 28-NOV-2002.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 19.7%; Score 125.6; DB 10; Length 2415;
Best Local Similarity 38.6%; Pred. No. 2e-27;
RESULT 358
ID ADL95396 standard; cDNA; 2415 BP.
DE Angiotensin converting enzyme-2 (ACE-2) coding sequence.
PN US6610497-B1.
PD 26-AUG-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 19.6%; Score 125; DB 11; Length 2415;
Best Local Similarity 57.3%; Pred. No. 3.1e-27;
RESULT 359
ID AAZ59465 standard; DNA; 2418 BP.
DE Human MPROT15 coding sequence #1.
PN JP11318472-A.
PD 24-NOV-1999.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 19.6%; Score 125; DB 3; Length 2418;
Best Local Similarity 57.3%; Pred. No. 3.1e-27;
RESULT 360
ID ACN43792 standard; cDNA; 3064 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2667.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 19.6%; Score 125; DB 13; Length 3064;
Best Local Similarity 57.3%; Pred. No. 3.4e-27;
RESULT 361
ID ACH03967 standard; cDNA; 3324 BP.
DE Human cDNA differentially expressed in lung cancer #172.
PN US2003065157-A1.
PD 03-APR-2003.
PA (LASE/) LASEK A W.
Query Match 19.6%; Score 125; DB 9; Length 3324;
Best Local Similarity 57.3%; Pred. No. 3.6e-27;
RESULT 362
ID ADC38727 standard; cDNA; 3325 BP.
DE Human cDNA encoding a secreted protein #41.
PN US2002193567-A1.
PD 19-DEC-2002.
PA (GEMY) GENETICS INST INC.
Query Match 19.6%; Score 125; DB 10; Length 3325;
Best Local Similarity 57.3%; Pred. No. 3.6e-27;
RESULT 363
ID AAC84366 standard; cDNA; 3334 BP.
DE Human Zace2 protein encoding cDNA.
PN WO200070032-A1.
PD 23-NOV-2000.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 19.6%; Score 125; DB 4; Length 3334;

Best Local Similarity 57.3%; Pred. No. 3.6e-27;
RESULT 364
ID ABX93333 standard; cDNA; 3334 BP.
DE cDNA encoding human zinc metallopeptidase Zace2.
PN US2002177211-A1.
PD 28-NOV-2002.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 19.6%; Score 125; DB 10; Length 3334;
Best Local Similarity 57.3%; Pred. No. 3.6e-27;
RESULT 365
ID AAA12764 standard; cDNA; 3396 BP.
DE cDNA encoding a human angiotensin converting enzyme-2 (ACE-2).
PN WO200018899-A2.
PD 06-APR-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 19.6%; Score 125; DB 3; Length 3396;
Best Local Similarity 57.3%; Pred. No. 3.6e-27;
RESULT 366
ID AAD02758 standard; cDNA; 3396 BP.
DE Human angiotensin converting enzyme-2 (ACE-2) cDNA.
PN US6194556-B1.
PD 27-FEB-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 19.6%; Score 125; DB 4; Length 3396;
Best Local Similarity 57.3%; Pred. No. 3.6e-27;
RESULT 367
ID AAD32586 standard; cDNA; 3396 BP.
DE Human ACE-2 full-length cDNA.
PN WO200212471-A2.
PD 14-FEB-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 19.6%; Score 125; DB 6; Length 3396;
Best Local Similarity 57.3%; Pred. No. 3.6e-27;
RESULT 368
ID ABK87623 standard; cDNA; 3396 BP.
DE cDNA encoding human angiotensin converting enzyme-2 (ACE-2) protein.
PN WO200239997-A2.
PD 23-MAY-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 19.6%; Score 125; DB 6; Length 3396;
Best Local Similarity 57.3%; Pred. No. 3.6e-27;
RESULT 369
ID ADA03343 standard; DNA; 3396 BP.
DE Human angiotensin converting enzyme 2-like protein gene.
PN WO200298448-A1.
PD 12-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 19.6%; Score 125; DB 8; Length 3396;
Best Local Similarity 57.3%; Pred. No. 3.6e-27;
RESULT 370
ID ACC79022 standard; cDNA; 3396 BP.
DE Human ACE-2 protein encoding cDNA SEQ ID NO:141.
PN WO200298906-A1.
PD 12-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 19.6%; Score 125; DB 8; Length 3396;
Best Local Similarity 57.3%; Pred. No. 3.6e-27;
RESULT 371
ID ADL95394 standard; cDNA; 3396 BP.
DE Human angiotensin converting enzyme-2 (ACE-2) cDNA.
PN US6610497-B1.
PD 26-AUG-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 19.6%; Score 125; DB 11; Length 3396;
Best Local Similarity 57.3%; Pred. No. 3.6e-27;
RESULT 372
ID ADH51356 standard; DNA; 3404 BP.
DE Human angiotensin-converting enzyme homologue ACE2 DNA.
PN WO2004000367-A1.
PD 31-DEC-2003.
PA (UYHE-) UNIV HEALTH NETWORK.
Query Match 19.6%; Score 125; DB 12; Length 3404;
Best Local Similarity 57.3%; Pred. No. 3.6e-27;
RESULT 373
ID ABS60632 standard; cDNA; 3405 BP.
DE Human cDNA encoding angiotensin converting enzyme 2 variant #1.
PN WO200261131-A2.
PD 08-AUG-2002.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
PA (TSUC/) TSUCHIHASHI Z.
PA (HUIL/) HUI L.
Query Match 19.6%; Score 125; DB 6; Length 3405;
Best Local Similarity 57.3%; Pred. No. 3.6e-27;
RESULT 374
ID ABS60371 standard; cDNA; 3405 BP.
DE Human cDNA encoding angiotensin converting enzyme 2.
PN WO200261131-A2.
PD 08-AUG-2002.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
PA (TSUC/) TSUCHIHASHI Z.
PA (HUIL/) HUI L.
Query Match 19.6%; Score 125; DB 6; Length 3405;
Best Local Similarity 57.3%; Pred. No. 3.6e-27;
RESULT 375
ID AAS21279 standard; cDNA; 3732 BP.
DE Human cDNA sequence encoding for PRO1885 polypeptide.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 4; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 376
ID ACA03638 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 8; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 377
ID ABX89176 standard; cDNA; 3732 BP.
DE DNA encoding novel secreted and transmembrane protein PRO1885.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 8; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 378
ID ACD41830 standard; cDNA; 3732 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #36.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 8; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 379
ID ACA04059 standard; cDNA; 3732 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 71.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 8; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 380
ID ADA45590 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 381
ID ADA76021 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003073212-A1.
PD 17-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 382
ID ADA18671 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 383
ID ADA61294 standard; cDNA; 3732 BP.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 384
ID ADB19079 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 385
ID ADB27620 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 386
ID ADA86099 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 387
ID ADB15663 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 388
ID ADA47449 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 389
ID ADA67244 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 390
ID ADB30251 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 391
ID ADA85547 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 392
ID ADA96759 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 393
ID ADA79063 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 394
ID ADA87202 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 395
ID ADB16404 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 396
ID ADA91496 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 397
ID ADB14559 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 398
ID ADB18520 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 399
ID ADA93735 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;

Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 400
ID ADB19631 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 401
ID ADB12943 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 402
ID ACD98459 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 403
ID ADA74197 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 404
ID ADB24430 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide SEQ ID NO 71.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 405
ID ADA81954 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 406
ID ADA74917 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 407
ID ADA84995 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 408
ID ADA84443 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 409
ID ADB29699 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 410
ID ADA80227 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 411
ID ADA75469 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 412
ID ADA46694 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 413
ID ADB24990 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide SEQ ID NO 71.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 414
ID ADA93166 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 415
ID ADB26516 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 416
ID ADB30803 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 417
ID ADA60731 standard; cDNA; 3732 BP.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 418

ID ADB23878 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide SEQ ID NO 71.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 419
ID ADA96207 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 420
ID ADA80779 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 421
ID ADA95655 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 422
ID ADB25964 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 423
ID ADB21449 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 424
ID ADA77228 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 425
ID ADB17968 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 426
ID ADA86651 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 427
ID ADA87754 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 428
ID ADA46142 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 429
ID ADB28172 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 430
ID ADB28724 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 431
ID ADA76676 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 432
ID ADA88306 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 433
ID ADA97311 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 434
ID ADB27068 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003022239-A1.
PD 30-JAN-2003.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 435
ID ADB22001 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003087344-A1.
PD 08-MAY-2003.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 436
ID ADA66692 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003068793-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 437
ID ADB22553 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 438
ID ADB23326 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide SEQ ID NO 71.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 439
ID ADA92048 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 440
ID ADB15111 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 441
ID ADB38363 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 442
ID ADB37811 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 443
ID ADB66283 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 444
ID ADB89363 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 445
ID ADB90095 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 446
ID ADB39196 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 447
ID ADB46819 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 448
ID ADB86426 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 449
ID ADB77031 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 450
ID ADB34188 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide SEQ ID NO 71.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 451
ID ADB35292 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide SEQ ID NO 71.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 452
ID ADB33636 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide SEQ ID NO 71.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 453
ID ADB34740 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide SEQ ID NO 71.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 454
ID ADB35844 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide SEQ ID NO 71.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;

Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 455
ID ADB46239 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 456
ID ADC50112 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 457
ID ADC71659 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 458
ID ADC59638 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 459
ID ADC52645 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID71.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 460
ID ADC56999 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID71.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 461
ID ADC60190 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 462
ID ADC50665 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 463
ID ADC65192 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 464
ID ADC54290 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID71.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 465
ID ADC53251 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID71.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 466
ID ADC58774 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID71.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 467
ID ADC55652 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID71.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 468
ID ADC58222 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID71.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 469
ID ADD02896 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 470
ID ADC89888 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 471
ID ADC69307 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 472
ID ADC48196 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 473

ID ADD09725 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 474
ID ADD04300 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 475
ID ADC80256 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 476
ID ADD10763 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 477
ID ADC47644 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 478
ID ADC79704 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 479
ID ADD09173 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 480
ID ADD40886 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 481
ID ADD52025 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 482
ID ADD52765 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 483
ID ADD53317 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 484
ID ADD51473 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 485
ID ADD02272 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 486
ID ADD01706 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 487
ID ADD53888 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 488
ID ADD92205 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 489
ID ADD91101 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 490
ID ADE03715 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 491
ID ADE32012 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.

PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 492
ID ADE21944 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 493
ID ADD79168 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 494
ID ADE41704 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 495
ID ADE17521 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 496
ID ADD91653 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 497
ID ADE33116 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 498
ID ADE33668 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 499
ID ADD79720 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 500
ID ADD92757 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 501
ID ADE19177 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 502
ID ADE18625 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 503
ID ADE42821 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 504
ID ADD95610 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 505
ID ADE22496 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 506
ID ADD78614 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 507
ID ADE32564 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 508
ID ADE42256 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 509
ID ADD80272 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003207418-A1.
PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 510
ID ADD89300 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 511
ID ADE40584 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 512
ID ADE04383 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 513
ID ADE92512 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 514
ID ADG21221 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 515
ID ADG22862 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 516
ID ADF97197 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 517
ID ADG80261 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 518
ID ADG79709 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 519
ID ADH55001 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 520
ID ADH55553 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 521
ID ADI64721 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 522
ID ADH81634 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 523
ID ADH81082 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 524
ID ACD23888 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 525
ID ACA67029 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 526
ID ADM82251 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 11; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 527
ID ADN15650 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 11; Length 3732;

Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 528
ID ADN16279 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 11; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 529
ID ADN15098 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 11; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 530
ID ADN14546 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 11; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 531
ID ADI63772 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 11; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 532
ID ADI63220 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 11; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 533
ID ADC80808 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 534
ID ADD76256 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 535
ID ADD87620 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 536
ID ADD86024 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 537
ID ADE75472 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 538
ID ADE23048 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 539
ID ADE23600 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 540
ID ADE24243 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 541
ID ADD87068 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 542
ID ADE88934 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 543
ID ADE18073 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 544
ID ADE88382 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 545
ID ADE94402 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 546

ID ADE90813 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 547
ID ADE94954 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 548
ID ADE93064 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 549
ID ADF34645 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 550
ID ADE91960 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 551
ID ADE90261 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 552
ID ADE91408 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 553
ID ADG01987 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 554
ID ADG21773 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 555
ID ADG19843 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 556
ID ADF97749 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 557
ID ADG23966 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 558
ID ADF98320 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 559
ID ADG03151 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 560
ID ADF98872 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 561
ID ADG16457 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 562
ID ADG04916 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 563
ID ADG19183 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 564
ID ADG13020 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.

PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 565
ID ADG08077 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 566
ID ADG15247 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 567
ID ADF96645 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 568
ID ADG05830 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 569
ID ADG23414 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 570
ID ADG03703 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 571
ID ADG24604 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 572
ID ADG06901 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 573
ID ADG07453 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 574
ID ADG54948 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 575
ID ADG60612 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 576
ID ADG61716 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 577
ID ADG81917 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 578
ID ADG57156 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 579
ID ADG56604 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 580
ID ADG55500 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 581
ID ADG58260 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 582
ID ADG70626 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207420-A1.
PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 583
ID ADG57708 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 584
ID ADG53292 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 585
ID ADG71178 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 586
ID ADG81365 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003207805-A1.
PD 06-NOV-2003.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 587
ID ADH30327 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 588
ID ADH11694 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 589
ID ADG52116 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 590
ID ADG53844 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 591
ID ADG80813 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 592
ID ADG56052 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 593
ID ADH12318 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 594
ID ADG61164 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 595
ID ADH28251 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 596
ID ADG54396 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 597
ID ADG59436 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 598
ID ADI80860 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 599
ID ADG09603 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 600
ID ADI15074 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;

RESULT 601
ID ADG08951 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 602
ID ADI14406 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 603
ID ADI18001 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 604
ID ADJ63282 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 605
ID ADJ77177 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 606
ID ADJ65299 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 607
ID ADM27435 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 608
ID ADM42159 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 609
ID ADM28021 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 610
ID ADI95503 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 13; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 611
ID ADI96055 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 18.7%; Score 119.8; DB 13; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-25;
RESULT 612
ID AAS14890 standard; cDNA; 2911 BP.
DE Human cDNA encoding novel human protein NHP #11.
PN WO200174896-A1.
PD 11-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 18.3%; Score 117; DB 4; Length 2911;
Best Local Similarity 57.6%; Pred. No. 9.5e-25;
RESULT 613
ID AAS14880 standard; cDNA; 2920 BP.
DE Human cDNA encoding novel human protein NHP #1.
PN WO200174896-A1.
PD 11-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 18.3%; Score 117; DB 4; Length 2920;
Best Local Similarity 57.6%; Pred. No. 9.5e-25;
RESULT 614
ID ADA03339 standard; DNA; 2920 BP.
DE Human angiotensin converting enzyme 2 gene.
PN WO200298448-A1.
PD 12-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 18.3%; Score 117; DB 8; Length 2920;
Best Local Similarity 57.6%; Pred. No. 9.5e-25;
RESULT 615
ID ACC79021 standard; cDNA; 2920 BP.
DE Human ACE-2 protein encoding cDNA SEQ ID NO:137.
PN WO200298906-A1.
PD 12-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 18.3%; Score 117; DB 8; Length 2920;
Best Local Similarity 57.6%; Pred. No. 9.5e-25;
RESULT 616
ID AAC84368 standard; cDNA; 2638 BP.
DE Mouse Zace2-5 protein encoding cDNA.
PN WO200070032-A1.
PD 23-NOV-2000.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 17.4%; Score 111.4; DB 4; Length 2638;
Best Local Similarity 56.9%; Pred. No. 4.7e-23;
RESULT 617
ID ABX93335 standard; cDNA; 2638 BP.
DE cDNA encoding mouse zinc metallopeptidase mZace-5.
PN US2002177211-A1.
PD 28-NOV-2002.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 17.4%; Score 111.4; DB 10; Length 2638;
Best Local Similarity 56.9%; Pred. No. 4.7e-23;
RESULT 618
ID AAC84370 standard; cDNA; 2638 BP.
DE Mouse Zace2-10 protein encoding cDNA.
PN WO200070032-A1.
PD 23-NOV-2000.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 16.9%; Score 108.2; DB 4; Length 2638;
Best Local Similarity 56.5%; Pred. No. 4.5e-22;
RESULT 619
ID ABX93337 standard; cDNA; 2638 BP.

DE cDNA encoding mouse zinc metallopeptidase mZace-10.
PN US2002177211-A1.
PD 28-NOV-2002.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 16.9%; Score 108.2; DB 10; Length 2638;
Best Local Similarity 56.5%; Pred. No. 4.5e-22;
RESULT 620
ID ADH51358 standard; DNA; 2739 BP.
DE Mouse angiotensin-converting enzyme homologue ACE2 DNA.
PN WO2004000367-A1.
PD 31-DEC-2003.
PA (UYHE-) UNIV HEALTH NETWORK.
Query Match 16.9%; Score 108.2; DB 12; Length 2739;
Best Local Similarity 56.5%; Pred. No. 4.6e-22;
RESULT 621
ID ABQ57861 standard; cDNA; 561 BP.
DE Human colon cancer related nucleotide sequence SEQ ID NO:1556.
PN WO200229086-A2.
PD 11-APR-2002.
PA (FARB) BAYER CORP.
Query Match 15.1%; Score 96.8; DB 6; Length 561;
Best Local Similarity 57.8%; Pred. No. 6.8e-19;
RESULT 622
ID AAZ59466 standard; DNA; 2262 BP.
DE Human MPROT15 coding sequence #2.
PN JP11318472-A.
PD 24-NOV-1999.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 15.1%; Score 96.8; DB 3; Length 2262;
Best Local Similarity 57.8%; Pred. No. 1.3e-18;
RESULT 623
ID ACN43791 standard; cDNA; 3072 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2666.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 15.1%; Score 96.8; DB 13; Length 3072;
Best Local Similarity 57.8%; Pred. No. 1.5e-18;
RESULT 624
ID ABK30270 standard; cDNA; 2350 BP.
DE Human G-protein-coupled protease #40.
PN US6331427-B1.
PD 18-DEC-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 10.9%; Score 69.4; DB 6; Length 2350;
Best Local Similarity 55.1%; Pred. No. 3.3e-10;
RESULT 625
ID AAS42515 standard; cDNA; 3474 BP.
DE Human cDNA encoding an mddt protein, clone LI:347572.1:2000MAY01.
PN WO200162922-A2.
PD 30-AUG-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 9.9%; Score 63; DB 5; Length 3474;
Best Local Similarity 55.8%; Pred. No. 3.6e-08;
RESULT 626
ID ABN36017 standard; DNA; 60 BP.
DE Human spliced transcript detection oligonucleotide SEQ ID NO:8765.
PN WO200210449-A2.
PD 07-FEB-2002.
PA (COMP-) COMPUGEN INC.
Query Match 9.4%; Score 60; DB 6; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.5e-08;
RESULT 627
ID AAQ90512 standard; DNA; 11288 BP.
DE CEA clone HindIII-Sau3A fragment.
PN WO9514100-A2.
PD 26-MAY-1995.
PA (WELL) WELLCOME FOUND LTD.
Query Match 8.5%; Score 54; DB 2; Length 11288;
Best Local Similarity 62.1%; Pred. No. 3.6e-05;
RESULT 628
ID AAS14778 standard; DNA; 11288 BP.
DE Human carcinoembryonic antigen (CEA) genomic DNA.
PN WO200174861-A2.
PD 11-OCT-2001.
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
Query Match 8.5%; Score 54; DB 5; Length 11288;
Best Local Similarity 62.1%; Pred. No. 3.6e-05;
RESULT 629
ID AAV52967 standard; DNA; 15056 BP.
DE Carcinoembryonic antigen gene 5' flanking region.
PN WO9839467-A2.
PD 11-SEP-1998.
PA (CALY-) CALYDON INC.
Query Match 8.5%; Score 54; DB 2; Length 15056;
Best Local Similarity 62.1%; Pred. No. 4.1e-05;
RESULT 630
ID AAZ99933 standard; DNA; 15056 BP.
DE DNA sequence of comprising a carcinoembryonic antigen TRE.
PN WO200015820-A1.
PD 23-MAR-2000.
PA (CALY-) CALYDON INC.
Query Match 8.5%; Score 54; DB 3; Length 15056;
Best Local Similarity 62.1%; Pred. No. 4.1e-05;
RESULT 631
ID AAA46851 standard; DNA; 15056 BP.
DE Nucleotide sequence of a CEA-TRE.
PN WO200039319-A2.
PD 06-JUL-2000.
PA (CALY-) CALYDON INC.
Query Match 8.5%; Score 54; DB 3; Length 15056;
Best Local Similarity 62.1%; Pred. No. 4.1e-05;
RESULT 632
ID AAH43620 standard; cDNA; 15056 BP.
DE CEA-TRE.
PN WO200173093-A2.
PD 04-OCT-2001.
PA (CALY-) CALYDON INC.
Query Match 8.5%; Score 54; DB 5; Length 15056;
Best Local Similarity 62.1%; Pred. No. 4.1e-05;
RESULT 633
ID AAF87238 standard; DNA; 15056 BP.
DE CEA-TRE fusion protein coding sequence.
PN WO200172341-A2.
PD 04-OCT-2001.
PA (CALY-) CALYDON INC.
Query Match 8.5%; Score 54; DB 5; Length 15056;
Best Local Similarity 62.1%; Pred. No. 4.1e-05;
RESULT 634
ID ABK99582 standard; DNA; 15056 BP.
DE Prostate-specific antigen transcriptional regulatory elelment (TRE).
PN US2002068049-A1.
PD 06-JUN-2002.
PA (HEND/) HENDERSON D R.
PA (SCHU/) SCHUUR E R.
Query Match 8.5%; Score 54; DB 6; Length 15056;
Best Local Similarity 62.1%; Pred. No. 4.1e-05;
RESULT 635
ID ACD07309 standard; DNA; 15056 BP.
DE Human carcinoembryonic antigen (CEA) TRE.
PN US2003044383-A1.
PD 06-MAR-2003.
PA (HEND/) HENDERSON D R.
PA (SCHU/) SCHUUR E R.
Query Match 8.5%; Score 54; DB 8; Length 15056;
Best Local Similarity 62.1%; Pred. No. 4.1e-05;
RESULT 636
ID ADA71938 standard; DNA; 2000 BP.
DE Rice gene, SEQ ID 5263.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 7.5%; Score 48.2; DB 8; Length 2000;
Best Local Similarity 14.5%; Pred. No. 0.00095;
RESULT 637
ID ABN53251 standard; DNA; 65 BP.

DE Mouse spliced transcript detection oligonucleotide SEQ ID NO:25999.
PN WO200210449-A2.
PD 07-FEB-2002.
PA (COMP-) COMPUGEN INC.
Query Match 7.5%; Score 48; DB 6; Length 65;
Best Local Similarity 84.4%; Pred. No. 0.00022;
RESULT 638
ID ADL45106 standard; DNA; 531 BP.
DE Human ovarian cancer DNA marker #18996.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 7.2%; Score 45.8; DB 5; Length 531;
Best Local Similarity 59.7%; Pred. No. 0.0028;
RESULT 639
ID AAI76073 standard; DNA; 51 BP.
DE Human silent SNP containing nucleic acid SEQ:3014.
PN WO200140521-A2.
PD 07-JUN-2001.
PA (CURA-) CURAGEN CORP.
Query Match 6.7%; Score 43; DB 4; Length 51;
Best Local Similarity 90.2%; Pred. No. 0.0068;
RESULT 640
ID ADL13839 standard; DNA; 600 BP.
DE Osteoarthritis-associated polymorphic nucleotide #371.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.6%; Score 42; DB 10; Length 600;
Best Local Similarity 50.2%; Pred. No. 0.043;
RESULT 641
ID AAI76072 standard; DNA; 51 BP.
DE Human silent SNP containing nucleic acid SEQ:3013.
PN WO200140521-A2.
PD 07-JUN-2001.
PA (CURA-) CURAGEN CORP.
Query Match 6.5%; Score 41.4; DB 4; Length 51;
Best Local Similarity 88.2%; Pred. No. 0.021;
RESULT 642
ID ABQ76673 standard; DNA; 160820 BP.
DE Androgen receptor signalling pathway-associated DNA AB043547.
PN WO200282081-A2.
PD 17-OCT-2002.
PA (UYRP) UNIV ROCHESTER.
Query Match 6.3%; Score 40.2; DB 8; Length 160820;
Best Local Similarity 54.4%; Pred. No. 2.1;
RESULT 643
ID AAQ90511 standard; DNA; 14556 BP.
DE CEA genomic clone.
PN WO9514100-A2.
PD 26-MAY-1995.
PA (WELL) WELLCOME FOUND LTD.
Query Match 6.2%; Score 39.8; DB 2; Length 14556;
Best Local Similarity 72.1%; Pred. No. 0.9;
RESULT 644
ID ACN45006 standard; DNA; 67810 BP.
DE Human genomic sequence hCG32956.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 6.2%; Score 39.8; DB 11; Length 67810;
Best Local Similarity 59.1%; Pred. No. 1.8;
RESULT 645
ID ADA71938 standard; DNA; 2000 BP.
DE Rice gene, SEQ ID 5263.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 6.1%; Score 39; DB 8; Length 2000;
Best Local Similarity 9.2%; Pred. No. 0.63;
RESULT 646
ID ADQ23378 standard; DNA; 2336 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6198.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 5.9%; Score 37.8; DB 12; Length 2336;
Best Local Similarity 52.2%; Pred. No. 1.6;
RESULT 647
ID ADQ25297 standard; DNA; 3404 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 8117.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 5.8%; Score 37; DB 12; Length 3404;
Best Local Similarity 51.5%; Pred. No. 3.3;
RESULT 648
ID ACH67311 standard; DNA; 599 BP.
DE Human genome derived single exon probe #506.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 5.7%; Score 36.6; DB 12; Length 599;
Best Local Similarity 57.4%; Pred. No. 1.9;
RESULT 649
ID AAD36766 standard; DNA; 8483 BP.
DE Human melanin-concentrating hormone receptor 1 (MCHR1) genomic DNA.
PN WO200236076-A2.
PD 10-MAY-2002.
PA (MERI) MERCK & CO INC.
PA (BANY) BANYU PHARM CO LTD.
Query Match 5.7%; Score 36.6; DB 6; Length 8483;
Best Local Similarity 50.3%; Pred. No. 6.7;
RESULT 650
ID ADH76849 standard; DNA; 122557 BP.
DE Melanin-concentrating hormone receptor 1 locus clone.
PN WO2003104489-A2.
PD 18-DEC-2003.
PA (UYPH-) UNIV PHILIPPS MARBURG.
Query Match 5.7%; Score 36.6; DB 12; Length 122557;
Best Local Similarity 50.3%; Pred. No. 23;
RESULT 651
ID AAF68619 standard; cDNA; 558 BP.
DE Human lung tumour protein related nucleotide sequence SEQ ID NO:554.
PN WO200100828-A2.
PD 04-JAN-2001.
PA (CORI-) CORIXA CORP.
Query Match 5.7%; Score 36.4; DB 5; Length 558;
Best Local Similarity 51.2%; Pred. No. 2.2;
RESULT 652
ID ABK38530 standard; cDNA; 558 BP.
DE cDNA encoding clone #26027 of lung tumour protein.
PN WO200204514-A2.
PD 17-JAN-2002.
PA (CORI-) CORIXA CORP.
Query Match 5.7%; Score 36.4; DB 6; Length 558;
Best Local Similarity 51.2%; Pred. No. 2.2;
RESULT 653
ID ACA10859 standard; cDNA; 558 BP.
DE Human lung neuroendocrine carcinoma library MLN1 cDNA, SEQ ID 554.
PN US2002197669-A1.
PD 26-DEC-2002.
PA (BANG/) BANGUR C S.
PA (FANG/) FANGER G R.
PA (WANG/) WANG A.
PA (WANG/) WANG T.
PA (SWIT/) SWITZER A P.
PA (MCNE/) MCNEILL P D.
PA (CLAP/) CLAPPER J D.
Query Match 5.7%; Score 36.4; DB 8; Length 558;
Best Local Similarity 51.2%; Pred. No. 2.2;
RESULT 654
ID ABX99810 standard; cDNA; 558 BP.
DE Lung cancer therapyand diagnosis associated cDNA #537.

PN US2002172952-A1.
PD 21-NOV-2002.
PA (CORI-) CORIXA CORP.
Query Match 5.7%; Score 36.4; DB 8; Length 558;
Best Local Similarity 51.2%; Pred. No. 2.2;
RESULT 655
ID ADH46073 standard; cDNA; 558 BP.
DE Human lung tumour cDNA clone, SEQ ID No 554.
PN WO2003037267-A2.
PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match 5.7%; Score 36.4; DB 10; Length 558;
Best Local Similarity 51.2%; Pred. No. 2.2;
RESULT 656
ID ADE71825 standard; cDNA; 558 BP.
DE Human lung tumour protein cDNA #537.
PN US2003125245-A1.
PD 03-JUL-2003.
PA (WANG/) WANG T.
PA (BANG/) BANGUR C S.
Query Match 5.7%; Score 36.4; DB 12; Length 558;
Best Local Similarity 51.2%; Pred. No. 2.2;
RESULT 657
ID ADJ19992 standard; cDNA; 558 BP.
DE Human lung cancer-related cDNA - SEQ ID 554.
PN US2003211510-A1.
PD 13-NOV-2003.
PA (CORI-) CORIXA CORP.
Query Match 5.7%; Score 36.4; DB 13; Length 558;
Best Local Similarity 51.2%; Pred. No. 2.2;
RESULT 658
ID ABV58001 standard; cDNA; 616 BP.
DE Human prostate expression marker cDNA 57992.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.7%; Score 36.4; DB 5; Length 616;
Best Local Similarity 59.8%; Pred. No. 2.3;
RESULT 659
ID AAK72778 standard; DNA; 2458 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27590.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.7%; Score 36.4; DB 4; Length 2458;
Best Local Similarity 74.6%; Pred. No. 4.3;
RESULT 660
ID ABD33536 standard; DNA; 88445 BP.
DE Human cancer-associated (CA) gene HD07-106.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 5.6%; Score 36; DB 13; Length 88445;
Best Local Similarity 48.1%; Pred. No. 30;
RESULT 661
ID AAT85403 standard; cDNA; 2625 BP.
DE Human cadherin-11 coding sequence.
PN US5646250-A.
PD 08-JUL-1997.
PA (DOHE-) DOHENY EYE INST.
Query Match 5.6%; Score 35.8; DB 2; Length 2625;
Best Local Similarity 50.9%; Pred. No. 6.8;
RESULT 662
ID AAT61925 standard; cDNA; 2625 BP.
DE Full length human cadherin-11 cDNA.
PN US5597725-A.
PD 28-JAN-1997.
PA (DOHE-) DOHENY EYE INST.
Query Match 5.6%; Score 35.8; DB 2; Length 2625;
Best Local Similarity 50.9%; Pred. No. 6.8;
RESULT 663
ID AAV83124 standard; cDNA; 2625 BP.
DE Cadherin-11 cDNA.
PN WO9849560-A1.
PD 05-NOV-1998.
PA (UYBR-) UNIV BRITISH COLUMBIA.
Query Match 5.6%; Score 35.8; DB 2; Length 2625;
Best Local Similarity 50.9%; Pred. No. 6.8;
RESULT 664
ID AAF55586 standard; DNA; 2625 BP.
DE Nucleotide sequence of a human cadherin-11 polypeptide.
PN WO200117557-A1.
PD 15-MAR-2001.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
Query Match 5.6%; Score 35.8; DB 5; Length 2625;
Best Local Similarity 50.9%; Pred. No. 6.8;
RESULT 665
ID ADP18641 standard; cDNA; 2625 BP.
DE Human TAT400 cDNA used to treat cancer SeqID 1.
PN WO2004045516-A2.
PD 03-JUN-2004.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 35.8; DB 12; Length 2625;
Best Local Similarity 50.9%; Pred. No. 6.8;
RESULT 666
ID ADP26918 standard; cDNA; 2625 BP.
DE Human OB-cadherin encoding cDNA SEQ ID NO:19.
PN EP1428893-A2.
PD 16-JUN-2004.
PA (SPRE/) SPRECHER E.
PA (BERG/) BERGMAN R.
Query Match 5.6%; Score 35.8; DB 12; Length 2625;
Best Local Similarity 50.9%; Pred. No. 6.8;
RESULT 667
ID ADR24809 standard; DNA; 2625 BP.
DE Breast cancer prognosis marker #670.
PN WO2004065545-A2.
PD 05-AUG-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
PA (NECA-) NETHERLANDS CANCER INST.
Query Match 5.6%; Score 35.8; DB 13; Length 2625;
Best Local Similarity 50.9%; Pred. No. 6.8;
RESULT 668
ID ABX63597 standard; cDNA; 3403 BP.
DE Human cDNA #597 differentially expressed in activated vascular tissue.
PN US2002137081-A1.
PD 26-SEP-2002.
PA (BAND/) BANDMAN O.
Query Match 5.6%; Score 35.8; DB 8; Length 3403;
Best Local Similarity 50.9%; Pred. No. 7.7;
RESULT 669
ID ADJ56330 standard; cDNA; 3403 BP.
DE Human cDNA differentially expressed in MYCN activated cells SeqID 136.
PN US2003119009-A1.
PD 26-JUN-2003.
PA (STUA/) STUART S G.
PA (NUCH/) NUCHTERN J G.
PA (PLON/) PLON S E.
PA (SHOH/) SHOHET J M.
Query Match 5.6%; Score 35.8; DB 10; Length 3403;
Best Local Similarity 50.9%; Pred. No. 7.7;
RESULT 670
ID ADR48217 standard; cDNA; 3654 BP.
DE Human cadherin 11 type 2 OB-cadherin encoding cDNA SEQ:5.
PN WO2004074510-A1.
PD 02-SEP-2004.
PA (GARV-) GARVAN INST MEDICAL RES.
Query Match 5.6%; Score 35.8; DB 13; Length 3654;
Best Local Similarity 50.9%; Pred. No. 8;
RESULT 671
ID ADH17152 standard; cDNA; 3661 BP.
DE Human OB-cadherin-1 cDNA.
PN WO2003097854-A2.
PD 27-NOV-2003.
PA (SUGE-) SUGEN INC.
Query Match 5.6%; Score 35.8; DB 12; Length 3661;

Best Local Similarity 50.9%; Pred. No. 8;
RESULT 672
ID AAQ44392 standard; cDNA to mRNA; 3712 BP.
DE Sequence of human OSF-4-1 cDNA.
PN EP585801-A2.
PD 09-MAR-1994.
PA (FARH) HOECHST JAPAN LTD.
Query Match 5.6%; Score 35.8; DB 2; Length 3712;
Best Local Similarity 50.9%; Pred. No. 8;
RESULT 673
ID ACN42737 standard; cDNA; 5690 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:1612.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 5.6%; Score 35.8; DB 13; Length 5690;
Best Local Similarity 50.9%; Pred. No. 9.8;
RESULT 674
ID ADQ59437 standard; DNA; 339234 BP.
DE Human cancer-associated (CA) gene sequence SEQ ID NO:73.
PN WO2004058288-A1.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 5.6%; Score 35.6; DB 12; Length 339234;
Best Local Similarity 49.5%; Pred. No. 76;
RESULT 675
ID AAC12675 standard; cDNA; 352 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 16750.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 5.5%; Score 35.2; DB 3; Length 352;
Best Local Similarity 52.2%; Pred. No. 4.1;
RESULT 676
ID ADB37661 standard; DNA; 29993 BP.
DE Human chemically pretreated EYA4 gene SEQ ID NO:3.
PN WO2003072812-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.5%; Score 35.2; DB 10; Length 29993;
Best Local Similarity 44.7%; Pred. No. 32;
RESULT 677
ID AAS46746 standard; DNA; 38342 BP.
DE Tumour suppressor gene derived chemically modified sequence #470.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.5%; Score 35.2; DB 4; Length 38342;
Best Local Similarity 44.7%; Pred. No. 36;
RESULT 678
ID ABK31507 standard; DNA; 38342 BP.
DE Signal transduction associated gene modified complementary DNA #175.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.5%; Score 35.2; DB 6; Length 38342;
Best Local Similarity 44.7%; Pred. No. 36;
RESULT 679
Query Match 5.5%; Score 35; DB 11; Length 110000;
Best Local Similarity 50.9%; Pred. No. 68;
RESULT 680
ID ADC24763 standard; DNA; 334462 BP.
DE Human wild type HNL4X genomic sequence.
PN WO2003045998-A2.
PD 05-JUN-2003.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (INSP) INST PASTEUR.
PA (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.
Query Match 5.5%; Score 35; DB 10; Length 334462;
Best Local Similarity 54.2%; Pred. No. 1.1e+02;
RESULT 681
ID AAV03031 standard; DNA; 652 BP.
DE Meloidogyne incognita cellulase MI-eng3 gene.
PN WO9801569-A1.
PD 15-JAN-1998.
PA (RIJK-) RIJKSLANDBOUWHOGESCHOOL.
Query Match 5.4%; Score 34.8; DB 2; Length 652;
Best Local Similarity 49.5%; Pred. No. 7.2;
RESULT 682
ID AAC84170 standard; DNA; 978 BP.
DE Mouse OX2RH1 degenerate nucleotide sequence.
PN WO200070045-A1.
PD 23-NOV-2000.
PA (MEDI-) MEDICAL RES COUNCIL.
PA (SCHE) SCHERING CORP.
Query Match 5.4%; Score 34.8; DB 5; Length 978;
Best Local Similarity 32.0%; Pred. No. 8.7;
RESULT 683
ID ADI73592 standard; DNA; 426 BP.
DE Human ovarian cancer DNA marker #6334.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.4%; Score 34.2; DB 5; Length 426;
Best Local Similarity 67.6%; Pred. No. 9;
RESULT 684
ID ADL38722 standard; DNA; 426 BP.
DE Human ovarian cancer DNA marker #12612.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.4%; Score 34.2; DB 5; Length 426;
Best Local Similarity 67.6%; Pred. No. 9;
RESULT 685
ID ACA48447 standard; DNA; 1290 BP.
DE Prokaryotic essential gene #30104.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.4%; Score 34.2; DB 8; Length 1290;
Best Local Similarity 49.7%; Pred. No. 15;
RESULT 686
ID AAZ88922 standard; DNA; 26379 BP.
DE Human wolframin genomic DNA.
PN DE19845277-C1.
PD 09-MAR-2000.
PA (UYMU-) UNIV MUENCHEN MAXIMILIANS LUDWIG.
Query Match 5.4%; Score 34.2; DB 3; Length 26379;
Best Local Similarity 50.3%; Pred. No. 62;
RESULT 687
ID AAA08954 standard; DNA; 67212 BP.
DE WFS1 variant genomic DNA.
PN WO200018787-A1.
PD 06-APR-2000.
PA (UNIW) UNIV WASHINGTON.
PA (PERM/) PERMUTT M A.
PA (INOU/) INOUE H.
PA (MUEC/) MUECKLER M.
Query Match 5.4%; Score 34.2; DB 3; Length 67212;
Best Local Similarity 50.3%; Pred. No. 96;
RESULT 688
ID AAH88703 standard; DNA; 123219 BP.
DE Human DNA sequence SEQ ID 543.
PN WO200151659-A2.
PD 19-JUL-2001.
PA (GEST) GENSET.
Query Match 5.4%; Score 34.2; DB 4; Length 123219;
Best Local Similarity 50.3%; Pred. No. 1.3e+02;
RESULT 689
ID ADB63048 standard; cDNA; 822 BP.
DE Human cDNA encoding clone SKMUS20073150.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.3%; Score 34; DB 10; Length 822;

Best Local Similarity 48.5%; Pred. No. 14;
RESULT 690
ID ADQ23008 standard; DNA; 7161 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5828.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 5.3%; Score 34; DB 12; Length 7161;
Best Local Similarity 48.5%; Pred. No. 39;
RESULT 691
ID AAI59270 standard; cDNA; 11116 BP.
DE Human polynucleotide SEQ ID NO 1473.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.3%; Score 34; DB 4; Length 11116;
Best Local Similarity 48.5%; Pred. No. 48;
RESULT 692
ID ACN44738 standard; DNA; 174703 BP.
DE Human genomic sequence hCG40040.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 5.3%; Score 34; DB 11; Length 174703;
Best Local Similarity 54.9%; Pred. No. 1.7e+02;
RESULT 693
ID ADL13771 standard; DNA; 201766 BP.
DE Osteoarthritis-associated polymorphic nucleotide #303.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.3%; Score 34; DB 10; Length 201766;
Best Local Similarity 59.2%; Pred. No. 1.8e+02;
RESULT 694
ID ABQ56434 standard; cDNA; 453 BP.
DE Human colon cancer related nucleotide sequence SEQ ID NO:129.
PN WO200229086-A2.
PD 11-APR-2002.
PA (FARB) BAYER CORP.
Query Match 5.3%; Score 33.8; DB 6; Length 453;
Best Local Similarity 52.5%; Pred. No. 12;
RESULT 695
ID AAI12904 standard; DNA; 1982 BP.
DE Probe #2837 for gene expression analysis in human cervical cell sample.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 5.3%; Score 33.8; DB 4; Length 1982;
Best Local Similarity 60.2%; Pred. No. 25;
RESULT 696
ID ABA54603 standard; DNA; 1982 BP.
DE Human foetal liver single exon nucleic acid probe #2908.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 5.3%; Score 33.8; DB 4; Length 1982;
Best Local Similarity 60.2%; Pred. No. 25;
RESULT 697
ID AAI34262 standard; DNA; 1982 BP.
DE Probe #2948 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 5.3%; Score 33.8; DB 4; Length 1982;
Best Local Similarity 60.2%; Pred. No. 25;
RESULT 698
ID ABA44155 standard; DNA; 1982 BP.
DE Human breast cell single exon nucleic acid probe #2850.
PN WO200157271-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 5.3%; Score 33.8; DB 4; Length 1982;
Best Local Similarity 60.2%; Pred. No. 25;
RESULT 699
ID ABA24389 standard; DNA; 1982 BP.
DE Probe #2855 for gene expression analysis in human heart cell sample.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 5.3%; Score 33.8; DB 4; Length 1982;
Best Local Similarity 60.2%; Pred. No. 25;
RESULT 700
ID AAK28338 standard; DNA; 1982 BP.
DE Human bone marrow expressed single exon probe SEQ ID NO: 2895.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 5.3%; Score 33.8; DB 4; Length 1982;
Best Local Similarity 60.2%; Pred. No. 25;
RESULT 701
ID AAK02895 standard; DNA; 1982 BP.
DE Human brain expressed single exon probe SEQ ID NO: 2886.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 5.3%; Score 33.8; DB 4; Length 1982;
Best Local Similarity 60.2%; Pred. No. 25;
RESULT 702
ID ABS02847 standard; DNA; 1982 BP.
DE Human genome-derived single exon probe from lung SEQ ID No 2838.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 5.3%; Score 33.8; DB 6; Length 1982;
Best Local Similarity 60.2%; Pred. No. 25;
RESULT 703
ID ABL07230 standard; cDNA; 73947 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 16172.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.3%; Score 33.8; DB 4; Length 73947;
Best Local Similarity 50.3%; Pred. No. 1.3e+02;
RESULT 704
ID ACH01384 standard; DNA; 96898 BP.
DE Human BIVM gene.
PN WO2003089595-A2.
PD 30-OCT-2003.
PA (UYSF-) UNIV SOUTH FLORIDA.
Query Match 5.3%; Score 33.8; DB 10; Length 96898;
Best Local Similarity 47.4%; Pred. No. 1.5e+02;
RESULT 705
ID ABX34872 standard; cDNA; 384 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #37.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 5.3%; Score 33.6; DB 8; Length 384;
Best Local Similarity 48.8%; Pred. No. 13;
RESULT 706
ID ABV06229 standard; cDNA; 476 BP.
DE Human prostate expression marker cDNA 6220.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.3%; Score 33.6; DB 5; Length 476;
Best Local Similarity 57.1%; Pred. No. 15;
RESULT 707
ID AAS45431 standard; DNA; 5337 BP.
DE Chemically pretreated complementary DNA associated with cell cycle #68.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.

Query Match 5.3%; Score 33.6; DB 4; Length 5337;
Best Local Similarity 61.4%; Pred. No. 45;
RESULT 708
ID ACC41529 standard; DNA; 639 BP.
DE Perennial ryegrass LpZTa2 fragment.
PN WO200290491-A2.
PD 14-NOV-2002.
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
PA (AGRE-) AGRESEARCH LTD.
Query Match 5.2%; Score 33.4; DB 8; Length 639;
Best Local Similarity 55.7%; Pred. No. 19;
RESULT 709
ID ABZ82389 standard; cDNA; 1900 BP.
DE Perennial ryegrass ZTa cDNA.
PN WO200290491-A2.
PD 14-NOV-2002.
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
PA (AGRE-) AGRESEARCH LTD.
Query Match 5.2%; Score 33.4; DB 8; Length 1900;
Best Local Similarity 55.7%; Pred. No. 32;
RESULT 710
ID ACA52666 standard; DNA; 2514 BP.
DE Prokaryotic essential gene #34323.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.2%; Score 33.4; DB 8; Length 2514;
Best Local Similarity 47.8%; Pred. No. 36;
RESULT 711
ID ABN80298 standard; DNA; 7219 BP.
DE Human chemically modified disease associated gene SEQ ID NO 315.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 33.4; DB 6; Length 7219;
Best Local Similarity 51.0%; Pred. No. 59;
RESULT 712
ID AAL36286 standard; DNA; 11337 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 2651.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.2%; Score 33.4; DB 4; Length 11337;
Best Local Similarity 50.3%; Pred. No. 73;
RESULT 713
ID ABX59274 standard; cDNA; 11337 BP.
DE cDNA encoding novel human musculoskeletal system antigen #1618.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 5.2%; Score 33.4; DB 8; Length 11337;
Best Local Similarity 50.3%; Pred. No. 73;
RESULT 714
ID ADJ30024 standard; DNA; 11337 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2651.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.2%; Score 33.4; DB 12; Length 11337;
Best Local Similarity 50.3%; Pred. No. 73;
RESULT 715
ID ABL11264 standard; cDNA; 11572 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 28274.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.2%; Score 33.4; DB 4; Length 11572;
Best Local Similarity 53.4%; Pred. No. 74;
RESULT 716
ID ABL19466 standard; DNA; 23307 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 9871.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.2%; Score 33.4; DB 4; Length 23307;
Best Local Similarity 53.4%; Pred. No. 1e+02;
RESULT 717
ID ABL29416 standard; DNA; 31193 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 39721.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.2%; Score 33.4; DB 4; Length 31193;
Best Local Similarity 53.4%; Pred. No. 1.2e+02;
RESULT 718
ID ABA18136 standard; DNA; 412 BP.
DE Human nervous system related polynucleotide SEQ ID NO 10467.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.2%; Score 33.2; DB 5; Length 412;
Best Local Similarity 49.4%; Pred. No. 18;
RESULT 719
ID ABA18135 standard; DNA; 412 BP.
DE Human nervous system related polynucleotide SEQ ID NO 10466.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.2%; Score 33.2; DB 5; Length 412;
Best Local Similarity 49.4%; Pred. No. 18;
RESULT 720
ID ABZ16504 standard; DNA; 453 BP.
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 4309.
PN WO200216655-A2.
PD 28-FEB-2002.
PA (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 5.2%; Score 33.2; DB 6; Length 453;
Best Local Similarity 50.0%; Pred. No. 19;
RESULT 721
ID ADH82310 standard; DNA; 957 BP.
DE Enterococcus faecalis polynucleotide #195.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 5.2%; Score 33.2; DB 10; Length 957;
Best Local Similarity 50.0%; Pred. No. 27;
RESULT 722
ID ABK35485 standard; DNA; 3867 BP.
DE Human endometrial cancer related gene, CDH11.
PN WO200209573-A2.
PD 07-FEB-2002.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
Query Match 5.2%; Score 33.2; DB 6; Length 3867;
Best Local Similarity 57.8%; Pred. No. 51;
RESULT 723
ID ABZ35374 standard; cDNA; 3867 BP.
DE Human gene expression profile polynucleotide SEQ ID NO 485.
PN WO200274979-A2.
PD 26-SEP-2002.
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
Query Match 5.2%; Score 33.2; DB 6; Length 3867;
Best Local Similarity 57.8%; Pred. No. 51;
RESULT 724
ID ADH17153 standard; cDNA; 3867 BP.
DE Human OB-cadherin-2 cDNA.
PN WO2003097854-A2.
PD 27-NOV-2003.
PA (SUGE-) SUGEN INC.
Query Match 5.2%; Score 33.2; DB 12; Length 3867;
Best Local Similarity 57.8%; Pred. No. 51;
RESULT 725
ID AAQ44393 standard; cDNA to mRNA; 3914 BP.

DE Sequence of human OSF-4-2 cDNA.
PN EP585801-A2.
PD 09-MAR-1994.
PA (FARH) HOECHST JAPAN LTD.
Query Match 5.2%; Score 33.2; DB 2; Length 3914;
Best Local Similarity 57.8%; Pred. No. 51;
RESULT 726
ID ADQ22593 standard; DNA; 3948 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5413.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 5.2%; Score 33.2; DB 12; Length 3948;
Best Local Similarity 57.8%; Pred. No. 52;
RESULT 727
ID ABV15398 standard; cDNA; 362 BP.
DE Human prostate expression marker cDNA 15389.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.2%; Score 33; DB 5; Length 362;
Best Local Similarity 57.1%; Pred. No. 20;
RESULT 728
ID ABV36190 standard; cDNA; 390 BP.
DE Human prostate expression marker cDNA 36181.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.2%; Score 33; DB 5; Length 390;
Best Local Similarity 57.1%; Pred. No. 20;
RESULT 729
ID ABV45242 standard; cDNA; 390 BP.
DE Human prostate expression marker cDNA 45233.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.2%; Score 33; DB 5; Length 390;
Best Local Similarity 57.1%; Pred. No. 20;
RESULT 730
ID ABZ14991 standard; DNA; 2000 BP.
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 2796.
PN WO200216655-A2.
PD 28-FEB-2002.
PA (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 5.2%; Score 33; DB 6; Length 2000;
Best Local Similarity 57.1%; Pred. No. 43;
RESULT 731
ID ABL06956 standard; cDNA; 3866 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 15350.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.2%; Score 33; DB 4; Length 3866;
Best Local Similarity 52.6%; Pred. No. 59;
RESULT 732
ID ABL21788 standard; DNA; 4097 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 16837.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.2%; Score 33; DB 4; Length 4097;
Best Local Similarity 52.6%; Pred. No. 60;
RESULT 733
ID AAX13453 standard; DNA; 5101 BP.
DE Enterococcus faecalis genome contig SEQ ID NO:516.
PN WO9850555-A2.
PD 12-NOV-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.2%; Score 33; DB 2; Length 5101;
Best Local Similarity 51.0%; Pred. No. 67;
RESULT 734
ID ABS99248 standard; DNA; 5101 BP.
DE Enterococcus faecalis contig sequence #516.
PN US2002120116-A1.
PD 29-AUG-2002.
PA (KUNS/) KUNSCH C A.
PA (DILL/) DILLON P J.
PA (BARA/) BARASH S.
Query Match 5.2%; Score 33; DB 6; Length 5101;
Best Local Similarity 51.0%; Pred. No. 67;
RESULT 735
ID AAH62695 standard; DNA; 5811 BP.
DE Shrimp white spot Bacilliform virus (WSBV) gene 6.
PN WO200138351-A2.
PD 31-MAY-2001.
PA (PENY-) PE CORP NY.
PA (THIR-) THIRD INST OCEANOGRAPHY STATE OCEANI C A.
PA (SINO-) SINOGENOMAX CO LTD.
Query Match 5.2%; Score 33; DB 4; Length 5811;
Best Local Similarity 50.3%; Pred. No. 71;
RESULT 736
ID AAS46431 standard; DNA; 11327 BP.
DE Tumour suppressor gene derived chemically modified sequence #153.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 33; DB 4; Length 11327;
Best Local Similarity 45.5%; Pred. No. 97;
RESULT 737
ID AAS45389 standard; DNA; 15732 BP.
DE Chemically pretreated complementary DNA associated with cell cycle #47.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 33; DB 4; Length 15732;
Best Local Similarity 57.1%; Pred. No. 1.1e+02;
RESULT 738
ID ABK28234 standard; DNA; 15732 BP.
DE DNA transcription associated complementary genomic DNA #54.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.2%; Score 33; DB 6; Length 15732;
Best Local Similarity 57.1%; Pred. No. 1.1e+02;
RESULT 739
ID ACN43940 standard; DNA; 79831 BP.
DE Mouse genomic sequence mCG11506.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 5.2%; Score 33; DB 11; Length 79831;
Best Local Similarity 49.7%; Pred. No. 2.4e+02;
RESULT 740
ID AAZ01425 standard; DNA; 1038602 BP.
DE Complete genome sequence of Chlamydia trachomatis.
PN WO9928475-A2.
PD 10-JUN-1999.
PA (GEST) GENSET.
Query Match 5.2%; Score 33; DB 2; Length 110000;
Best Local Similarity 60.7%; Pred. No. 2.8e+02;
RESULT 741
Query Match 5.2%; Score 33; DB 2; Length 110000;
Best Local Similarity 60.7%; Pred. No. 2.8e+02;
RESULT 742
ID AAH62689 standard; DNA; 305107 BP.
DE Shrimp white spot Bacilliform virus (WSBV) genomic sequence.
PN WO200138351-A2.
PD 31-MAY-2001.
PA (PENY-) PE CORP NY.
PA (THIR-) THIRD INST OCEANOGRAPHY STATE OCEANI C A.
PA (SINO-) SINOGENOMAX CO LTD.
Query Match 5.2%; Score 33; DB 4; Length 305107;
Best Local Similarity 50.3%; Pred. No. 4.5e+02;
RESULT 743
ID AAX07129 standard; DNA; 477 BP.

DE Staphylococcus aureus mutant P10C18 virulence gene.
PN WO9901473-A2.
PD 14-JAN-1999.
PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
Query Match 5.1%; Score 32.8; DB 2; Length 477;
Best Local Similarity 45.0%; Pred. No. 26;
RESULT 744
ID ADA30754 standard; DNA; 822 BP.
DE DNA encoding Acinetobacter baumannii protein #2041.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.1%; Score 32.8; DB 9; Length 822;
Best Local Similarity 54.0%; Pred. No. 33;
RESULT 745
ID ADH84260 standard; DNA; 933 BP.
DE Enterococcus faecalis polynucleotide #2145.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 5.1%; Score 32.8; DB 10; Length 933;
Best Local Similarity 59.8%; Pred. No. 35;
RESULT 746
ID ADM01805 standard; cDNA; 2893 BP.
DE Human cDNA of the invention SEQ ID NO:490.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.1%; Score 32.8; DB 11; Length 2893;
Best Local Similarity 46.5%; Pred. No. 59;
RESULT 747
ID AAX12960 standard; DNA; 21126 BP.
DE Enterococcus faecalis genome contig SEQ ID NO:23.
PN WO9850555-A2.
PD 12-NOV-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.1%; Score 32.8; DB 2; Length 21126;
Best Local Similarity 59.8%; Pred. No. 1.5e+02;
RESULT 748
ID ABS98755 standard; DNA; 21126 BP.
DE Enterococcus faecalis contig sequence #23.
PN US2002120116-A1.
PD 29-AUG-2002.
PA (KUNS/) KUNSCH C A.
PA (DILL/) DILLON P J.
PA (BARA/) BARASH S.
Query Match 5.1%; Score 32.8; DB 6; Length 21126;
Best Local Similarity 59.8%; Pred. No. 1.5e+02;
RESULT 749
ID AAK67282 standard; DNA; 33147 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22094.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.1%; Score 32.8; DB 4; Length 33147;
Best Local Similarity 56.5%; Pred. No. 1.8e+02;
RESULT 750
ID ABK42692 standard; DNA; 12822 BP.
DE Genomic sequence #591 encoding novel human connective tissue polypeptide.
PN WO200155343-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.1%; Score 32.6; DB 4; Length 12822;
Best Local Similarity 48.6%; Pred. No. 1.4e+02;
RESULT 751
ID ADB60848 standard; DNA; 12822 BP.
DE Connective tissue related genomic DNA #591.
PN US2003054375-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.1%; Score 32.6; DB 9; Length 12822;
Best Local Similarity 48.6%; Pred. No. 1.4e+02;
RESULT 752
ID AAS61418 standard; DNA; 17918 BP.
DE Human gene regulation-associated gene oligonucleotide #373.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 32.6; DB 6; Length 17918;
Best Local Similarity 50.3%; Pred. No. 1.6e+02;
RESULT 753
ID AAZ29254 standard; DNA; 978 BP.
DE Rifin 3198 gene.
PN WO9955381-A1.
PD 04-NOV-1999.
PA (USNA) US SEC OF NAVY.
Query Match 5.1%; Score 32.4; DB 3; Length 978;
Best Local Similarity 50.0%; Pred. No. 47;
RESULT 754
ID AAA70279 standard; DNA; 1047 BP.
DE Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:412.
PN WO200025728-A2.
PD 11-MAY-2000.
PA (HOFF/) HOFFMAN S.
PA (CARU/) CARUCCI D.
PA (GARD/) GARDNER M.
PA (VENT/) VENTER J C.
Query Match 5.1%; Score 32.4; DB 3; Length 1047;
Best Local Similarity 50.0%; Pred. No. 49;
RESULT 755
ID ABK31369 standard; DNA; 5956 BP.
DE Signal transduction associated gene modified complementary DNA #106.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 32.4; DB 6; Length 5956;
Best Local Similarity 55.3%; Pred. No. 1.1e+02;
RESULT 756
ID ABL70326 standard; DNA; 5956 BP.
DE Chemically treated cell signalling DNA sequence complementary to#108.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 32.4; DB 6; Length 5956;
Best Local Similarity 55.3%; Pred. No. 1.1e+02;
RESULT 757
ID AAS61273 standard; DNA; 5956 BP.
DE Human gene regulation-associated gene oligonucleotide #228.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 32.4; DB 6; Length 5956;
Best Local Similarity 55.3%; Pred. No. 1.1e+02;
RESULT 758
ID AAS61208 standard; DNA; 5992 BP.
DE Human gene regulation-associated gene oligonucleotide #163.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 32.4; DB 6; Length 5992;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
RESULT 759
ID ABL32091 standard; DNA; 12733 BP.
DE Human immune system associated gene SEQ ID NO: 64.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.1%; Score 32.4; DB 6; Length 12733;
Best Local Similarity 64.9%; Pred. No. 1.6e+02;
RESULT 760
ID ADL13732 standard; DNA; 160203 BP.
DE Osteoarthritis-associated polymorphic nucleotide #264.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.

Query Match 5.1%; Score 32.4; DB 10; Length 160203;
Best Local Similarity 53.1%; Pred. No. 5.1e+02;
RESULT 761
ID ADE81671 standard; cDNA; 500 BP.
DE Arabidopsis thaliana expressed polynucleotide seq id 442.
PN US2003115639-A1.
PD 19-JUN-2003.
PA (GORL/) GORLACH J.
PA (ANYY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T M.
PA (YUYY/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHEW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
PA (KRIC/) KRICKER M.
PA (SLAT/) SLATER T.
PA (DAVI/) DAVIS K R.
PA (ALLE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURB/) HURBAN P.
Query Match 5.0%; Score 32.2; DB 10; Length 500;
Best Local Similarity 56.9%; Pred. No. 40;
RESULT 762
ID ADP74633 standard; DNA; 2361 BP.
DE Nucleotide sequence of GPI10/PIG-B polypeptide.
PN WO2004048567-A2.
PD 10-JUN-2004.
PA (EISA) EISAI CO LTD.
Query Match 5.0%; Score 32.2; DB 12; Length 2361;
Best Local Similarity 50.3%; Pred. No. 82;
RESULT 763
ID ABL02978 standard; cDNA; 4466 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 3416.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.0%; Score 32.2; DB 4; Length 4466;
Best Local Similarity 51.0%; Pred. No. 1.1e+02;
RESULT 764
ID ABL70158 standard; DNA; 5551 BP.
DE Chemically treated cell signalling DNA sequence complementary to#24.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.0%; Score 32.2; DB 6; Length 5551;
Best Local Similarity 56.0%; Pred. No. 1.2e+02;
RESULT 765
ID AAS61100 standard; DNA; 5551 BP.
DE Human gene regulation-associated gene oligonucleotide #55.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.0%; Score 32.2; DB 6; Length 5551;
Best Local Similarity 56.0%; Pred. No. 1.2e+02;
RESULT 766
ID AAX34650 standard; DNA; 11463 BP.
DE Starch branching enzyme II (SBE II) gene sequence.
PN WO9914314-A1.
PD 25-MAR-1999.
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
PA (AUSU) UNIV AUSTRALIAN NAT.
PA (GOOD-) GOODMAN FIELDER LTD.
PA (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.
Query Match 5.0%; Score 32.2; DB 2; Length 11463;
Best Local Similarity 63.6%; Pred. No. 1.7e+02;
RESULT 767
ID AAH78338 standard; cDNA; 11475 BP.
DE Nucleotide sequence of a starch branching enzyme designated F2.
PN WO200162934-A1.
PD 30-AUG-2001.
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
PA (GOOD-) GOODMAN FIELDER LTD.
PA (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.
Query Match 5.0%; Score 32.2; DB 5; Length 11475;
Best Local Similarity 63.6%; Pred. No. 1.7e+02;
RESULT 768
ID ADF89961 standard; DNA; 11476 BP.
DE A. tauschii starch branching enzyme IIa (SBEIIa) gene.
PN WO2003094600-A1.
PD 20-NOV-2003.
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
Query Match 5.0%; Score 32.2; DB 12; Length 11476;
Best Local Similarity 63.6%; Pred. No. 1.7e+02;
RESULT 769
ID AAV74393 standard; DNA; 15598 BP.
DE Staphylococcus aureus contig SEQ ID #82.
PN EP786519-A2.
PD 30-JUL-1997.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.0%; Score 32.2; DB 2; Length 15598;
Best Local Similarity 48.6%; Pred. No. 2e+02;
RESULT 770
ID AAK70623 standard; DNA; 26410 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25435.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.0%; Score 32.2; DB 4; Length 26410;
Best Local Similarity 51.8%; Pred. No. 2.5e+02;
RESULT 771
ID AAZ23899 standard; DNA; 49999 BP.
DE Human LOBO homologue genomic DNA.
PN WO9950284-A2.
PD 07-OCT-1999.
PA (ROSE/) ROSENTHAL A.
Query Match 5.0%; Score 32.2; DB 2; Length 49999;
Best Local Similarity 56.0%; Pred. No. 3.4e+02;
RESULT 772
ID ABN62299 standard; cDNA; 495 BP.
DE Human cancer related polynucleotide SEQ ID NO 2266.
PN WO200214500-A2.
PD 21-FEB-2002.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 5.0%; Score 32; DB 6; Length 495;
Best Local Similarity 55.4%; Pred. No. 46;
RESULT 773
ID AAI94881 standard; cDNA; 718 BP.
DE Human neuroblastoma expressed polynucleotide SEQ ID NO 956.
PN WO200166719-A1.
PD 13-SEP-2001.
PA (CHIB-) CHIBA PREFECTURE.
PA (HISM) HISAMITSU PHARM CO LTD.
Query Match 5.0%; Score 32; DB 4; Length 718;
Best Local Similarity 48.5%; Pred. No. 54;
RESULT 774
ID AAL18876 standard; cDNA; 820 BP.
DE Human breast cancer expressed polynucleotide 11333.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 5.0%; Score 32; DB 4; Length 820;
Best Local Similarity 49.4%; Pred. No. 58;
RESULT 775
ID ABZ16038 standard; DNA; 1431 BP.
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 3843.
PN WO200216655-A2.
PD 28-FEB-2002.
PA (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.

Query Match 5.0%; Score 32; DB 6; Length 1431;
Best Local Similarity 55.4%; Pred. No. 75;
RESULT 776
ID ADA71951 standard; DNA; 2000 BP.
DE Rice gene, SEQ ID 5276.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 5.0%; Score 32; DB 8; Length 2000;
Best Local Similarity 50.7%; Pred. No. 88;
RESULT 777
ID AAX20302 standard; DNA; 2324 BP.
DE Borrelia burgdorferi polynucleotide sequence #55.
PN WO9858943-A1.
PD 30-DEC-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (MEDI-) MEDIMMUNE INC.
Query Match 5.0%; Score 32; DB 2; Length 2324;
Best Local Similarity 48.4%; Pred. No. 94;
RESULT 778
ID ABQ67022 standard; DNA; 4661 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 52.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.0%; Score 32; DB 6; Length 4661;
Best Local Similarity 54.2%; Pred. No. 1.3e+02;
RESULT 779
ID ABQ67018 standard; DNA; 17234 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 48.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.0%; Score 32; DB 6; Length 17234;
Best Local Similarity 54.2%; Pred. No. 2.4e+02;
RESULT 780
ID ACD19193 standard; DNA; 43360 BP.
DE E. coli 0157 unique DNA sequence OZID_206.
PN US2003023075-A1.
PD 30-JAN-2003.
PA (BLAT/) BLATTNER F R.
PA (BURL/) BURLAND V D.
PA (PERN/) PERNA N T.
PA (PLUN/) PLUNKETT G.
PA (WELC/) WELCH R.
Query Match 5.0%; Score 32; DB 9; Length 43360;
Best Local Similarity 55.4%; Pred. No. 3.7e+02;
RESULT 781
ID ADC00771 standard; DNA; 43450 BP.
DE Enterohaemorragic E. coli 0157:H7-specific nucleic acid SEQ ID NO: 816.
PN JP2002355074-A.
PD 10-DEC-2002.
PA (UYTS-) UNIV TSUKUBA.
Query Match 5.0%; Score 32; DB 10; Length 43450;
Best Local Similarity 55.4%; Pred. No. 3.7e+02;
RESULT 782
ID ACD19247 standard; DNA; 45325 BP.
DE E. coli 0157 locus of Enterocyte Effacement, LEE.
PN US2003023075-A1.
PD 30-JAN-2003.
PA (BLAT/) BLATTNER F R.
PA (BURL/) BURLAND V D.
PA (PERN/) PERNA N T.
PA (PLUN/) PLUNKETT G.
PA (WELC/) WELCH R.
Query Match 5.0%; Score 32; DB 9; Length 45325;
Best Local Similarity 55.4%; Pred. No. 3.8e+02;
RESULT 783
ID ACN43972 standard; DNA; 47601 BP.
DE Mouse genomic sequence mCG12024.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 5.0%; Score 32; DB 11; Length 47601;
Best Local Similarity 47.9%; Pred. No. 3.8e+02;
RESULT 784
ID ABD33341 standard; DNA; 66126 BP.
DE Murine cancer-associated (CA) gene MD07-062.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 5.0%; Score 32; DB 13; Length 66126;
Best Local Similarity 53.1%; Pred. No. 4.5e+02;
RESULT 785
ID ADQ59368 standard; DNA; 100944 BP.
DE Human cancer-associated (CA) gene sequence SEQ ID NO:4.
PN WO2004058288-A1.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 5.0%; Score 32; DB 12; Length 100944;
Best Local Similarity 51.4%; Pred. No. 5.5e+02;
RESULT 786
Query Match 5.0%; Score 32; DB 6; Length 110000;
Best Local Similarity 54.2%; Pred. No. 5.6e+02;
RESULT 787
ID ACN43866 standard; DNA; 117754 BP.
DE Human genomic sequence hCG37475.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 5.0%; Score 32; DB 11; Length 117754;
Best Local Similarity 53.1%; Pred. No. 5.8e+02;
RESULT 788
ID AAH21613 standard; DNA; 168575 BP.
DE Human hypocretin receptor 2 (HCRTR2) gene SEQ ID NO:1.
PN WO200130991-A2.
PD 03-MAY-2001.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.0%; Score 32; DB 4; Length 168575;
Best Local Similarity 58.3%; Pred. No. 6.9e+02;
RESULT 789
ID ADQ20606 standard; DNA; 195917 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 3426.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 5.0%; Score 32; DB 12; Length 195917;
Best Local Similarity 55.4%; Pred. No. 7.3e+02;
RESULT 790
ID AAT70426 standard; cDNA; 616 BP.
DE Mouse peripherin cDNA with replaced non-coding sequence.
PN WO9711169-A2.
PD 27-MAR-1997.
PA (QUEE-) QUEEN ELIZABETH COLLEGE DUBLIN.
Query Match 5.0%; Score 31.8; DB 2; Length 616;
Best Local Similarity 52.8%; Pred. No. 58;
RESULT 791
ID ACC41531 standard; DNA; 797 BP.
DE Perennial ryegrass LpZTa4 fragment.
PN WO200290491-A2.
PD 14-NOV-2002.
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
PA (AGRE-) AGRESEARCH LTD.
Query Match 5.0%; Score 31.8; DB 8; Length 797;
Best Local Similarity 54.8%; Pred. No. 66;
RESULT 792
ID ABT13288 standard; DNA; 870 BP.
DE Breast specific related polynucleotide SEQ ID No 3.
PN WO200277232-A2.
PD 03-OCT-2002.
PA (DIAD-) DIADEXUS INC.
Query Match 5.0%; Score 31.8; DB 8; Length 870;
Best Local Similarity 61.4%; Pred. No. 69;
RESULT 793
ID ACC41527 standard; DNA; 996 BP.
DE Consensus contig nucleotide sequence of perennial ryegrass LpZTa.

PN WO200290491-A2.
PD 14-NOV-2002.
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
PA (AGRE-) AGRESEARCH LTD.
Query Match 5.0%; Score 31.8; DB 8; Length 996;
Best Local Similarity 54.8%; Pred. No. 73;
RESULT 794
ID ABQ68621 standard; DNA; 1102 BP.
DE Listeria monocytogenes 4b contig DNA sequence #1387.
PN WO200228891-A2.
PD 11-APR-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 5.0%; Score 31.8; DB 6; Length 1102;
Best Local Similarity 56.1%; Pred. No. 77;
RESULT 795
ID ADP73028 standard; DNA; 1121 BP.
DE Renal toxin progression gene marker #1617.
PN WO2004048598-A2.
PD 10-JUN-2004.
PA (GENE-) GENE LOGIC INC.
Query Match 5.0%; Score 31.8; DB 12; Length 1121;
Best Local Similarity 52.7%; Pred. No. 77;
RESULT 796
ID ABZ16866 standard; DNA; 2000 BP.
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 4671.
PN WO200216655-A2.
PD 28-FEB-2002.
PA (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 5.0%; Score 31.8; DB 6; Length 2000;
Best Local Similarity 45.7%; Pred. No. 1e+02;
RESULT 797
ID ADJ40625 standard; cDNA; 2000 BP.
DE Plant cDNA #1625.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
PA (ZHUT/) ZHU T.
Query Match 5.0%; Score 31.8; DB 12; Length 2000;
Best Local Similarity 51.0%; Pred. No. 1e+02;
RESULT 798
ID ACA22385 standard; DNA; 2655 BP.
DE Prokaryotic essential gene #4042.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.0%; Score 31.8; DB 8; Length 2655;
Best Local Similarity 54.8%; Pred. No. 1.2e+02;
RESULT 799
ID ABL99880 standard; cDNA; 2741 BP.
DE Human secretory polynucleotide (sptm) 135.
PN WO200220756-A2.
PD 14-MAR-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.0%; Score 31.8; DB 6; Length 2741;
Best Local Similarity 46.1%; Pred. No. 1.2e+02;
RESULT 800
ID ABL20562 standard; DNA; 3027 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 13159.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.0%; Score 31.8; DB 4; Length 3027;
Best Local Similarity 49.7%; Pred. No. 1.2e+02;
RESULT 801
ID ABL27222 standard; DNA; 3383 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 33139.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.0%; Score 31.8; DB 4; Length 3383;
Best Local Similarity 50.2%; Pred. No. 1.3e+02;
RESULT 802
ID ABZ10151 standard; DNA; 3720 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #291.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.0%; Score 31.8; DB 8; Length 3720;
Best Local Similarity 49.7%; Pred. No. 1.3e+02;
RESULT 803
ID ADB54211 standard; DNA; 3720 BP.
DE Pretreated genomic DNA region 135.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.0%; Score 31.8; DB 10; Length 3720;
Best Local Similarity 49.7%; Pred. No. 1.3e+02;
RESULT 804
ID ADE84145 standard; DNA; 3720 BP.
DE Human lymphoid cell proliferative disorder gene derived DNA #81.
PN WO2003044226-A2.
PD 30-MAY-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.0%; Score 31.8; DB 10; Length 3720;
Best Local Similarity 49.7%; Pred. No. 1.3e+02;
RESULT 805
ID ADS89511 standard; DNA; 3720 BP.
DE Oligonucleotide of the invention SEQ ID NO:527.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.0%; Score 31.8; DB 13; Length 3720;
Best Local Similarity 49.7%; Pred. No. 1.3e+02;
RESULT 806
ID ADB54250 standard; DNA; 6274 BP.
DE Pretreated genomic DNA region 174.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.0%; Score 31.8; DB 10; Length 6274;
Best Local Similarity 51.0%; Pred. No. 1.7e+02;
RESULT 807
ID AAV74362 standard; DNA; 6730 BP.
DE Staphylococcus aureus contig SEQ ID #51.
PN EP786519-A2.
PD 30-JUL-1997.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.0%; Score 31.8; DB 2; Length 6730;
Best Local Similarity 57.6%; Pred. No. 1.8e+02;
RESULT 808
ID ABQ71073 standard; DNA; 12278 BP.
DE Listeria monocytogenes 4b contig DNA sequence #1015.
PN WO200228891-A2.
PD 11-APR-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 5.0%; Score 31.8; DB 6; Length 12278;
Best Local Similarity 56.1%; Pred. No. 2.4e+02;
RESULT 809
ID ABL12192 standard; cDNA; 15372 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 31058.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.0%; Score 31.8; DB 4; Length 15372;

Best Local Similarity 50.3%; Pred. No. 2.6e+02;
RESULT 810
ID ADO79402 standard; DNA; 76600 BP.
DE DLG1 region, SEQ ID 1.
PN WO2004047514-A2.
PD 10-JUN-2004.
PA (SEQU-) SEQUENOM INC.
Query Match 5.0%; Score 31.8; DB 12; Length 76600;
Best Local Similarity 46.0%; Pred. No. 5.5e+02;
RESULT 811
Query Match 5.0%; Score 31.8; DB 2; Length 110000;
Best Local Similarity 51.8%; Pred. No. 6.5e+02;
RESULT 812
Query Match 5.0%; Score 31.8; DB 2; Length 110000;
Best Local Similarity 51.8%; Pred. No. 6.5e+02;
RESULT 813
Query Match 5.0%; Score 31.8; DB 6; Length 110000;
Best Local Similarity 56.1%; Pred. No. 6.5e+02;
RESULT 814
Query Match 5.0%; Score 31.8; DB 8; Length 110000;
Best Local Similarity 51.8%; Pred. No. 6.5e+02;
RESULT 815
ID ADQ59167 standard; DNA; 120670 BP.
DE MSI-H carcinoma genomic DNA sequence SEQ ID NO:4.
PN KR2004008012-A.
PD 28-JAN-2004.
PA (KIMH/) KIM H G.
PA (KIMN/) KIM N G.
PA (LEEJ/) LEE J S.
PA (RHEE/) RHEE H S.
Query Match 5.0%; Score 31.8; DB 12; Length 120670;
Best Local Similarity 57.6%; Pred. No. 6.8e+02;
RESULT 816
ID AAD55694 standard; DNA; 175561 BP.
DE Human THBS4 reference gene (GI 14916146).
PN WO2003020120-A2.
PD 13-MAR-2003.
PA (VITI-) VITIVITY INC.
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
Query Match 5.0%; Score 31.8; DB 8; Length 175561;
Best Local Similarity 48.1%; Pred. No. 8e+02;
RESULT 817
ID ADL08129 standard; DNA; 175561 BP.
DE Human gene associated with low HDL-C THBS4.
PN US2004043389-A1.
PD 04-MAR-2004.
PA (VITI-) VITIVITY INC.
Query Match 5.0%; Score 31.8; DB 12; Length 175561;
Best Local Similarity 48.1%; Pred. No. 8e+02;
RESULT 818
ID ABN61697 standard; cDNA; 562 BP.
DE Human cancer related polynucleotide SEQ ID NO 1664.
PN WO200214500-A2.
PD 21-FEB-2002.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 4.9%; Score 31.6; DB 6; Length 562;
Best Local Similarity 55.5%; Pred. No. 64;
RESULT 819
ID ABA13606 standard; cDNA; 663 BP.
DE Human nervous system related polynucleotide SEQ ID NO 2613.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.9%; Score 31.6; DB 5; Length 663;
Best Local Similarity 55.5%; Pred. No. 70;
RESULT 820
ID ACC41528 standard; DNA; 800 BP.
DE Perennial ryegrass LpZTa1 fragment.
PN WO200290491-A2.
PD 14-NOV-2002.
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
PA (AGRE-) AGRESEARCH LTD.

Query Match 4.9%; Score 31.6; DB 8; Length 800;
Best Local Similarity 55.5%; Pred. No. 76;
RESULT 821
ID ACA47638 standard; DNA; 3891 BP.
DE Prokaryotic essential gene #29295.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.9%; Score 31.6; DB 8; Length 3891;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
RESULT 822
ID ABL70589 standard; DNA; 6129 BP.
DE Chemically treated cell signalling DNA sequence#240.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.9%; Score 31.6; DB 6; Length 6129;
Best Local Similarity 45.3%; Pred. No. 2e+02;
RESULT 823
ID AAS61300 standard; DNA; 6129 BP.
DE Human gene regulation-associated gene oligonucleotide #255.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.9%; Score 31.6; DB 6; Length 6129;
Best Local Similarity 45.3%; Pred. No. 2e+02;
RESULT 824
ID AAS45504 standard; DNA; 8996 BP.
DE Chemically pretreated genomic DNA associated with cell cycle #105.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.9%; Score 31.6; DB 4; Length 8996;
Best Local Similarity 50.0%; Pred. No. 2.3e+02;
RESULT 825
ID ABK28436 standard; DNA; 8996 BP.
DE DNA transcription associated complementary genomic DNA #155.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.9%; Score 31.6; DB 6; Length 8996;
Best Local Similarity 50.0%; Pred. No. 2.3e+02;
RESULT 826
ID AAV99811 standard; DNA; 16075 BP.
DE Gum gene cluster.
PN WO9856942-A1.
PD 17-DEC-1998.
PA (SHIN-) SHINETSU BIO INC.
PA (SHIE) SHINETSU CHEM CO LTD.
Query Match 4.9%; Score 31.6; DB 2; Length 16075;
Best Local Similarity 62.8%; Pred. No. 3.1e+02;
RESULT 827
ID AAN70753 standard; DNA; 16079 BP.
DE Sequence of segment of Xanthomonas campestris DNA that contains a gene
DE cluster that directs Xanthan biosynthesis.
PN WO8705938-A.
PD 08-OCT-1987.
PA (GETT-) GETTY SCI DEV CO.
Query Match 4.9%; Score 31.6; DB 1; Length 16079;
Best Local Similarity 62.8%; Pred. No. 3.1e+02;
RESULT 828
ID ABL12300 standard; cDNA; 91507 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 31382.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.9%; Score 31.6; DB 4; Length 91507;
Best Local Similarity 46.6%; Pred. No. 6.9e+02;
RESULT 829
Query Match 4.9%; Score 31.6; DB 6; Length 110000;
Best Local Similarity 50.0%; Pred. No. 7.5e+02;
RESULT 830
Query Match 4.9%; Score 31.6; DB 6; Length 110000;

Best Local Similarity 47.9%; Pred. No. 7.5e+02;
RESULT 831
Query Match 4.9%; Score 31.6; DB 10; Length 110000;
Best Local Similarity 55.5%; Pred. No. 7.5e+02;
RESULT 832
Query Match 4.9%; Score 31.6; DB 12; Length 110000;
Best Local Similarity 50.0%; Pred. No. 7.5e+02;
RESULT 833
Query Match 4.9%; Score 31.6; DB 12; Length 110000;
Best Local Similarity 50.0%; Pred. No. 7.5e+02;
RESULT 834
Query Match 4.9%; Score 31.6; DB 12; Length 110000;
Best Local Similarity 50.0%; Pred. No. 7.5e+02;
RESULT 835
ID ADC24703 standard; DNA; 335199 BP.
DE Human wild type HNL4Y genomic sequence.
PN WO2003045998-A2.
PD 05-JUN-2003.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (INSP) INST PASTEUR.
PA (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.
Query Match 4.9%; Score 31.6; DB 10; Length 335199;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 836
ID ACC55515 standard; cDNA; 178 BP.
DE Rice endosperm EST #23.
PN CN1366081-A.
PD 28-AUG-2002.
PA (UYZH-) UNIV ZHEJIANG.
Query Match 4.9%; Score 31.4; DB 10; Length 178;
Best Local Similarity 51.0%; Pred. No. 43;
RESULT 837
ID ACH47940 standard; cDNA; 438 BP.
DE Human lung tumour cDNA #73.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 4.9%; Score 31.4; DB 9; Length 438;
Best Local Similarity 49.7%; Pred. No. 66;
RESULT 838
ID ABL93469 standard; cDNA; 469 BP.
DE Arabidopsis thaliana nucleic acid sequence Ref:2027234 SEQ ID NO:234.
PN US2002023280-A1.
PD 21-FEB-2002.
PA (GORL/) GORLACH J.
PA (ANYY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T M.
PA (YUYY/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHEW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
PA (KRIC/) KRICKER M.
PA (SLAT/) SLATER T.
PA (DAVI/) DAVIS K R.
PA (ALLE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURB/) HURBAN P.
Query Match 4.9%; Score 31.4; DB 6; Length 469;
Best Local Similarity 47.3%; Pred. No. 68;
RESULT 839
ID ABK30905 standard; cDNA; 554 BP.
DE Plant dwarfing/stunting related cDNA seq ID 319.
PN WO200208410-A2.
PD 31-JAN-2002.
PA (DOWC) DOW CHEM CO.
PA (REDD/) REDDY S A.
PA (LARR/) LARRINUA M I.
PA (RUEG/) RUEGGER M.
PA (WEGL/) WEGLARZ T.
PA (BLAK/) BLAKESLEE B.
PA (ORIE/) ORIEDO V B J.
PA (SAVI/) SAVICKAS J P.
PA (MCCR/) MCCRERY A D.
PA (MILL/) MILLER A B.
PA (POGU/) POGUE P G.
PA (DELL/) DELLA-CIOPPA R G.
PA (WOLF/) WOLFE M G.
PA (ZHEN/) ZHENG W.
PA (GACH/) GACHOTTE D.
PA (GROS/) GROSLEY R.
PA (PELL/) PELL R.
Query Match 4.9%; Score 31.4; DB 6; Length 554;
Best Local Similarity 48.6%; Pred. No. 74;
RESULT 840
ID ABV52833 standard; cDNA; 615 BP.
DE Human prostate expression marker cDNA 52824.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.9%; Score 31.4; DB 5; Length 615;
Best Local Similarity 53.7%; Pred. No. 77;
RESULT 841
ID AAS45053 standard; cDNA; 843 BP.
DE cDNA encoding novel human secretory protein, Seq ID No 134.
PN WO200166689-A2.
PD 13-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.9%; Score 31.4; DB 5; Length 843;
Best Local Similarity 49.7%; Pred. No. 90;
RESULT 842
ID AAS45241 standard; cDNA; 865 BP.
DE cDNA encoding novel human secretory protein, Seq ID No 510.
PN WO200166689-A2.
PD 13-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.9%; Score 31.4; DB 5; Length 865;
Best Local Similarity 49.7%; Pred. No. 91;
RESULT 843
ID AAC45923 standard; DNA; 1779 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 48258.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.9%; Score 31.4; DB 3; Length 1779;
Best Local Similarity 47.3%; Pred. No. 1.3e+02;
RESULT 844
ID AAC40484 standard; DNA; 1786 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 28468.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.9%; Score 31.4; DB 3; Length 1786;
Best Local Similarity 47.3%; Pred. No. 1.3e+02;
RESULT 845
ID AAS75385 standard; cDNA; 1887 BP.
DE DNA encoding novel human diagnostic protein #11189.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.9%; Score 31.4; DB 5; Length 1887;
Best Local Similarity 52.7%; Pred. No. 1.3e+02;
RESULT 846
ID ABA19513 standard; DNA; 2274 BP.
DE Human nervous system related polynucleotide SEQ ID NO 11844.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.9%; Score 31.4; DB 5; Length 2274;

Best Local Similarity 54.9%; Pred. No. 1.4e+02;
RESULT 847
ID ADG79245 standard; cDNA; 2291 BP.
DE Human secreted protein cDNA of the invention SEQ ID NO:51.
PN WO200268638-A1.
PD 06-SEP-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.9%; Score 31.4; DB 6; Length 2291;
Best Local Similarity 54.9%; Pred. No. 1.4e+02;
RESULT 848
ID ADB62538 standard; cDNA; 2642 BP.
DE Human cDNA encoding clone HLUNG20012140.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 4.9%; Score 31.4; DB 10; Length 2642;
Best Local Similarity 54.9%; Pred. No. 1.5e+02;
RESULT 849
ID ADQ24937 standard; DNA; 2972 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7757.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.9%; Score 31.4; DB 12; Length 2972;
Best Local Similarity 49.7%; Pred. No. 1.6e+02;
RESULT 850
ID ABK31457 standard; DNA; 5860 BP.
DE Signal transduction associated gene modified complementary DNA #150.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.9%; Score 31.4; DB 6; Length 5860;
Best Local Similarity 45.9%; Pred. No. 2.2e+02;
RESULT 851
ID ABL70524 standard; DNA; 5860 BP.
DE Chemically treated cell signalling DNA sequence complementary to#207.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.9%; Score 31.4; DB 6; Length 5860;
Best Local Similarity 45.9%; Pred. No. 2.2e+02;
RESULT 852
ID AAS61373 standard; DNA; 5860 BP.
DE Human gene regulation-associated gene oligonucleotide #328.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.9%; Score 31.4; DB 6; Length 5860;
Best Local Similarity 45.9%; Pred. No. 2.2e+02;
RESULT 853
ID ADQ59482 standard; DNA; 43709 BP.
DE Human cancer-associated (CA) gene sequence SEQ ID NO:118.
PN WO2004058288-A1.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 4.9%; Score 31.4; DB 12; Length 43709;
Best Local Similarity 56.2%; Pred. No. 5.6e+02;
RESULT 854
Query Match 4.9%; Score 31.4; DB 10; Length 110000;
Best Local Similarity 45.9%; Pred. No. 8.6e+02;
RESULT 855
ID ADQ97266 standard; DNA; 355211 BP.
DE Human cancer associated sequence HD08-023, SEQ ID 242.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 4.9%; Score 31.4; DB 12; Length 110000;
Best Local Similarity 45.9%; Pred. No. 8.6e+02;
RESULT 856
ID ADL13873 standard; DNA; 183178 BP.
DE Osteoarthritis-associated polymorphic nucleotide #405.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 4.9%; Score 31.4; DB 10; Length 183178;
Best Local Similarity 52.7%; Pred. No. 1.1e+03;
RESULT 857
ID ACN44210 standard; DNA; 238484 BP.
DE Human genomic sequence hCG28803.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 4.9%; Score 31.4; DB 11; Length 238484;
Best Local Similarity 51.8%; Pred. No. 1.2e+03;
RESULT 858
ID ADQ55747 standard; DNA; 454 BP.
DE Novel canine microarray-related DNA sequence SeqID7049.
PN WO2004063324-A2.
PD 29-JUL-2004.
PA (GENE-) GENE LOGIC INC.
PA (PFIZ) PFIZER PROD INC.
Query Match 4.9%; Score 31.2; DB 13; Length 454;
Best Local Similarity 53.2%; Pred. No. 77;
RESULT 859
ID ABA21279 standard; DNA; 475 BP.
DE Human nervous system related polynucleotide SEQ ID NO 13610.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.9%; Score 31.2; DB 5; Length 475;
Best Local Similarity 57.0%; Pred. No. 79;
RESULT 860
ID ACA33327 standard; DNA; 528 BP.
DE Prokaryotic essential gene #14984.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.9%; Score 31.2; DB 8; Length 528;
Best Local Similarity 66.2%; Pred. No. 83;
RESULT 861
ID AAS53105 standard; DNA; 531 BP.
DE Enterococcus faecalis DNA for cellular proliferation protein #533.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.9%; Score 31.2; DB 4; Length 531;
Best Local Similarity 66.2%; Pred. No. 83;
RESULT 862
ID ADH84609 standard; DNA; 537 BP.
DE Enterococcus faecalis polynucleotide #2494.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 4.9%; Score 31.2; DB 10; Length 537;
Best Local Similarity 66.2%; Pred. No. 84;
RESULT 863
ID ABV20146 standard; cDNA; 626 BP.
DE Human prostate expression marker cDNA 20137.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.9%; Score 31.2; DB 5; Length 626;
Best Local Similarity 50.7%; Pred. No. 90;
RESULT 864
ID ABV25979 standard; cDNA; 626 BP.
DE Human prostate expression marker cDNA 25970.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.9%; Score 31.2; DB 5; Length 626;
Best Local Similarity 50.7%; Pred. No. 90;
RESULT 865
ID AAH51406 standard; DNA; 1001 BP.
DE Human UGT1A7 related DNA containing a biallelic polymorphism SEQ ID 297.

PN WO200058508-A2.
PD 05-OCT-2000.
PA (GEST) GENSET.
Query Match 4.9%; Score 31.2; DB 3; Length 1001;
Best Local Similarity 48.8%; Pred. No. 1.1e+02;
RESULT 866
ID AAH51407 standard; DNA; 1001 BP.
DE Human UGT1A7 related DNA containing a biallelic polymorphism SEQ ID 298.
PN WO200058508-A2.
PD 05-OCT-2000.
PA (GEST) GENSET.
Query Match 4.9%; Score 31.2; DB 3; Length 1001;
Best Local Similarity 48.8%; Pred. No. 1.1e+02;
RESULT 867
ID ADH84072 standard; DNA; 1536 BP.
DE Enterococcus faecalis polynucleotide #1957.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 4.9%; Score 31.2; DB 10; Length 1536;
Best Local Similarity 50.7%; Pred. No. 1.4e+02;
RESULT 868
ID ACN89539 standard; DNA; 1876 BP.
DE Breast cancer related marker, seq id 10689.
PN US20030099974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 4.9%; Score 31.2; DB 11; Length 1876;
Best Local Similarity 54.3%; Pred. No. 1.5e+02;
RESULT 869
ID ABL12784 standard; cDNA; 3644 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 32834.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.9%; Score 31.2; DB 4; Length 3644;
Best Local Similarity 57.0%; Pred. No. 2e+02;
RESULT 870
ID ABL11242 standard; cDNA; 5471 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 28208.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.9%; Score 31.2; DB 4; Length 5471;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
RESULT 871
ID AAX13264 standard; DNA; 6005 BP.
DE Enterococcus faecalis genome contig SEQ ID NO:327.
PN WO9850555-A2.
PD 12-NOV-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.9%; Score 31.2; DB 2; Length 6005;
Best Local Similarity 66.2%; Pred. No. 2.6e+02;
RESULT 872
ID ABS99059 standard; DNA; 6005 BP.
DE Enterococcus faecalis contig sequence #327.
PN US2002120116-A1.
PD 29-AUG-2002.
PA (KUNS/) KUNSCH C A.
PA (DILL/) DILLON P J.
PA (BARA/) BARASH S.
Query Match 4.9%; Score 31.2; DB 6; Length 6005;
Best Local Similarity 66.2%; Pred. No. 2.6e+02;
RESULT 873
ID ABA20292 standard; DNA; 6454 BP.
DE Human nervous system related polynucleotide SEQ ID NO 12623.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.9%; Score 31.2; DB 5; Length 6454;
Best Local Similarity 50.0%; Pred. No. 2.7e+02;
RESULT 874
ID ADM98582 standard; DNA; 7837 BP.
DE Geranylgeranyl pyrophosphate synthase DNA #2.
PN US2004072323-A1.
PD 15-APR-2004.
PA (MATS/) MATSUDA S P T.
PA (HART/) HART E A.
Query Match 4.9%; Score 31.2; DB 12; Length 7837;
Best Local Similarity 66.2%; Pred. No. 2.9e+02;
RESULT 875
ID ABL10576 standard; cDNA; 10241 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 26210.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.9%; Score 31.2; DB 4; Length 10241;
Best Local Similarity 57.0%; Pred. No. 3.3e+02;
RESULT 876
ID AAZ35272 standard; DNA; 12571 BP.
DE Soybean retroelement Calypso 1-2.
PN WO9960842-A2.
PD 02-DEC-1999.
PA (WRIG/) WRIGHT D A.
PA (VOYT/) VOYTAS D F.
Query Match 4.9%; Score 31.2; DB 3; Length 12571;
Best Local Similarity 51.0%; Pred. No. 3.6e+02;
RESULT 877
ID ABL34071 standard; DNA; 13503 BP.
DE Human immune system associated gene SEQ ID NO: 2044.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.9%; Score 31.2; DB 6; Length 13503;
Best Local Similarity 58.7%; Pred. No. 3.8e+02;
RESULT 878
ID ACN44388 standard; DNA; 55544 BP.
DE Mouse genomic sequence mCG18573.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 4.9%; Score 31.2; DB 11; Length 55544;
Best Local Similarity 54.3%; Pred. No. 7.3e+02;
RESULT 879
Query Match 4.9%; Score 31.2; DB 12; Length 57652;
Best Local Similarity 50.7%; Pred. No. 7.4e+02;
RESULT 880
ID AAF22292 standard; DNA; 86584 BP.
DE BAC containing repeats from centromeres 1-4 #15.
PN WO200055325-A2.
PD 21-SEP-2000.
PA (UYCH-) UNIV CHICAGO.
Query Match 4.9%; Score 31.2; DB 3; Length 86584;
Best Local Similarity 50.0%; Pred. No. 8.9e+02;
RESULT 881
ID AAF22297 standard; DNA; 96583 BP.
DE BAC containing repeats from centromeres 1-4 #20.
PN WO200055325-A2.
PD 21-SEP-2000.
PA (UYCH-) UNIV CHICAGO.
Query Match 4.9%; Score 31.2; DB 3; Length 96583;
Best Local Similarity 50.0%; Pred. No. 9.3e+02;
RESULT 882
Query Match 4.9%; Score 31.2; DB 6; Length 110000;
Best Local Similarity 50.7%; Pred. No. 9.9e+02;
RESULT 883
ID ADQ97960 standard; DNA; 390183 BP.
DE Human cancer associated sequence HD11-029, SEQ ID 937.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 4.9%; Score 31.2; DB 12; Length 110000;
Best Local Similarity 55.6%; Pred. No. 9.9e+02;
RESULT 884
ID ACN43872 standard; DNA; 122859 BP.

DE Mouse genomic sequence mCG10301.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 4.9%; Score 31.2; DB 11; Length 122859;
Best Local Similarity 49.4%; Pred. No. 1e+03;
RESULT 885
ID ACN44188 standard; DNA; 144179 BP.
DE Mouse genomic sequence mCG15699.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 4.9%; Score 31.2; DB 11; Length 144179;
Best Local Similarity 63.2%; Pred. No. 1.1e+03;
RESULT 886
ID ABS55200 standard; DNA; 341511 BP.
DE Genomic DNA encoding human transporter protein.
Query Match 4.9%; Score 31.2; DB 6; Length 341511;
Best Local Similarity 50.7%; Pred. No. 1.6e+03;
RESULT 887
ID ADC86642 standard; DNA; 349881 BP.
DE Human GPCR gene SEQ ID NO:1095.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 4.9%; Score 31.2; DB 10; Length 349881;
Best Local Similarity 48.8%; Pred. No. 1.6e+03;
RESULT 888
ID AAC94710 standard; cDNA; 445 BP.
DE Cat flea hindgut and Malpighian tubule (HMT) cDNA, SEQ ID NO:1205.
PN WO200061621-A2.
PD 19-OCT-2000.
PA (HESK-) HESKA CORP.
Query Match 4.9%; Score 31; DB 3; Length 445;
Best Local Similarity 52.3%; Pred. No. 88;
RESULT 889
ID ACH23722 standard; cDNA; 495 BP.
DE Human adult ovary cDNA #2102.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 4.9%; Score 31; DB 9; Length 495;
Best Local Similarity 50.0%; Pred. No. 93;
RESULT 890
ID ABT18394 standard; DNA; 612 BP.
DE Aspergillus fumigatus essential gene #752.
PN WO200286090-A2.
PD 31-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.9%; Score 31; DB 8; Length 612;
Best Local Similarity 55.0%; Pred. No. 1e+02;
RESULT 891
ID ABT18988 standard; DNA; 612 BP.
DE Aspergillus fumigatus essential gene #1346.
PN WO200286090-A2.
PD 31-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.9%; Score 31; DB 8; Length 612;
Best Local Similarity 55.0%; Pred. No. 1e+02;
RESULT 892
ID AAV75357 standard; DNA; 626 BP.
DE Staphylococcus aureus contig SEQ ID #1046.
PN EP786519-A2.
PD 30-JUL-1997.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.9%; Score 31; DB 2; Length 626;
Best Local Similarity 48.6%; Pred. No. 1e+02;
RESULT 893
ID AAC46969 standard; DNA; 642 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 52078.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.9%; Score 31; DB 3; Length 642;
Best Local Similarity 51.0%; Pred. No. 1e+02;
RESULT 894
ID ACF65883 standard; DNA; 754 BP.
DE Photorhabdus luminescens nucleotide sequence #4350.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 4.9%; Score 31; DB 10; Length 754;
Best Local Similarity 49.1%; Pred. No. 1.1e+02;
RESULT 895
ID ACF67120 standard; DNA; 759 BP.
DE Photorhabdus luminescens nucleotide sequence #5587.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 4.9%; Score 31; DB 10; Length 759;
Best Local Similarity 49.1%; Pred. No. 1.1e+02;
RESULT 896
ID ACF66251 standard; DNA; 762 BP.
DE Photorhabdus luminescens nucleotide sequence #4718.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 4.9%; Score 31; DB 10; Length 762;
Best Local Similarity 49.1%; Pred. No. 1.1e+02;
RESULT 897
ID AAC52074 standard; DNA; 768 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 70326.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.9%; Score 31; DB 3; Length 768;
Best Local Similarity 51.0%; Pred. No. 1.1e+02;
RESULT 898
ID ACF66612 standard; DNA; 775 BP.
DE Photorhabdus luminescens nucleotide sequence #5079.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 4.9%; Score 31; DB 10; Length 775;
Best Local Similarity 49.1%; Pred. No. 1.1e+02;
RESULT 899
ID ABT20808 standard; DNA; 846 BP.
DE Aspergillus fumigatus essential gene #3166.
PN WO200286090-A2.
PD 31-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.9%; Score 31; DB 8; Length 846;
Best Local Similarity 55.0%; Pred. No. 1.2e+02;
RESULT 900
ID ADT41915 standard; cDNA; 903 BP.
DE Bacterial polynucleotide #16666.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 4.9%; Score 31; DB 13; Length 903;
Best Local Similarity 53.8%; Pred. No. 1.2e+02;
RESULT 901
ID AAT98708 standard; DNA; 978 BP.
DE DNA encoding a S. pneumoniae 30S ribosomal protein S9.
PN WO9743303-A1.

PD 20-NOV-1997.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 4.9%; Score 31; DB 2; Length 978;
Best Local Similarity 64.8%; Pred. No. 1.3e+02;
RESULT 902
ID ADT46572 standard; cDNA; 990 BP.
DE Bacterial polynucleotide #21323.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 4.9%; Score 31; DB 13; Length 990;
Best Local Similarity 57.9%; Pred. No. 1.3e+02;
RESULT 903
ID ABT20210 standard; DNA; 1087 BP.
DE Aspergillus fumigatus essential gene #2568.
PN WO200286090-A2.
PD 31-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.9%; Score 31; DB 8; Length 1087;
Best Local Similarity 55.0%; Pred. No. 1.3e+02;
RESULT 904
ID ADK16608 standard; DNA; 1821 BP.
DE Nanoarchaeum equitans cancer-associated (CA) gene #280.
PN WO2003093434-A2.
PD 13-NOV-2003.
PA (DIVE-) DIVERSA CORP.
Query Match 4.9%; Score 31; DB 12; Length 1821;
Best Local Similarity 47.2%; Pred. No. 1.7e+02;
RESULT 905
ID ABT17800 standard; DNA; 2612 BP.
DE Aspergillus fumigatus essential gene #158.
PN WO200286090-A2.
PD 31-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.9%; Score 31; DB 8; Length 2612;
Best Local Similarity 55.0%; Pred. No. 2e+02;
RESULT 906
ID AAN60611 standard; DNA; 2647 BP.
DE Vector sequence derived from bean golden mosaic virus.
PN JP61132188-A.
PD 19-JUN-1986.
PA (TEIJ) TEIJIN LTD.
Query Match 4.9%; Score 31; DB 1; Length 2647;
Best Local Similarity 59.8%; Pred. No. 2e+02;
RESULT 907
ID AAN70630 standard; DNA; 2647 BP.
DE DNA -b sequence of Bean Golden Mossaic virus.
PN JP61257186-A.
PD 14-NOV-1986.
PA (TEIJ) TEIJIN LTD.
Query Match 4.9%; Score 31; DB 1; Length 2647;
Best Local Similarity 59.8%; Pred. No. 2e+02;
RESULT 908
ID ABL05870 standard; cDNA; 3060 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 12092.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.9%; Score 31; DB 4; Length 3060;
Best Local Similarity 55.0%; Pred. No. 2.2e+02;
RESULT 909
ID ABT19614 standard; DNA; 3087 BP.
DE Aspergillus fumigatus essential gene #1972.
PN WO200286090-A2.
PD 31-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.9%; Score 31; DB 8; Length 3087;
Best Local Similarity 55.0%; Pred. No. 2.2e+02;

RESULT 910
ID ADN73088 standard; cDNA; 3255 BP.
DE Thale cress cDNA upregulated in E2Fa/Dpa expressing plants SeqID 983.
PN WO2004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPDESIGN NV.
Query Match 4.9%; Score 31; DB 12; Length 3255;
Best Local Similarity 68.3%; Pred. No. 2.2e+02;
RESULT 911
ID ABS79014 standard; DNA; 5446 BP.
DE E. coli CFT073 genomic sequence #181.
PN WO200259320-A2.
PD 01-AUG-2002.
PA (WISC) WISCONSIN ALUMNI RES FOUND.
Query Match 4.9%; Score 31; DB 6; Length 5446;
Best Local Similarity 62.0%; Pred. No. 2.8e+02;
RESULT 912
ID ADH80581 standard; DNA; 7246 BP.
DE Escherichia coli CFT073 genome contig #181.
PN US2003165870-A1.
PD 04-SEP-2003.
PA (BLAT/) BLATTNER F R.
PA (WELC/) WELCH R A.
PA (BURL/) BURLAND V D.
Query Match 4.9%; Score 31; DB 10; Length 7246;
Best Local Similarity 62.0%; Pred. No. 3.2e+02;
RESULT 913
ID ABA89015 standard; DNA; 7268 BP.
DE Escherichia coli polynucleotide SEQ ID NO 597.
PN WO200166572-A2.
PD 13-SEP-2001.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
Query Match 4.9%; Score 31; DB 4; Length 7268;
Best Local Similarity 62.0%; Pred. No. 3.2e+02;
RESULT 914
ID AAA70206 standard; DNA; 7503 BP.
DE Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:339.
PN WO200025728-A2.
PD 11-MAY-2000.
PA (HOFF/) HOFFMAN S.
PA (CARU/) CARUCCI D.
PA (GARD/) GARDNER M.
PA (VENT/) VENTER J C.
Query Match 4.9%; Score 31; DB 3; Length 7503;
Best Local Similarity 48.1%; Pred. No. 3.3e+02;
RESULT 915
ID ABL56201 standard; DNA; 50000 BP.
DE AmEPV genome fragment#3.
PN WO200212526-A2.
PD 14-FEB-2002.
PA (UYFL) UNIV FLORIDA.
Query Match 4.9%; Score 31; DB 6; Length 50000;
Best Local Similarity 51.0%; Pred. No. 8e+02;
RESULT 916
ID ADQ97885 standard; DNA; 62130 BP.
DE Mouse cancer associated sequence MD11-019, SEQ ID 862.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 4.9%; Score 31; DB 12; Length 62130;
Best Local Similarity 48.6%; Pred. No. 8.8e+02;
RESULT 917
Query Match 4.9%; Score 31; DB 10; Length 110000;
Best Local Similarity 49.1%; Pred. No. 1.1e+03;
RESULT 918
Query Match 4.9%; Score 31; DB 12; Length 110000;
Best Local Similarity 47.2%; Pred. No. 1.1e+03;
RESULT 919
ID ABK83573 standard; cDNA; 130263 BP.
DE Human cDNA differentially expressed in granulocytic cells #144.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.

Query Match 4.9%; Score 31; DB 6; Length 130263;
Best Local Similarity 64.8%; Pred. No. 1.2e+03;

RESULT 920
ID ABK83566 standard; cDNA; 147724 BP.
DE Human cDNA differentially expressed in granulocytic cells #137.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 4.9%; Score 31; DB 6; Length 147724;
Best Local Similarity 57.9%; Pred. No. 1.3e+03;

RESULT 921
ID ACF65379 standard; DNA; 182624 BP.
DE Photorhabdus luminescens nucleotide sequence #32.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 4.9%; Score 31; DB 10; Length 182624;
Best Local Similarity 49.1%; Pred. No. 1.4e+03;

RESULT 922
ID ABK89296 standard; DNA; 326014 BP.
DE Human gene for novel serine/threonine serine kinase.
Query Match 4.9%; Score 31; DB 6; Length 326014;
Best Local Similarity 48.6%; Pred. No. 1.8e+03;

RESULT 923
ID ADQ94981 standard; DNA; 326014 BP.
DE Human kinase genomic DNA.
Query Match 4.9%; Score 31; DB 12; Length 326014;
Best Local Similarity 48.6%; Pred. No. 1.8e+03;

RESULT 924
ID ADP43517 standard; DNA; 347001 BP.
DE Human MAD1-like 1 DNA #7.
PN US2004115650-A1.
PD 17-JUN-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 4.9%; Score 31; DB 12; Length 347001;
Best Local Similarity 50.3%; Pred. No. 1.9e+03;

RESULT 925
ID ADC87010 standard; DNA; 349999 BP.
DE Human GPCR gene SEQ ID NO:1463.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 4.9%; Score 31; DB 10; Length 349999;
Best Local Similarity 51.0%; Pred. No. 1.9e+03;

RESULT 926
ID ABL81744 standard; cDNA; 447 BP.
DE Human ovarian cancer related cDNA clone SEQ ID NO:4722.
PN WO200192581-A2.
PD 06-DEC-2001.
PA (CORI-) CORIXA CORP.
Query Match 4.8%; Score 30.8; DB 6; Length 447;
Best Local Similarity 54.4%; Pred. No. 1e+02;

RESULT 927
ID AAA09483 standard; DNA; 450 BP.
DE Human Zsig24 degenerate open reading frame.
PN WO200024767-A2.
PD 04-MAY-2000.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 4.8%; Score 30.8; DB 3; Length 450;
Best Local Similarity 34.2%; Pred. No. 1e+02;

RESULT 928
ID ABX10910 standard; DNA; 450 BP.
DE Novel human membrane associated protein Zsig24, degenerate DNA.
PN US2002164701-A1.
PD 07-NOV-2002.
PA (SHEP/) SHEPPARD P O.
PA (JELI/) JELINEK L J.
PA (WHIT/) WHITMORE T E.
Query Match 4.8%; Score 30.8; DB 10; Length 450;
Best Local Similarity 34.2%; Pred. No. 1e+02;

RESULT 929
ID ACH91992 standard; DNA; 456 BP.
DE Human genome derived single exon probe #25187.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 4.8%; Score 30.8; DB 12; Length 456;
Best Local Similarity 57.1%; Pred. No. 1e+02;

RESULT 930
ID ACN56190 standard; cDNA; 498 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-032-Q6-N6-H12, SEQ:10971.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.8%; Score 30.8; DB 13; Length 498;
Best Local Similarity 48.3%; Pred. No. 1.1e+02;

RESULT 931
ID AAH11028 standard; cDNA; 520 BP.
DE Human cDNA clone (3'-primer) SEQ ID NO:7863.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 4.8%; Score 30.8; DB 4; Length 520;
Best Local Similarity 49.7%; Pred. No. 1.1e+02;

RESULT 932
ID ACH77597 standard; DNA; 563 BP.
DE Human genome derived single exon probe #10792.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 4.8%; Score 30.8; DB 12; Length 563;
Best Local Similarity 49.4%; Pred. No. 1.1e+02;

RESULT 933
ID ACH69131 standard; DNA; 573 BP.
DE Human genome derived single exon probe #2326.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 4.8%; Score 30.8; DB 12; Length 573;
Best Local Similarity 51.1%; Pred. No. 1.1e+02;

RESULT 934
ID AAK92512 standard; cDNA; 592 BP.
DE Human cDNA 3'-end sequence, SEQ ID NO: 972.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 4.8%; Score 30.8; DB 4; Length 592;
Best Local Similarity 54.4%; Pred. No. 1.2e+02;

RESULT 935
ID ADL28939 standard; cDNA; 592 BP.
DE 3' end of a human cDNA molecule SeqID 972.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 4.8%; Score 30.8; DB 12; Length 592;
Best Local Similarity 54.4%; Pred. No. 1.2e+02;

RESULT 936
ID AAI96874 standard; cDNA; 728 BP.
DE Human neuroblastoma expressed polynucleotide SEQ ID NO 2949.
PN WO200166719-A1.
PD 13-SEP-2001.
PA (CHIB-) CHIBA PREFECTURE.
PA (HISM) HISAMITSU PHARM CO LTD.
Query Match 4.8%; Score 30.8; DB 4; Length 728;
Best Local Similarity 55.7%; Pred. No. 1.3e+02;

RESULT 937
ID ABN99152 standard; DNA; 769 BP.
DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 920.
PN US2002023281-A1.
PD 21-FEB-2002.
PA (GORL/) GORLACH J.
PA (ANYY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T M.
PA (YUYY/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHEW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
PA (KRIC/) KRICKER M.
PA (SLAT/) SLATER T.
PA (DAVI/) DAVIS K R.
PA (ALLE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURB/) HURBAN P.
Query Match 4.8%; Score 30.8; DB 6; Length 769;
Best Local Similarity 50.7%; Pred. No. 1.3e+02;
RESULT 938
ID AAI95931 standard; cDNA; 788 BP.
DE Human neuroblastoma expressed polynucleotide SEQ ID NO 2006.
PN WO200166719-A1.
PD 13-SEP-2001.
PA (CHIB-) CHIBA PREFECTURE.
PA (HISM) HISAMITSU PHARM CO LTD.
Query Match 4.8%; Score 30.8; DB 4; Length 788;
Best Local Similarity 55.7%; Pred. No. 1.3e+02;
RESULT 939
ID AAA01854 standard; cDNA; 815 BP.
DE Human colon cancer cell line polynucleotide sequence SEQ ID NO:1845.
PN WO9958675-A2.
PD 18-NOV-1999.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 4.8%; Score 30.8; DB 3; Length 815;
Best Local Similarity 51.6%; Pred. No. 1.3e+02;
RESULT 940
ID AAA01853 standard; cDNA; 843 BP.
DE Human colon cancer cell line polynucleotide sequence SEQ ID NO:1844.
PN WO9958675-A2.
PD 18-NOV-1999.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 4.8%; Score 30.8; DB 3; Length 843;
Best Local Similarity 51.6%; Pred. No. 1.4e+02;
RESULT 941
ID ACA47999 standard; DNA; 960 BP.
DE Prokaryotic essential gene #29656.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.8%; Score 30.8; DB 8; Length 960;
Best Local Similarity 48.3%; Pred. No. 1.5e+02;
RESULT 942
ID ADS51320 standard; cDNA; 1016 BP.
DE Bacterial polynucleotide #6063.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 4.8%; Score 30.8; DB 13; Length 1016;
Best Local Similarity 52.3%; Pred. No. 1.5e+02;
RESULT 943
ID AAT89511 standard; DNA; 1347 BP.
DE Xanthosine N7 methyltransferase (XMT) encoding DNA.
PN WO9735960-A1.
PD 02-OCT-1997.
PA (UYHA-) UNIV HAWAII.
Query Match 4.8%; Score 30.8; DB 2; Length 1347;
Best Local Similarity 52.3%; Pred. No. 1.7e+02;
RESULT 944
ID AAV61944 standard; cDNA; 1347 BP.
DE Coffee XMT cDNA.
PN WO9842848-A1.
PD 01-OCT-1998.
PA (UYHA-) UNIV HAWAII.
Query Match 4.8%; Score 30.8; DB 2; Length 1347;
Best Local Similarity 52.3%; Pred. No. 1.7e+02;
RESULT 945
ID AAV07574 standard; DNA; 1347 BP.
DE Xanthosine N7 methyltransferase antisense sequence.
PN WO9836053-A2.
PD 20-AUG-1998.
PA (UYHA-) UNIV HAWAII.
Query Match 4.8%; Score 30.8; DB 2; Length 1347;
Best Local Similarity 52.3%; Pred. No. 1.7e+02;
RESULT 946
ID AAV07573 standard; cDNA; 1347 BP.
DE Xanthosine N7 methyltransferase cDNA.
PN WO9836053-A2.
PD 20-AUG-1998.
PA (UYHA-) UNIV HAWAII.
Query Match 4.8%; Score 30.8; DB 2; Length 1347;
Best Local Similarity 52.3%; Pred. No. 1.7e+02;
RESULT 947
ID AAD31536 standard; cDNA; 1347 BP.
DE Arabica coffee xanthosine-N7-methyltransferase (XMT) cDNA.
PN US6348641-B1.
PD 19-FEB-2002.
PA (UYHA-) UNIV HAWAII.
Query Match 4.8%; Score 30.8; DB 6; Length 1347;
Best Local Similarity 52.3%; Pred. No. 1.7e+02;
RESULT 948
ID ADB31378 standard; cDNA; 1497 BP.
DE Testosterone regulated prostate cancer gene #49.
PN US6506607-B1.
PD 14-JAN-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 4.8%; Score 30.8; DB 10; Length 1497;
Best Local Similarity 23.3%; Pred. No. 1.8e+02;
RESULT 949
ID ACF74767 standard; DNA; 1653 BP.
DE Staphylococcus aureus DNA #2447.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 4.8%; Score 30.8; DB 8; Length 1653;
Best Local Similarity 58.9%; Pred. No. 1.9e+02;
RESULT 950
ID ABZ16311 standard; DNA; 2000 BP.
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 4116.
PN WO200216655-A2.
PD 28-FEB-2002.
PA (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 4.8%; Score 30.8; DB 6; Length 2000;
Best Local Similarity 51.4%; Pred. No. 2e+02;
RESULT 951
ID ADR25523 standard; DNA; 2058 BP.
DE Breast cancer prognosis marker #1384.
PN WO2004065545-A2.
PD 05-AUG-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
PA (NECA-) NETHERLANDS CANCER INST.
Query Match 4.8%; Score 30.8; DB 13; Length 2058;

Best Local Similarity 51.6%; Pred. No. 2.1e+02;
RESULT 952
ID ADP56317 standard; cDNA; 2058 BP.
DE Human PRO cDNA sequence SEQ ID NO:2293.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 4.8%; Score 30.8; DB 13; Length 2058;
Best Local Similarity 51.6%; Pred. No. 2.1e+02;
RESULT 953
ID AAS26348 standard; cDNA; 2109 BP.
DE Human cDNA encoding a novel secreted protein, Seq ID 527.
PN WO200155322-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.8%; Score 30.8; DB 4; Length 2109;
Best Local Similarity 54.4%; Pred. No. 2.1e+02;
RESULT 954
ID ABX73689 standard; DNA; 2109 BP.
DE Human novel polynucleotide #517.
PN US2002132753-A1.
PD 19-SEP-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 4.8%; Score 30.8; DB 8; Length 2109;
Best Local Similarity 54.4%; Pred. No. 2.1e+02;
RESULT 955
ID AAS25895 standard; cDNA; 2221 BP.
DE Human cDNA encoding a novel secreted protein, Seq ID 74.
PN WO200155322-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.8%; Score 30.8; DB 4; Length 2221;
Best Local Similarity 54.4%; Pred. No. 2.1e+02;
RESULT 956
ID ABX73236 standard; DNA; 2221 BP.
DE Human novel polynucleotide #64.
PN US2002132753-A1.
PD 19-SEP-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 4.8%; Score 30.8; DB 8; Length 2221;
Best Local Similarity 54.4%; Pred. No. 2.1e+02;
RESULT 957
ID AAH17654 standard; cDNA; 2338 BP.
DE Human cDNA sequence SEQ ID NO:17206.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 4.8%; Score 30.8; DB 4; Length 2338;
Best Local Similarity 57.1%; Pred. No. 2.2e+02;
RESULT 958
ID AAL49930 standard; cDNA; 2647 BP.
DE Human molecule for disease detection and treatment coding sequence #4.
PN WO200270709-A2.
PD 12-SEP-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 4.8%; Score 30.8; DB 6; Length 2647;
Best Local Similarity 51.6%; Pred. No. 2.3e+02;
RESULT 959
ID ADB63605 standard; cDNA; 2773 BP.
DE Human cDNA encoding clone THYMU20052460.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 4.8%; Score 30.8; DB 10; Length 2773;
Best Local Similarity 57.1%; Pred. No. 2.4e+02;
RESULT 960
ID AAK94668 standard; cDNA; 2853 BP.
DE Human full-length cDNA, SEQ ID NO: 3664.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 4.8%; Score 30.8; DB 4; Length 2853;
Best Local Similarity 54.4%; Pred. No. 2.4e+02;
RESULT 961
ID ADL31631 standard; cDNA; 2853 BP.
DE Full length human cDNA clone SeqID 3664.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 4.8%; Score 30.8; DB 12; Length 2853;
Best Local Similarity 54.4%; Pred. No. 2.4e+02;
RESULT 962
ID ADB58248 standard; DNA; 2950 BP.
DE Toxicity-related gene, SEQ ID 3274.
PN WO2003064624-A2.
PD 07-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 4.8%; Score 30.8; DB 10; Length 2950;
Best Local Similarity 52.3%; Pred. No. 2.5e+02;
RESULT 963
ID ABT41956 standard; DNA; 2950 BP.
DE Toxicity modelling related rat gene SEQ ID No 1658.
PN WO200295000-A2.
PD 28-NOV-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 4.8%; Score 30.8; DB 10; Length 2950;
Best Local Similarity 52.3%; Pred. No. 2.5e+02;
RESULT 964
ID ABL42496 standard; cDNA; 2956 BP.
DE Nucleophosmin 9.68 cDNA.
PN WO200206471-A1.
PD 24-JAN-2002.
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
Query Match 4.8%; Score 30.8; DB 6; Length 2956;
Best Local Similarity 55.7%; Pred. No. 2.5e+02;
RESULT 965
ID ADQ23232 standard; DNA; 3093 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6052.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.8%; Score 30.8; DB 12; Length 3093;
Best Local Similarity 57.1%; Pred. No. 2.5e+02;
RESULT 966
ID ADR73227 standard; DNA; 3126 BP.
DE Thale cress DNA regulating element (DRE) #5.
PN WO2004081173-A2.
PD 23-SEP-2004.
PA (EVOG-) EVOGENE LTD.
Query Match 4.8%; Score 30.8; DB 13; Length 3126;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
RESULT 967
ID ACN37890 standard; cDNA; 3169 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA324280, SEQ ID NO:1074.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 4.8%; Score 30.8; DB 13; Length 3169;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
RESULT 968
ID AAF59626 standard; cDNA; 4172 BP.
DE Human cell cycle and proliferation protein CCYPR-37 cDNA, SEQ ID NO:91.
PN WO200107471-A2.
PD 01-FEB-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 4.8%; Score 30.8; DB 4; Length 4172;
Best Local Similarity 50.0%; Pred. No. 2.9e+02;
RESULT 969
ID ACN37644 standard; cDNA; 4493 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA324062, SEQ ID NO:664.
PN WO2004030615-A2.

PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 4.8%; Score 30.8; DB 13; Length 4493;
Best Local Similarity 50.0%; Pred. No. 3e+02;
RESULT 970
ID ADF81603 standard; DNA; 4510 BP.
DE Leukaemia-related DNA sequence #2159.
PN WO2003039443-A2.
PD 15-MAY-2003.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAFE/) HAFERLACH T.
PA (SCHO/) SCHOCH C.
PA (KERN/) KERN W.
Query Match 4.8%; Score 30.8; DB 10; Length 4510;
Best Local Similarity 50.0%; Pred. No. 3e+02;
RESULT 971
ID AAH24065 standard; DNA; 4590 BP.
DE Yeast AOD9604-associated DNA sequence, SEQ ID NO:1.
PN WO200133977-A1.
PD 17-MAY-2001.
PA (META-) METABOLIC PHARM LTD.
Query Match 4.8%; Score 30.8; DB 5; Length 4590;
Best Local Similarity 9.9%; Pred. No. 3e+02;
RESULT 972
ID AAH98623 standard; cDNA; 4686 BP.
DE Human EST-derived coding sequence SEQ ID NO: 480.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.8%; Score 30.8; DB 4; Length 4686;
Best Local Similarity 50.0%; Pred. No. 3e+02;
RESULT 973
ID ADE09726 standard; DNA; 4686 BP.
DE Novel DNA-related contig nucleotide sequence #448.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 4.8%; Score 30.8; DB 10; Length 4686;
Best Local Similarity 50.0%; Pred. No. 3e+02;
RESULT 974
ID ADE09741 standard; DNA; 4686 BP.
DE Novel DNA-related contig nucleotide sequence #463.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 4.8%; Score 30.8; DB 10; Length 4686;
Best Local Similarity 50.0%; Pred. No. 3e+02;
RESULT 975
ID ADS11318 standard; DNA; 4686 BP.
DE Human therapeutic contig DNA - SEQ ID 1555.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 4.8%; Score 30.8; DB 13; Length 4686;
Best Local Similarity 50.0%; Pred. No. 3e+02;
RESULT 976
ID ADS11319 standard; DNA; 4686 BP.
DE Human therapeutic contig DNA - SEQ ID 1556.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 4.8%; Score 30.8; DB 13; Length 4686;
Best Local Similarity 50.0%; Pred. No. 3e+02;
RESULT 977
ID ADS09966 standard; DNA; 4688 BP.
DE Human therapeutic DNA - SEQ ID 203.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 4.8%; Score 30.8; DB 13; Length 4688;
Best Local Similarity 50.0%; Pred. No. 3e+02;
RESULT 978
ID ADS09965 standard; DNA; 4817 BP.
DE Human therapeutic DNA - SEQ ID 202.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 4.8%; Score 30.8; DB 13; Length 4817;
Best Local Similarity 50.0%; Pred. No. 3.1e+02;
RESULT 979
ID AAF62416 standard; DNA; 5000 BP.
DE A thaliana VRN1 gene.
PN WO200121822-A1.
PD 29-MAR-2001.
PA (PLAN-) PLANT BIOSCIENCE LTD.
Query Match 4.8%; Score 30.8; DB 4; Length 5000;
Best Local Similarity 53.3%; Pred. No. 3.1e+02;
RESULT 980
ID AAC74994 standard; cDNA; 5108 BP.
DE Human ORFX ORF549 polynucleotide sequence SEQ ID NO:1097.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 4.8%; Score 30.8; DB 3; Length 5108;
Best Local Similarity 50.0%; Pred. No. 3.2e+02;
RESULT 981
ID ABL32873 standard; DNA; 5250 BP.
DE Human immune system associated gene SEQ ID NO: 846.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.8%; Score 30.8; DB 6; Length 5250;
Best Local Similarity 55.6%; Pred. No. 3.2e+02;
RESULT 982
ID ADQ24871 standard; DNA; 5284 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7691.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.8%; Score 30.8; DB 12; Length 5284;
Best Local Similarity 48.5%; Pred. No. 3.2e+02;
RESULT 983
ID AAA10595 standard; DNA; 6741 BP.
DE Gene encoding a subunit of cellulose synthase.
PN JP2000060568-A.
PD 29-FEB-2000.
PA (MIZU/) MIZUNO K.
PA (OJIP) OJI PAPER CO.
Query Match 4.8%; Score 30.8; DB 3; Length 6741;
Best Local Similarity 17.0%; Pred. No. 3.6e+02;
RESULT 984
ID AAQ42541 standard; DNA; 8700 BP.
DE BglII/HpaII fragment of pTu32.
PN EP543195-A2.
PD 26-MAY-1993.
PA (THOM) THOMAE GMBH KARL.
Query Match 4.8%; Score 30.8; DB 2; Length 8700;
Best Local Similarity 53.3%; Pred. No. 4.1e+02;
RESULT 985
ID AAZ25496 standard; cDNA; 8700 BP.
DE S. epidermis plasmid sequence encoding epiA, B, C, D, P, Q, Y' and Y''.
PN US5962253-A.
PD 05-OCT-1999.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
Query Match 4.8%; Score 30.8; DB 2; Length 8700;
Best Local Similarity 53.3%; Pred. No. 4.1e+02;
RESULT 986
ID ABL16716 standard; DNA; 13837 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 1621.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.8%; Score 30.8; DB 4; Length 13837;
Best Local Similarity 49.4%; Pred. No. 5e+02;
RESULT 987

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ID   ADB68445 standard; DNA; 44096 BP.
DE   Human DCAL genomic DNA.
PN   WO2003055997-A1.
PD   10-JUL-2003.
PA   (ORDE-) ORDER OF SISTERS OF MERCY IN QUEENSLAND.
  Query Match             4.8%;  Score 30.8;  DB 10;  Length 44096;
  Best Local Similarity   63.5%;  Pred. No. 8.6e+02;
RESULT 988
  Query Match             4.8%;  Score 30.8;  DB 6;  Length 65237;
  Best Local Similarity   54.4%;  Pred. No. 1e+03;
RESULT 989
  Query Match             4.8%;  Score 30.8;  DB 6;  Length 65237;
  Best Local Similarity   54.4%;  Pred. No. 1e+03;
RESULT 990
  Query Match             4.8%;  Score 30.8;  DB 8;  Length 65237;
  Best Local Similarity   54.4%;  Pred. No. 1e+03;
RESULT 991
ID   ADO25290 standard; DNA; 80928 BP.
DE   Human protein kinase C iota/lambda genomic sequence.
PN   WO2004041212-A2.
PD   21-MAY-2004.
PA   (SACK/) SACKTOR T C.
PA   (CRAR/) CRARY J F.
PA   (HERN/) HERNANDEZ A I.
PA   (MIRR/) MIRRA S.
PA   (SHAO/) SHAO C.
  Query Match             4.8%;  Score 30.8;  DB 12;  Length 80928;
  Best Local Similarity   50.7%;  Pred. No. 1.1e+03;
RESULT 992
  Query Match             4.8%;  Score 30.8;  DB 10;  Length 92000;
  Best Local Similarity   54.4%;  Pred. No. 1.2e+03;
RESULT 993
ID   ABD33254 standard; DNA; 97415 BP.
DE   Murine cancer-associated (CA) gene MD07-043.
PN   WO2004058146-A2.
PD   15-JUL-2004.
PA   (SAGR-) SAGRES DISCOVERY INC.
  Query Match             4.8%;  Score 30.8;  DB 13;  Length 97415;
  Best Local Similarity   58.9%;  Pred. No. 1.2e+03;
RESULT 994
  Query Match             4.8%;  Score 30.8;  DB 6;  Length 110000;
  Best Local Similarity   55.7%;  Pred. No. 1.3e+03;
RESULT 995
ID   ABQ69245 standard; DNA; 3011208 BP.
DE   Listeria innocua DNA sequence #684.
PN   WO200228891-A2.
PD   11-APR-2002.
PA   (INSP ) INST PASTEUR.
PA   (CNRS ) CNRS CENT NAT RECH SCI.
  Query Match             4.8%;  Score 30.8;  DB 6;  Length 110000;
  Best Local Similarity   55.7%;  Pred. No. 1.3e+03;
RESULT 996
ID   ADO34435 standard; DNA; 634886 BP.
DE   Human SLIT-3 genomic sequence.
PN   WO2004042358-A2.
PD   21-MAY-2004.
PA   (DECO-) DECODE GENETICS EHF.
  Query Match             4.8%;  Score 30.8;  DB 12;  Length 110000;
  Best Local Similarity   50.0%;  Pred. No. 1.3e+03;
RESULT 997
ID   ABK83568 standard; DNA; 201143 BP.
DE   Human DNA differentially expressed in granulocytic cells #139.
PN   WO200228999-A2.
PD   11-APR-2002.
PA   (GENE-) GENE LOGIC INC.
  Query Match             4.8%;  Score 30.8;  DB 6;  Length 201143;
  Best Local Similarity   57.1%;  Pred. No. 1.7e+03;
RESULT 998
ID   ADQ59395 standard; DNA; 209612 BP.
DE   Human cancer-associated (CA) gene sequence SEQ ID NO:31.
PN   WO2004058288-A1.
PD   15-JUL-2004.
PA   (SAGR-) SAGRES DISCOVERY INC.
  Query Match             4.8%;  Score 30.8;  DB 12;  Length 209612;
  Best Local Similarity   52.3%;  Pred. No. 1.7e+03;
RESULT 999
ID   ACH17381 standard; cDNA; 401 BP.
DE   Human adult heart cDNA #1695.
PN   US2003073623-A1.
PD   17-APR-2003.
PA   (DRMA/) DRMANAC R T.
PA   (LABA/) LABAT I.
PA   (STAC/) STACHE-CRAIN B.
PA   (DICK/) DICKSON M C.
PA   (JONE/) JONES L W.
  Query Match             4.8%;  Score 30.6;  DB 9;  Length 401;
  Best Local Similarity   51.9%;  Pred. No. 1.1e+02;
RESULT 1000
ID   ABV57971 standard; cDNA; 500 BP.
DE   Human prostate expression marker cDNA 57962.
PN   WO200160860-A2.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match             4.8%;  Score 30.6;  DB 5;  Length 500;
  Best Local Similarity   58.1%;  Pred. No. 1.2e+02;
RESULT 1001
ID   ADD34721 standard; DNA; 563 BP.
DE   Mouse mitochondrial DNA sequence SEQ ID NO:2500.
PN   WO2003020220-A2.
PD   13-MAR-2003.
PA   (UYEM-) UNIV EMORY.
  Query Match             4.8%;  Score 30.6;  DB 10;  Length 563;
  Best Local Similarity   62.3%;  Pred. No. 1.3e+02;
RESULT 1002
ID   AAH05803 standard; cDNA; 571 BP.
DE   Human cDNA clone (5'-primer) SEQ ID NO:2638.
PN   EP1074617-A2.
PD   07-FEB-2001.
PA   (HELI-) HELIX RES INST.
  Query Match             4.8%;  Score 30.6;  DB 4;  Length 571;
  Best Local Similarity   55.1%;  Pred. No. 1.3e+02;
RESULT 1003
ID   ADD34722 standard; DNA; 589 BP.
DE   Mouse mitochondrial DNA sequence SEQ ID NO:2501.
PN   WO2003020220-A2.
PD   13-MAR-2003.
PA   (UYEM-) UNIV EMORY.
  Query Match             4.8%;  Score 30.6;  DB 10;  Length 589;
  Best Local Similarity   62.3%;  Pred. No. 1.3e+02;
RESULT 1004
ID   ADN13760 standard; cDNA; 606 BP.
DE   Human prostate/colon/lung/breast cancer-related cDNA 1275, SEQ:1275.
PN   WO2004039943-A2.
PD   13-MAY-2004.
PA   (CHIR ) CHIRON CORP.
  Query Match             4.8%;  Score 30.6;  DB 12;  Length 606;
  Best Local Similarity   47.9%;  Pred. No. 1.4e+02;
RESULT 1005
ID   AAZ60396 standard; DNA; 1020 BP.
DE   A diacylglycerol acyl transferase related sequence K07B1.4.
PN   WO200001713-A2.
PD   13-JAN-2000.
PA   (CALJ ) CALGENE LLC.
  Query Match             4.8%;  Score 30.6;  DB 3;  Length 1020;
  Best Local Similarity   56.4%;  Pred. No. 1.7e+02;
RESULT 1006
ID   AAC37023 standard; DNA; 1970 BP.
DE   Arabidopsis thaliana DNA fragment SEQ ID NO: 15904.
PN   EP1033405-A2.
PD   06-SEP-2000.
  Query Match             4.8%;  Score 30.6;  DB 3;  Length 1970;
  Best Local Similarity   52.8%;  Pred. No. 2.3e+02;
RESULT 1007
ID   ABN79836 standard; DNA; 2370 BP.
DE   Fungal ZBC gene sequence #73.
PN   WO200224865-A2.
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PD 28-MAR-2002.
PA (MICR-) MICROBIA INC.
Query Match 4.8%; Score 30.6; DB 6; Length 2370;
Best Local Similarity 50.3%; Pred. No. 2.5e+02;
RESULT 1008
ID AAV36165 standard; cDNA; 2491 BP.
DE Human trident transcription factor gene promoter region.
PN EP846761-A1.
PD 10-JUN-1998.
PA (INTR-) INTROGENE BV.
Query Match 4.8%; Score 30.6; DB 2; Length 2491;
Best Local Similarity 62.3%; Pred. No. 2.6e+02;
RESULT 1009
ID ABZ09975 standard; DNA; 2527 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #115.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.8%; Score 30.6; DB 8; Length 2527;
Best Local Similarity 53.8%; Pred. No. 2.6e+02;
RESULT 1010
ID ABZ10121 standard; DNA; 2527 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #261.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.8%; Score 30.6; DB 8; Length 2527;
Best Local Similarity 53.8%; Pred. No. 2.6e+02;
RESULT 1011
ID AAF16064 standard; cDNA; 2871 BP.
DE Human prostate cancer antigen nucleotide sequence SEQ ID NO:499.
PN WO200055174-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 4.8%; Score 30.6; DB 3; Length 2871;
Best Local Similarity 50.3%; Pred. No. 2.8e+02;
RESULT 1012
ID ABL16854 standard; DNA; 4947 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 2035.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.8%; Score 30.6; DB 4; Length 4947;
Best Local Similarity 48.1%; Pred. No. 3.6e+02;
RESULT 1013
ID ABL32316 standard; DNA; 5527 BP.
DE Human immune system associated gene SEQ ID NO: 289.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.8%; Score 30.6; DB 6; Length 5527;
Best Local Similarity 53.8%; Pred. No. 3.8e+02;
RESULT 1014
ID ABL54337 standard; DNA; 5527 BP.
DE Chemically treated apoptosis gene #19.
PN WO200177164-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.8%; Score 30.6; DB 6; Length 5527;
Best Local Similarity 53.8%; Pred. No. 3.8e+02;
RESULT 1015
ID ADB54325 standard; DNA; 5527 BP.
DE Pretreated genomic DNA region 249.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.8%; Score 30.6; DB 10; Length 5527;
Best Local Similarity 53.8%; Pred. No. 3.8e+02;
RESULT 1016
ID ADB54197 standard; DNA; 5527 BP.
DE Pretreated genomic DNA region 121.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.8%; Score 30.6; DB 10; Length 5527;
Best Local Similarity 53.8%; Pred. No. 3.8e+02;
RESULT 1017
ID ABL32338 standard; DNA; 5559 BP.
DE Human immune system associated gene SEQ ID NO: 311.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.8%; Score 30.6; DB 6; Length 5559;
Best Local Similarity 49.7%; Pred. No. 3.8e+02;
RESULT 1018
ID ABL32853 standard; DNA; 5999 BP.
DE Human immune system associated gene SEQ ID NO: 826.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.8%; Score 30.6; DB 6; Length 5999;
Best Local Similarity 55.0%; Pred. No. 3.9e+02;
RESULT 1019
ID ABK28192 standard; DNA; 5999 BP.
DE DNA transcription associated complementary genomic DNA #33.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.8%; Score 30.6; DB 6; Length 5999;
Best Local Similarity 55.0%; Pred. No. 3.9e+02;
RESULT 1020
ID ABL54343 standard; DNA; 6059 BP.
DE Chemically treated apoptosis gene #22.
PN WO200177164-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.8%; Score 30.6; DB 6; Length 6059;
Best Local Similarity 46.2%; Pred. No. 3.9e+02;
RESULT 1021
ID ACC42327 standard; cDNA; 6614 BP.
DE Human MAP kinase cascade activator #46 cDNA.
PN WO2003008589-A1.
PD 30-JAN-2003.
PA (ASAH) ASAHI KASEI KOGYO KK.
Query Match 4.8%; Score 30.6; DB 8; Length 6614;
Best Local Similarity 50.3%; Pred. No. 4.1e+02;
RESULT 1022
ID ADH14289 standard; cDNA; 6636 BP.
DE Human retinoblastoma 1 (RB1CC1) cDNA.
PN WO2003102028-A1.
PD 11-DEC-2003.
PA (OKAB/) OKABE H.
PA (IKEG/) IKEGAWA S.
PA (CHAN/) CHANO T.
Query Match 4.8%; Score 30.6; DB 12; Length 6636;
Best Local Similarity 50.3%; Pred. No. 4.1e+02;
RESULT 1023
ID ABL33895 standard; DNA; 6899 BP.
DE Human immune system associated gene SEQ ID NO: 1868.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.8%; Score 30.6; DB 6; Length 6899;
Best Local Similarity 51.9%; Pred. No. 4.2e+02;
RESULT 1024
ID AAK68674 standard; DNA; 9259 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23486.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.8%; Score 30.6; DB 4; Length 9259;
Best Local Similarity 55.0%; Pred. No. 4.8e+02;
RESULT 1025
ID AAK78818 standard; DNA; 10127 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33630.

PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.8%; Score 30.6; DB 4; Length 10127;
Best Local Similarity 47.6%; Pred. No. 5e+02;
RESULT 1026
ID AAK85169 standard; DNA; 23815 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39981.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.8%; Score 30.6; DB 4; Length 23815;
Best Local Similarity 55.0%; Pred. No. 7.5e+02;
RESULT 1027
ID AAK68678 standard; DNA; 23815 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23490.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.8%; Score 30.6; DB 4; Length 23815;
Best Local Similarity 55.0%; Pred. No. 7.5e+02;
RESULT 1028
ID ABS55821 standard; DNA; 69327 BP.
DE Human transporter protein gene.
Query Match 4.8%; Score 30.6; DB 6; Length 69327;
Best Local Similarity 49.7%; Pred. No. 1.2e+03;
RESULT 1029
ID ADL15741 standard; DNA; 69327 BP.
DE Novel human transporter genomic DNA.
Query Match 4.8%; Score 30.6; DB 12; Length 69327;
Best Local Similarity 49.7%; Pred. No. 1.2e+03;
RESULT 1030
Query Match 4.8%; Score 30.6; DB 12; Length 110000;
Best Local Similarity 48.1%; Pred. No. 1.5e+03;
RESULT 1031
ID ABL34175 standard; DNA; 113515 BP.
DE Human immune system associated gene SEQ ID NO: 2148.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.8%; Score 30.6; DB 6; Length 113515;
Best Local Similarity 44.4%; Pred. No. 1.5e+03;
RESULT 1032
ID ABK84797 standard; cDNA; 149671 BP.
DE Human cDNA differentially expressed in granulocytic cells #1368.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 4.8%; Score 30.6; DB 6; Length 149671;
Best Local Similarity 45.3%; Pred. No. 1.7e+03;
RESULT 1033
ID ADB70361 standard; cDNA; 149671 BP.
DE Moesin cDNA SEQ ID NO:53.
PN WO2003021229-A2.
PD 13-MAR-2003.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
Query Match 4.8%; Score 30.6; DB 9; Length 149671;
Best Local Similarity 45.3%; Pred. No. 1.7e+03;
RESULT 1034
ID ADJ37140 standard; cDNA; 149671 BP.
DE Human malignant pleural mesothelioma (MPM) cDNA #23.
PN US2003219760-A1.
PD 27-NOV-2003.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
Query Match 4.8%; Score 30.6; DB 12; Length 149671;
Best Local Similarity 45.3%; Pred. No. 1.7e+03;
RESULT 1035
ID ADO47191 standard; DNA; 200000 BP.
DE DNA sequence of a human immunoglobulin heavy chain variable region.
PN WO2004029249-A1.
PD 08-APR-2004.
PA (CENT-) CENTENARY INST CANCER MEDICINE & CELL BI.
Query Match 4.8%; Score 30.6; DB 12; Length 200000;
Best Local Similarity 58.1%; Pred. No. 1.9e+03;
RESULT 1036
ID ADP65796 standard; DNA; 270150 BP.
DE Human 16p133 sequence section 7 of 8 DNA.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 4.8%; Score 30.6; DB 11; Length 270150;
Best Local Similarity 49.1%; Pred. No. 2.2e+03;
RESULT 1037
ID ACC41530 standard; DNA; 246 BP.
DE Perennial ryegrass LpZTa3 fragment.
PN WO200290491-A2.
PD 14-NOV-2002.
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
PA (AGRE-) AGRESEARCH LTD.
Query Match 4.8%; Score 30.4; DB 8; Length 246;
Best Local Similarity 53.0%; Pred. No. 1e+02;
RESULT 1038
ID ABX54609 standard; cDNA; 391 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #4538.
PN US2002137160-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 4.8%; Score 30.4; DB 8; Length 391;
Best Local Similarity 47.4%; Pred. No. 1.3e+02;
RESULT 1039
ID AAF94893 standard; cDNA; 396 BP.
DE Human ovarian cancer associated coding sequence SEQ ID NO: 84.
PN WO200118046-A2.
PD 15-MAR-2001.
PA (CORI-) CORIXA CORP.
Query Match 4.8%; Score 30.4; DB 4; Length 396;
Best Local Similarity 51.1%; Pred. No. 1.3e+02;
RESULT 1040
ID ABL48843 standard; cDNA; 396 BP.
DE Ovarian carcinoma sequence isolate 24694.
PN US2002004491-A1.
PD 10-JAN-2002.
PA (XUJJ/) XU J.
PA (STOL/) STOLK J A.
PA (ALGA/) ALGATE P A.
PA (FLIN/) FLING S P.
Query Match 4.8%; Score 30.4; DB 6; Length 396;
Best Local Similarity 51.1%; Pred. No. 1.3e+02;
RESULT 1041
ID ABT03160 standard; cDNA; 396 BP.
DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 84.
PN WO200239885-A2.
PD 23-MAY-2002.
PA (CORI-) CORIXA CORP.
Query Match 4.8%; Score 30.4; DB 6; Length 396;
Best Local Similarity 51.1%; Pred. No. 1.3e+02;
RESULT 1042
ID ADM10753 standard; cDNA; 396 BP.
DE Human ovarian carcinoma-associated cDNA 24694.
PN US2003206918-A1.
PD 06-NOV-2003.
PA (CORI-) CORIXA CORP.
Query Match 4.8%; Score 30.4; DB 11; Length 396;
Best Local Similarity 51.1%; Pred. No. 1.3e+02;
RESULT 1043
ID ADJ11083 standard; cDNA; 396 BP.
DE Representative human ovarian carcinoma cDNA SeqID 84.
PN US2003232056-A1.
PD 18-DEC-2003.
PA (CORI-) CORIXA CORP.
Query Match 4.8%; Score 30.4; DB 12; Length 396;
Best Local Similarity 51.1%; Pred. No. 1.3e+02;
RESULT 1044

ID ADM43344 standard; cDNA; 396 BP.
DE Human ovarian carcinoma cDNA #84.
PN US2003129192-A1.
PD 10-JUL-2003.
PA (CORI-) CORIXA CORP.
Query Match 4.8%; Score 30.4; DB 12; Length 396;
Best Local Similarity 51.1%; Pred. No. 1.3e+02;
RESULT 1045
ID ADP93425 standard; cDNA; 436 BP.
DE Cotton expressed sequence tag, EST, #2436.
PN US2004123338-A1.
PD 24-JUN-2004.
PA (FINC/) FINCHER K L.
Query Match 4.8%; Score 30.4; DB 12; Length 436;
Best Local Similarity 53.3%; Pred. No. 1.3e+02;
RESULT 1046
ID AAK58136 standard; cDNA; 477 BP.
DE Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:3196.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.8%; Score 30.4; DB 4; Length 477;
Best Local Similarity 53.8%; Pred. No. 1.4e+02;
RESULT 1047
ID ABZ22262 standard; DNA; 615 BP.
DE Schwann cell specific enhancer consensus SCE1 nucleotide sequence #2.
PN WO200288352-A2.
PD 07-NOV-2002.
PA (UYMC-) UNIV MCGILL.
Query Match 4.8%; Score 30.4; DB 8; Length 615;
Best Local Similarity 17.2%; Pred. No. 1.6e+02;
RESULT 1048
ID ABQ88798 standard; cDNA; 750 BP.
DE Human prostate expressed polynucleotide SEQ ID NO 54.
PN WO200255700-A2.
PD 18-JUL-2002.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 4.8%; Score 30.4; DB 6; Length 750;
Best Local Similarity 52.5%; Pred. No. 1.7e+02;
RESULT 1049
ID ABZ22275 standard; DNA; 997 BP.
DE Mouse and human consensus SCE1 nucleotide sequence #2.
PN WO200288352-A2.
PD 07-NOV-2002.
PA (UYMC-) UNIV MCGILL.
Query Match 4.8%; Score 30.4; DB 8; Length 997;
Best Local Similarity 17.2%; Pred. No. 2e+02;
RESULT 1050
ID AAC57525 standard; DNA; 1001 BP.
DE Arachidonic acid metabolism related genomic biallelic marker #159.
PN WO200047771-A2.
PD 17-AUG-2000.
PA (GEST) GENSET.
Query Match 4.8%; Score 30.4; DB 3; Length 1001;
Best Local Similarity 51.5%; Pred. No. 2e+02;
RESULT 1051
ID ADI45546 standard; cDNA; 1093 BP.
DE Wheat isoprenoid biosynthesis-associated cDNA #6.
PN US2004010815-A1.
PD 15-JAN-2004.
PA (LANG/) LANGE B M.
PA (GHAS/) GHASSEMIAN M.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (MOUG/) MOUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
PA (ZHUT/) ZHU T.
Query Match 4.8%; Score 30.4; DB 12; Length 1093;
Best Local Similarity 55.8%; Pred. No. 2e+02;
RESULT 1052
ID ADQ08647 standard; DNA; 1288 BP.
DE Ciona intestinalis nervous system associated gene SeqID49.
PN JP2004057127-A.
PD 26-FEB-2004.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
Query Match 4.8%; Score 30.4; DB 12; Length 1288;
Best Local Similarity 63.9%; Pred. No. 2.2e+02;
RESULT 1053
ID ACA46752 standard; DNA; 2031 BP.
DE Prokaryotic essential gene #28409.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.8%; Score 30.4; DB 8; Length 2031;
Best Local Similarity 53.3%; Pred. No. 2.7e+02;
RESULT 1054
ID ABT42212 standard; DNA; 2246 BP.
DE Toxicity modelling related rat gene SEQ ID No 1914.
PN WO200295000-A2.
PD 28-NOV-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 4.8%; Score 30.4; DB 10; Length 2246;
Best Local Similarity 61.2%; Pred. No. 2.9e+02;
RESULT 1055
ID AAH55053 standard; DNA; 3078 BP.
DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:4417.
PN WO200134809-A2.
PD 17-MAY-2001.
PA (GLAX) GLAXO GROUP LTD.
Query Match 4.8%; Score 30.4; DB 4; Length 3078;
Best Local Similarity 53.3%; Pred. No. 3.3e+02;
RESULT 1056
ID ABL29032 standard; DNA; 3086 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 38569.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.8%; Score 30.4; DB 4; Length 3086;
Best Local Similarity 49.4%; Pred. No. 3.3e+02;
RESULT 1057
ID ABL15156 standard; cDNA; 3191 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 39950.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.8%; Score 30.4; DB 4; Length 3191;
Best Local Similarity 59.1%; Pred. No. 3.4e+02;
RESULT 1058
ID ABL15158 standard; cDNA; 3255 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 39956.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.8%; Score 30.4; DB 4; Length 3255;
Best Local Similarity 59.1%; Pred. No. 3.4e+02;
RESULT 1059
ID AAQ46544 standard; DNA; 3292 BP.
DE Yeast SSRP DNA sequence.
PN WO9313222-A1.
PD 08-JUL-1993.
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
Query Match 4.8%; Score 30.4; DB 2; Length 3292;
Best Local Similarity 47.8%; Pred. No. 3.4e+02;
RESULT 1060
ID AAV09625 standard; DNA; 3292 BP.
DE S. cerevisiae SSRP1 genomic DNA.
PN US5705334-A.
PD 06-JAN-1998.
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
Query Match 4.8%; Score 30.4; DB 2; Length 3292;

Best Local Similarity 47.8%; Pred. No. 3.4e+02;
RESULT 1061
ID ADA18598 standard; cDNA; 3292 BP.
DE Yeast DNA structure specific recognition protein (SSRP) cDNA.
PN US6475791-B1.
PD 05-NOV-2002.
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
Query Match 4.8%; Score 30.4; DB 10; Length 3292;
Best Local Similarity 47.8%; Pred. No. 3.4e+02;
RESULT 1062
ID ABK33953 standard; DNA; 3720 BP.
DE Human DNA for staging of Astrocytomas #19.
PN WO200202808-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.8%; Score 30.4; DB 6; Length 3720;
Best Local Similarity 50.0%; Pred. No. 3.6e+02;
RESULT 1063
ID ABZ10151 standard; DNA; 3720 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #291.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.8%; Score 30.4; DB 8; Length 3720;
Best Local Similarity 50.0%; Pred. No. 3.6e+02;
RESULT 1064
ID ABZ10005 standard; DNA; 3720 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #145.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.8%; Score 30.4; DB 8; Length 3720;
Best Local Similarity 50.0%; Pred. No. 3.6e+02;
RESULT 1065
ID ADA20408 standard; DNA; 3720 BP.
DE Prostate tumour related genomic DNA sample #37.
PN WO2002103042-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.8%; Score 30.4; DB 8; Length 3720;
Best Local Similarity 50.0%; Pred. No. 3.6e+02;
RESULT 1066
ID ADA84215 standard; DNA; 3720 BP.
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:73.
PN WO2002103041-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.8%; Score 30.4; DB 8; Length 3720;
Best Local Similarity 50.0%; Pred. No. 3.6e+02;
RESULT 1067
ID ADB54083 standard; DNA; 3720 BP.
DE Pretreated genomic DNA region 7.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.8%; Score 30.4; DB 10; Length 3720;
Best Local Similarity 50.0%; Pred. No. 3.6e+02;
RESULT 1068
ID ADB54211 standard; DNA; 3720 BP.
DE Pretreated genomic DNA region 135.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.8%; Score 30.4; DB 10; Length 3720;
Best Local Similarity 50.0%; Pred. No. 3.6e+02;
RESULT 1069
ID ADE84069 standard; DNA; 3720 BP.
DE Human lymphoid cell proliferative disorder gene derived DNA #5.
PN WO2003044226-A2.
PD 30-MAY-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.8%; Score 30.4; DB 10; Length 3720;
Best Local Similarity 50.0%; Pred. No. 3.6e+02;
RESULT 1070
ID ADE84145 standard; DNA; 3720 BP.
DE Human lymphoid cell proliferative disorder gene derived DNA #81.
PN WO2003044226-A2.
PD 30-MAY-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.8%; Score 30.4; DB 10; Length 3720;
Best Local Similarity 50.0%; Pred. No. 3.6e+02;
RESULT 1071
ID ADS89511 standard; DNA; 3720 BP.
DE Oligonucleotide of the invention SEQ ID NO:527.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.8%; Score 30.4; DB 13; Length 3720;
Best Local Similarity 50.0%; Pred. No. 3.6e+02;
RESULT 1072
ID ADS89237 standard; DNA; 3720 BP.
DE Oligonucleotide of the invention SEQ ID NO:253.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.8%; Score 30.4; DB 13; Length 3720;
Best Local Similarity 50.0%; Pred. No. 3.6e+02;
RESULT 1073
ID ABK52154 standard; DNA; 3893 BP.
DE Haemophilus influenzae strain A640164 BASB207 protein.
PN WO200232946-A2.
PD 25-APR-2002.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
Query Match 4.8%; Score 30.4; DB 6; Length 3893;
Best Local Similarity 53.3%; Pred. No. 3.7e+02;
RESULT 1074
ID ABL09800 standard; cDNA; 4510 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 23882.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.8%; Score 30.4; DB 4; Length 4510;
Best Local Similarity 49.4%; Pred. No. 4e+02;
RESULT 1075
ID ADS89480 standard; DNA; 4784 BP.
DE Oligonucleotide of the invention SEQ ID NO:496.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.8%; Score 30.4; DB 13; Length 4784;
Best Local Similarity 47.0%; Pred. No. 4.1e+02;
RESULT 1076
ID ADS89754 standard; DNA; 4784 BP.
DE Oligonucleotide of the invention SEQ ID NO:770.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.8%; Score 30.4; DB 13; Length 4784;
Best Local Similarity 47.0%; Pred. No. 4.1e+02;
RESULT 1077
ID ADR10423 standard; cDNA; 5202 BP.
DE Full length human cDNA useful for treating neurological disease Seq 3929.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 4.8%; Score 30.4; DB 13; Length 5202;
Best Local Similarity 53.3%; Pred. No. 4.2e+02;
RESULT 1078
ID AAQ31188 standard; cDNA; 5629 BP.
DE Alpha 6A integrin subunit cDNA.
PN WO9219647-A1.
PD 12-NOV-1992.
PA (SCRI) SCRIPPS RES INST.
Query Match 4.8%; Score 30.4; DB 2; Length 5629;
Best Local Similarity 47.0%; Pred. No. 4.4e+02;
RESULT 1079

ID AAV74495 standard; DNA; 6157 BP.
DE Staphylococcus aureus contig SEQ ID #184.
PN EP786519-A2.
PD 30-JUL-1997.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.8%; Score 30.4; DB 2; Length 6157;
Best Local Similarity 59.1%; Pred. No. 4.6e+02;
RESULT 1080
ID AAK73264 standard; DNA; 6550 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28076.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.8%; Score 30.4; DB 4; Length 6550;
Best Local Similarity 48.3%; Pred. No. 4.7e+02;
RESULT 1081
ID AAX84324 standard; DNA; 7312 BP.
DE Stealth virus nucleic acid clone, SEQ ID NO: 16.
PN WO9934019-A1.
PD 08-JUL-1999.
PA (MART/) MARTIN W J.
Query Match 4.8%; Score 30.4; DB 2; Length 7312;
Best Local Similarity 15.4%; Pred. No. 5e+02;
RESULT 1082
ID ADS36481 standard; DNA; 19986 BP.
DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1695.
PN WO2004083403-A2.
PD 30-SEP-2004.
PA (APPL-) APPLERA CORP.
Query Match 4.8%; Score 30.4; DB 13; Length 19986;
Best Local Similarity 48.8%; Pred. No. 7.9e+02;
RESULT 1083
ID AAI67784 standard; DNA; 26747 BP.
DE Nucleotide sequence of human NRG-4 DNA contig #2.
PN WO200181540-A2.
PD 01-NOV-2001.
PA (YEDA) YEDA RES & DEV CO LTD.
Query Match 4.8%; Score 30.4; DB 6; Length 26747;
Best Local Similarity 44.8%; Pred. No. 9.1e+02;
RESULT 1084
ID ADB37663 standard; DNA; 29993 BP.
DE Human chemically pretreated EYA4 gene SEQ ID NO:5.
PN WO2003072812-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.8%; Score 30.4; DB 10; Length 29993;
Best Local Similarity 43.8%; Pred. No. 9.6e+02;
RESULT 1085
ID ACN44464 standard; DNA; 31645 BP.
DE Mouse genomic sequence mCG1941.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 4.8%; Score 30.4; DB 11; Length 31645;
Best Local Similarity 48.8%; Pred. No. 9.8e+02;
RESULT 1086
ID ACN45214 standard; DNA; 76670 BP.
DE Human genomic sequence hCG30268.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 4.8%; Score 30.4; DB 11; Length 76670;
Best Local Similarity 48.3%; Pred. No. 1.5e+03;
RESULT 1087
ID ADA02600 standard; DNA; 96593 BP.
DE Human RUNX1 carcinoma associated gene, SEQ ID NO:1118.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 4.8%; Score 30.4; DB 9; Length 96593;
Best Local Similarity 52.3%; Pred. No. 1.6e+03;
RESULT 1088
ID ADB72338 standard; DNA; 96593 BP.
DE Human RUNX1 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 4.8%; Score 30.4; DB 10; Length 96593;
Best Local Similarity 52.3%; Pred. No. 1.6e+03;
RESULT 1089
ID ADE95848 standard; DNA; 96593 BP.
DE Human RUNX1 gene genomic DNA sequence.
PN WO2003039484-A2.
PD 15-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 4.8%; Score 30.4; DB 10; Length 96593;
Best Local Similarity 52.3%; Pred. No. 1.6e+03;
RESULT 1090
Query Match 4.8%; Score 30.4; DB 10; Length 110000;
Best Local Similarity 57.3%; Pred. No. 1.7e+03;
RESULT 1091
Query Match 4.8%; Score 30.4; DB 10; Length 110000;
Best Local Similarity 57.3%; Pred. No. 1.7e+03;
RESULT 1092
Query Match 4.8%; Score 30.4; DB 12; Length 110000;
Best Local Similarity 53.3%; Pred. No. 1.7e+03;
RESULT 1093
ID ADQ97260 standard; DNA; 150830 BP.
DE Mouse cancer associated sequence MD1-08-023, SEQ ID 236.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 4.8%; Score 30.4; DB 12; Length 150830;
Best Local Similarity 61.2%; Pred. No. 2e+03;
RESULT 1094
ID ADQ17784 standard; DNA; 154394 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 601.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.8%; Score 30.4; DB 12; Length 154394;
Best Local Similarity 51.5%; Pred. No. 2e+03;
RESULT 1095
ID ADO47192 standard; DNA; 200000 BP.
DE DNA sequence of a human immunoglobulin heavy chain variable region.
PN WO2004029249-A1.
PD 08-APR-2004.
PA (CENT-) CENTENARY INST CANCER MEDICINE & CELL BI.
Query Match 4.8%; Score 30.4; DB 12; Length 200000;
Best Local Similarity 55.8%; Pred. No. 2.2e+03;
RESULT 1096
ID ACN44002 standard; DNA; 228139 BP.
DE Human genomic sequence hCG37533.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 4.8%; Score 30.4; DB 11; Length 228139;
Best Local Similarity 55.8%; Pred. No. 2.3e+03;
RESULT 1097
ID ABD32598 standard; DNA; 290547 BP.
DE Human cancer-associated genomic DNA HD7-220.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 4.8%; Score 30.4; DB 13; Length 290547;
Best Local Similarity 55.8%; Pred. No. 2.6e+03;
RESULT 1098
ID ABV53493 standard; cDNA; 270 BP.
DE Human prostate expression marker cDNA 53484.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.7%; Score 30.2; DB 5; Length 270;
Best Local Similarity 55.1%; Pred. No. 1.2e+02;
RESULT 1099
ID ADI81887 standard; cDNA; 311 BP.

DE A. thaliana array-associated cDNA SEQ ID 89.
PN DE10204843-A1.
PD 14-AUG-2003.
PA (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEI.
Query Match 4.7%; Score 30.2; DB 10; Length 311;
Best Local Similarity 58.2%; Pred. No. 1.3e+02;
RESULT 1100
ID ADF79973 standard; DNA; 502 BP.
DE Leukaemia-related DNA sequence #529.
PN WO2003039443-A2.
PD 15-MAY-2003.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAFE/) HAFERLACH T.
PA (SCHO/) SCHOCH C.
PA (KERN/) KERN W.
Query Match 4.7%; Score 30.2; DB 10; Length 502;
Best Local Similarity 50.3%; Pred. No. 1.6e+02;
RESULT 1101
ID AAH11037 standard; cDNA; 512 BP.
DE Human cDNA clone (3'-primer) SEQ ID NO:7872.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 4.7%; Score 30.2; DB 4; Length 512;
Best Local Similarity 51.6%; Pred. No. 1.7e+02;
RESULT 1102
ID ABV51900 standard; cDNA; 559 BP.
DE Human prostate expression marker cDNA 51891.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.7%; Score 30.2; DB 5; Length 559;
Best Local Similarity 60.2%; Pred. No. 1.7e+02;
RESULT 1103
ID ADT94974 standard; cDNA; 566 BP.
DE Colon cancer associated human cDNA sequence #493.
PN US2003087818-A1.
PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match 4.7%; Score 30.2; DB 11; Length 566;
Best Local Similarity 51.1%; Pred. No. 1.7e+02;
RESULT 1104
ID AAS25091 standard; cDNA; 580 BP.
DE Human ovarian PCR-subtracted cDNA library clone #1272.
PN WO200157207-A2.
PD 09-AUG-2001.
PA (CORI-) CORIXA CORP.
Query Match 4.7%; Score 30.2; DB 4; Length 580;
Best Local Similarity 50.3%; Pred. No. 1.8e+02;
RESULT 1105
ID AAH83736 standard; cDNA; 580 BP.
DE Human ovarian tumour associated polynucleotide sequence SEQ ID NO:1360.
PN WO200151513-A2.
PD 19-JUL-2001.
PA (CORI-) CORIXA CORP.
Query Match 4.7%; Score 30.2; DB 5; Length 580;
Best Local Similarity 50.3%; Pred. No. 1.8e+02;
RESULT 1106
ID AAA81722 standard; DNA; 776 BP.
DE N. meningitidis partial DNA sequence gnm_269 SEQ ID NO:269.
PN WO200022430-A2.
PD 20-APR-2000.
PA (CHIR) CHIRON CORP.
Query Match 4.7%; Score 30.2; DB 3; Length 776;
Best Local Similarity 54.1%; Pred. No. 2e+02;
RESULT 1107
ID AAC84178 standard; DNA; 1044 BP.
DE Human OX2RH1.2 degenerate nucleotide sequence.
PN WO200070045-A1.
PD 23-NOV-2000.
PA (MEDI-) MEDICAL RES COUNCIL.
PA (SCHE) SCHERING CORP.
Query Match 4.7%; Score 30.2; DB 5; Length 1044;
Best Local Similarity 28.9%; Pred. No. 2.3e+02;
RESULT 1108
ID ADL62288 standard; DNA; 1729 BP.
DE Human ovarian cancer DNA marker #20500.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.7%; Score 30.2; DB 5; Length 1729;
Best Local Similarity 50.3%; Pred. No. 2.9e+02;
RESULT 1109
ID ADN04881 standard; cDNA; 1740 BP.
DE Antipsoriatic cDNA sequence #655.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 30.2; DB 12; Length 1740;
Best Local Similarity 51.1%; Pred. No. 2.9e+02;
RESULT 1110
ID ADR25770 standard; DNA; 1740 BP.
DE Breast cancer prognosis marker #1631.
PN WO2004065545-A2.
PD 05-AUG-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
PA (NECA-) NETHERLANDS CANCER INST.
Query Match 4.7%; Score 30.2; DB 13; Length 1740;
Best Local Similarity 51.1%; Pred. No. 2.9e+02;
RESULT 1111
ID ADP55291 standard; cDNA; 1740 BP.
DE Human PRO cDNA sequence SEQ ID NO:1267.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 30.2; DB 13; Length 1740;
Best Local Similarity 51.1%; Pred. No. 2.9e+02;
RESULT 1112
ID AAC76623 standard; cDNA; 1741 BP.
DE Human ORFX ORF2178 polynucleotide sequence SEQ ID NO:4355.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 4.7%; Score 30.2; DB 3; Length 1741;
Best Local Similarity 51.1%; Pred. No. 2.9e+02;
RESULT 1113
ID AAQ89459 standard; DNA; 1761 BP.
DE Saccharomyces carlsbergensis homothallism endonuclease gene.
PN JP07067664-A.
PD 14-MAR-1995.
PA (KIRI) KIRIN BREWERY KK.
Query Match 4.7%; Score 30.2; DB 2; Length 1761;
Best Local Similarity 62.7%; Pred. No. 2.9e+02;
RESULT 1114
ID ADG75764 standard; DNA; 1980 BP.
DE Human protein modification and maintenance molecule DNA SeqID88.
PN WO2003083084-A2.
PD 09-OCT-2003.
PA (INCY-) INCYTE CORP.
Query Match 4.7%; Score 30.2; DB 10; Length 1980;
Best Local Similarity 50.3%; Pred. No. 3.1e+02;
RESULT 1115
ID ADC08430 standard; DNA; 1999 BP.
DE Rice DNA sequence Seq ID735 related to grain filling.
PN WO2003000905-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 4.7%; Score 30.2; DB 10; Length 1999;
Best Local Similarity 60.2%; Pred. No. 3.1e+02;
RESULT 1116
ID AAZ40800 standard; DNA; 2025 BP.
DE Secreted protein EST coding sequence 108-006-5-0-E6-FL.
PN WO9940189-A2.
PD 12-AUG-1999.
PA (GEST) GENSET.

Query Match 4.7%; Score 30.2; DB 2; Length 2025;
Best Local Similarity 51.1%; Pred. No. 3.1e+02;
RESULT 1117
ID ADP19098 standard; cDNA; 2025 BP.
DE Human secreted polynucleotide #354.
PN US2004110939-A1.
PD 10-JUN-2004.
PA (GEST) GENSET SA.
Query Match 4.7%; Score 30.2; DB 12; Length 2025;
Best Local Similarity 51.1%; Pred. No. 3.1e+02;
RESULT 1118
ID ADM77777 standard; cDNA; 2026 BP.
DE Human cDNA #19.
PN US2003162176-A1.
PD 28-AUG-2003.
PA (EDWA/) EDWARDS J D M.
PA (DUCL/) DUCLERT A.
PA (BOUG/) BOUGUELERET L.
Query Match 4.7%; Score 30.2; DB 11; Length 2026;
Best Local Similarity 51.1%; Pred. No. 3.1e+02;
RESULT 1119
ID AAH16357 standard; cDNA; 2032 BP.
DE Human cDNA sequence SEQ ID NO:15289.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 4.7%; Score 30.2; DB 4; Length 2032;
Best Local Similarity 51.1%; Pred. No. 3.1e+02;
RESULT 1120
ID ADP18644 standard; cDNA; 2032 BP.
DE Human TAT403 cDNA used to treat cancer SeqID 4.
PN WO2004045516-A2.
PD 03-JUN-2004.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 30.2; DB 12; Length 2032;
Best Local Similarity 51.1%; Pred. No. 3.1e+02;
RESULT 1121
ID ABL90103 standard; cDNA; 2051 BP.
DE Human polynucleotide SEQ ID NO 665.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 30.2; DB 6; Length 2051;
Best Local Similarity 51.1%; Pred. No. 3.2e+02;
RESULT 1122
ID ADE08845 standard; DNA; 2368 BP.
DE Novel DNA-related contig nucleotide sequence #89.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 4.7%; Score 30.2; DB 10; Length 2368;
Best Local Similarity 51.1%; Pred. No. 3.4e+02;
RESULT 1123
ID ADQ84180 standard; cDNA; 2411 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #994.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 4.7%; Score 30.2; DB 13; Length 2411;
Best Local Similarity 53.9%; Pred. No. 3.4e+02;
RESULT 1124
ID ACN38730 standard; cDNA; 2411 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA325031, SEQ ID NO:2429.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 30.2; DB 13; Length 2411;
Best Local Similarity 53.9%; Pred. No. 3.4e+02;
RESULT 1125
ID AAK91412 standard; DNA; 2417 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 4988.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 30.2; DB 4; Length 2417;
Best Local Similarity 49.1%; Pred. No. 3.4e+02;
RESULT 1126
ID AAI57780 standard; DNA; 2417 BP.
DE Human colorectal cancer antigen coding sequence SEQ ID NO: 317.
PN WO200155350-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 30.2; DB 4; Length 2417;
Best Local Similarity 49.1%; Pred. No. 3.4e+02;
RESULT 1127
ID ABS99957 standard; DNA; 2417 BP.
DE Genomic DNA #161 encoding human colorectal cancer related protein.
PN US2002119919-A1.
PD 29-AUG-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 4.7%; Score 30.2; DB 6; Length 2417;
Best Local Similarity 49.1%; Pred. No. 3.4e+02;
RESULT 1128
ID ADB93110 standard; DNA; 2417 BP.
DE Human colorectal cancer related polypeptide DNA #161.
PN US2003054420-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 30.2; DB 10; Length 2417;
Best Local Similarity 49.1%; Pred. No. 3.4e+02;
RESULT 1129
ID ABL11384 standard; cDNA; 3000 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 28634.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.7%; Score 30.2; DB 4; Length 3000;
Best Local Similarity 56.6%; Pred. No. 3.8e+02;
RESULT 1130
ID ADE85003 standard; DNA; 3880 BP.
DE Farnesyl transferase inhibitor modulated leukemia associated gene #222.
PN WO2003038129-A2.
PD 08-MAY-2003.
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
Query Match 4.7%; Score 30.2; DB 10; Length 3880;
Best Local Similarity 50.3%; Pred. No. 4.3e+02;
RESULT 1131
ID ADF81402 standard; DNA; 3881 BP.
DE Leukaemia-related DNA sequence #1958.
PN WO2003039443-A2.
PD 15-MAY-2003.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAFE/) HAFERLACH T.
PA (SCHO/) SCHOCH C.
PA (KERN/) KERN W.
Query Match 4.7%; Score 30.2; DB 10; Length 3881;
Best Local Similarity 50.3%; Pred. No. 4.3e+02;
RESULT 1132
ID ADF81401 standard; DNA; 3881 BP.
DE Leukaemia-related DNA sequence #1957.
PN WO2003039443-A2.
PD 15-MAY-2003.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAFE/) HAFERLACH T.
PA (SCHO/) SCHOCH C.
PA (KERN/) KERN W.
Query Match 4.7%; Score 30.2; DB 10; Length 3881;
Best Local Similarity 50.3%; Pred. No. 4.3e+02;
RESULT 1133
ID ADP03064 standard; cDNA; 3881 BP.

DE Human housekeeping gene cDNA #105.
PN JP2004135552-A.
PD 13-MAY-2004.
PA (NIGA) NGK INSULATORS LTD.
Query Match 4.7%; Score 30.2; DB 12; Length 3881;
Best Local Similarity 50.3%; Pred. No. 4.3e+02;
RESULT 1134
ID ADS88562 standard; cDNA; 3881 BP.
DE Human housekeeping gene cDNA sequence SEQ ID NO:105.
PN WO2004035785-A1.
PD 29-APR-2004.
PA (NIGA) NGK INSULATORS LTD.
Query Match 4.7%; Score 30.2; DB 13; Length 3881;
Best Local Similarity 50.3%; Pred. No. 4.3e+02;
RESULT 1135
ID AAQ89458 standard; DNA; 3899 BP.
DE Saccharomyces carlsbergensis homothallism gene.
PN JP07067664-A.
PD 14-MAR-1995.
PA (KIRI) KIRIN BREWERY KK.
Query Match 4.7%; Score 30.2; DB 2; Length 3899;
Best Local Similarity 62.7%; Pred. No. 4.3e+02;
RESULT 1136
ID ABK83818 standard; cDNA; 4117 BP.
DE Human cDNA differentially expressed in granulocytic cells #389.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 4.7%; Score 30.2; DB 6; Length 4117;
Best Local Similarity 50.3%; Pred. No. 4.4e+02;
RESULT 1137
ID ADN04350 standard; cDNA; 4117 BP.
DE Antipsoriatic cDNA sequence #375.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 30.2; DB 12; Length 4117;
Best Local Similarity 50.3%; Pred. No. 4.4e+02;
RESULT 1138
ID ADF81686 standard; DNA; 4298 BP.
DE Leukaemia-related DNA sequence #2242.
PN WO2003039443-A2.
PD 15-MAY-2003.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAFE/) HAFERLACH T.
PA (SCHO/) SCHOCH C.
PA (KERN/) KERN W.
Query Match 4.7%; Score 30.2; DB 10; Length 4298;
Best Local Similarity 50.3%; Pred. No. 4.5e+02;
RESULT 1139
ID ADQ21780 standard; DNA; 4373 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 4600.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.7%; Score 30.2; DB 12; Length 4373;
Best Local Similarity 50.3%; Pred. No. 4.5e+02;
RESULT 1140
ID ABV30288 standard; cDNA; 4397 BP.
DE Human prostate expression marker cDNA 30279.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.7%; Score 30.2; DB 5; Length 4397;
Best Local Similarity 50.3%; Pred. No. 4.5e+02;
RESULT 1141
ID ABL34198 standard; DNA; 5316 BP.
DE Human immune system associated gene SEQ ID NO: 2171.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 30.2; DB 6; Length 5316;
Best Local Similarity 60.2%; Pred. No. 4.9e+02;
RESULT 1142
ID ABL16217 standard; DNA; 5718 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 124.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.7%; Score 30.2; DB 4; Length 5718;
Best Local Similarity 60.2%; Pred. No. 5.1e+02;
RESULT 1143
ID ADL62872 standard; DNA; 5861 BP.
DE Human ovarian cancer DNA marker #21084.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.7%; Score 30.2; DB 5; Length 5861;
Best Local Similarity 50.3%; Pred. No. 5.2e+02;
RESULT 1144
ID ABK39977 standard; DNA; 5933 BP.
DE Human chemically pretreated gene sequence #30 strand 1.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 30.2; DB 6; Length 5933;
Best Local Similarity 52.8%; Pred. No. 5.2e+02;
RESULT 1145
ID ACN92290 standard; DNA; 5969 BP.
DE Breast cancer related marker, seq id 13440.
PN US2003099974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 4.7%; Score 30.2; DB 11; Length 5969;
Best Local Similarity 50.3%; Pred. No. 5.2e+02;
RESULT 1146
ID ABL33646 standard; DNA; 6024 BP.
DE Human immune system associated gene SEQ ID NO: 1619.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 30.2; DB 6; Length 6024;
Best Local Similarity 49.7%; Pred. No. 5.2e+02;
RESULT 1147
ID AAS61177 standard; DNA; 6223 BP.
DE Human gene regulation-associated gene oligonucleotide #132.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 30.2; DB 6; Length 6223;
Best Local Similarity 43.5%; Pred. No. 5.3e+02;
RESULT 1148
ID ABL33776 standard; DNA; 6239 BP.
DE Human immune system associated gene SEQ ID NO: 1749.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 30.2; DB 6; Length 6239;
Best Local Similarity 53.9%; Pred. No. 5.3e+02;
RESULT 1149
ID ABK28297 standard; DNA; 6239 BP.
DE DNA transcription associated genomic DNA #86.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 30.2; DB 6; Length 6239;
Best Local Similarity 53.9%; Pred. No. 5.3e+02;
RESULT 1150
ID ABL16216 standard; DNA; 7285 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 121.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.7%; Score 30.2; DB 4; Length 7285;
Best Local Similarity 60.2%; Pred. No. 5.7e+02;

RESULT 1151
ID AAK68352 standard; DNA; 8952 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23164.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 30.2; DB 4; Length 8952;
Best Local Similarity 52.8%; Pred. No. 6.3e+02;
RESULT 1152
ID ABL34433 standard; DNA; 10151 BP.
DE Human immune system associated gene SEQ ID NO: 2406.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 30.2; DB 6; Length 10151;
Best Local Similarity 52.8%; Pred. No. 6.7e+02;
RESULT 1153
ID ABL26686 standard; DNA; 22319 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 31531.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.7%; Score 30.2; DB 4; Length 22319;
Best Local Similarity 52.8%; Pred. No. 9.6e+02;
RESULT 1154
ID AAA35185 standard; DNA; 32351 BP.
DE Human adenosine receptor related polynucleotide 2nd SEQ ID NO:59.
PN WO200009525-A2.
PD 24-FEB-2000.
PA (UYEC-) UNIV EAST CAROLINA.
Query Match 4.7%; Score 30.2; DB 3; Length 32351;
Best Local Similarity 58.2%; Pred. No. 1.1e+03;
RESULT 1155
ID AAF21307 standard; DNA; 32351 BP.
DE Human low adenosine antisense oligonucleotide related sequence #2874.
PN WO200062736-A2.
PD 26-OCT-2000.
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
Query Match 4.7%; Score 30.2; DB 3; Length 32351;
Best Local Similarity 58.2%; Pred. No. 1.1e+03;
RESULT 1156
ID ABZ97001 standard; DNA; 32351 BP.
DE Human nucleic acid sequence.
PN WO200285308-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Query Match 4.7%; Score 30.2; DB 10; Length 32351;
Best Local Similarity 58.2%; Pred. No. 1.1e+03;
RESULT 1157
ID ABD20850 standard; DNA; 32351 BP.
DE Human pulmonary and inflammatory target DNA #461.
PN WO200285309-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Query Match 4.7%; Score 30.2; DB 11; Length 32351;
Best Local Similarity 58.2%; Pred. No. 1.1e+03;
RESULT 1158
ID AAA35189 standard; DNA; 40298 BP.
DE Human adenosine receptor related polynucleotide 2nd SEQ ID NO:63.
PN WO200009525-A2.
PD 24-FEB-2000.
PA (UYEC-) UNIV EAST CAROLINA.
Query Match 4.7%; Score 30.2; DB 3; Length 40298;
Best Local Similarity 58.2%; Pred. No. 1.3e+03;
RESULT 1159
ID AAF21311 standard; DNA; 40298 BP.
DE Human low adenosine antisense oligonucleotide related sequence #2878.
PN WO200062736-A2.
PD 26-OCT-2000.
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
Query Match 4.7%; Score 30.2; DB 3; Length 40298;
Best Local Similarity 58.2%; Pred. No. 1.3e+03;
RESULT 1160
ID ABZ97005 standard; DNA; 40298 BP.
DE Human nucleic acid sequence.
PN WO200285308-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Query Match 4.7%; Score 30.2; DB 10; Length 40298;
Best Local Similarity 58.2%; Pred. No. 1.3e+03;
RESULT 1161
ID ABD20854 standard; DNA; 40298 BP.
DE Human pulmonary and inflammatory target DNA #465.
PN WO200285309-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Query Match 4.7%; Score 30.2; DB 11; Length 40298;
Best Local Similarity 58.2%; Pred. No. 1.3e+03;
RESULT 1162
ID AAK68184 standard; DNA; 40308 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22996.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 30.2; DB 4; Length 40308;
Best Local Similarity 49.1%; Pred. No. 1.3e+03;
RESULT 1163
ID ADI82557 standard; DNA; 63437 BP.
DE Human modifier of p21 (MP21) gene sequence SeqID123.
PN WO2004005486-A2.
PD 15-JAN-2004.
PA (EXEL-) EXELIXIS INC.
Query Match 4.7%; Score 30.2; DB 12; Length 63437;
Best Local Similarity 53.9%; Pred. No. 1.5e+03;
RESULT 1164
ID ADA02834 standard; DNA; 96596 BP.
DE Human MEF2C carcinoma associated gene, SEQ ID NO:1352.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 4.7%; Score 30.2; DB 9; Length 96596;
Best Local Similarity 56.6%; Pred. No. 1.9e+03;
RESULT 1165
ID ADB72572 standard; DNA; 96596 BP.
DE Human MEF2C gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 4.7%; Score 30.2; DB 10; Length 96596;
Best Local Similarity 56.6%; Pred. No. 1.9e+03;
RESULT 1166
ID ADC85313 standard; DNA; 96596 BP.
DE Mouse Mef2c coding sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 4.7%; Score 30.2; DB 10; Length 96596;
Best Local Similarity 56.6%; Pred. No. 1.9e+03;
RESULT 1167
ID ADM74429 standard; DNA; 96596 BP.
DE Human carcinoma associated (CA) nucleic acid #49.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.
PA (ENGE/) ENGELHARD E K.
Query Match 4.7%; Score 30.2; DB 12; Length 96596;
Best Local Similarity 56.6%; Pred. No. 1.9e+03;
RESULT 1168
ID ADI03931 standard; DNA; 99916 BP.
DE Human enzyme protein encoding genomic DNA.
PN WO200268657-A2.
PD 06-SEP-2002.
PA (PEKE) PE CORP NY.
Query Match 4.7%; Score 30.2; DB 6; Length 99916;

Best Local Similarity 48.5%; Pred. No. 1.9e+03;
RESULT 1169
Query Match 4.7%; Score 30.2; DB 2; Length 110000;
Best Local Similarity 58.2%; Pred. No. 2e+03;
RESULT 1170
ID ABL57909 standard; DNA; 368004 BP.
DE Human transporter protein gene.
Query Match 4.7%; Score 30.2; DB 6; Length 110000;
Best Local Similarity 49.7%; Pred. No. 2e+03;
RESULT 1171
Query Match 4.7%; Score 30.2; DB 13; Length 110000;
Best Local Similarity 47.6%; Pred. No. 2e+03;
RESULT 1172
ID AAX20249 standard; DNA; 116277 BP.
DE Borrelia burgdorferi polynucleotide sequence #2.
PN WO9858943-A1.
PD 30-DEC-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (MEDI-) MEDIMMUNE INC.
Query Match 4.7%; Score 30.2; DB 2; Length 116277;
Best Local Similarity 58.2%; Pred. No. 2e+03;
RESULT 1173
ID ADQ97587 standard; DNA; 116297 BP.
DE Human cancer associated sequence HD10-009, SEQ ID 564.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 4.7%; Score 30.2; DB 12; Length 116297;
Best Local Similarity 48.5%; Pred. No. 2e+03;
RESULT 1174
ID ABD32544 standard; DNA; 130505 BP.
DE Human cancer-associated genomic DNA HD7-024.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 4.7%; Score 30.2; DB 13; Length 130505;
Best Local Similarity 51.9%; Pred. No. 2.1e+03;
RESULT 1175
ID ADQ97957 standard; DNA; 191284 BP.
DE Mouse cancer associated sequence MD11-029, SEQ ID 934.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 4.7%; Score 30.2; DB 12; Length 191284;
Best Local Similarity 51.9%; Pred. No. 2.5e+03;
RESULT 1176
ID ACN44126 standard; DNA; 209484 BP.
DE Human genomic sequence hCG16187.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 4.7%; Score 30.2; DB 11; Length 209484;
Best Local Similarity 60.2%; Pred. No. 2.6e+03;
RESULT 1177
ID ABL62553 standard; DNA; 247 BP.
DE Colon adenocarcinoma related gene sequence SEQ ID NO:890.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 4.7%; Score 30; DB 6; Length 247;
Best Local Similarity 55.9%; Pred. No. 1.4e+02;
RESULT 1178
ID ABN95941 standard; DNA; 442 BP.
DE Gene #2439 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 4.7%; Score 30; DB 6; Length 442;
Best Local Similarity 51.5%; Pred. No. 1.8e+02;
RESULT 1179
ID ADI62601 standard; cDNA; 529 BP.
DE Human apoptosis-associated cDNA SEQ ID 44.
PN WO2003058021-A2.
PD 17-JUL-2003.
PA (XANT-) XANTOS BIOMEDICINE AG.
Query Match 4.7%; Score 30; DB 10; Length 529;
Best Local Similarity 55.9%; Pred. No. 1.9e+02;
RESULT 1180
ID ADN12680 standard; cDNA; 576 BP.
DE Human prostate/colon/lung/breast cancer-related cDNA 195, SEQ:195.
PN WO2004039943-A2.
PD 13-MAY-2004.
PA (CHIR) CHIRON CORP.
Query Match 4.7%; Score 30; DB 12; Length 576;
Best Local Similarity 48.8%; Pred. No. 2e+02;
RESULT 1181
ID AAC79806 standard; cDNA; 580 BP.
DE Human secreted protein gene 8 SEQ ID NO:18.
PN WO200058336-A1.
PD 05-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 30; DB 3; Length 580;
Best Local Similarity 51.5%; Pred. No. 2e+02;
RESULT 1182
ID ACA22190 standard; DNA; 666 BP.
DE Prokaryotic essential gene #3847.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.7%; Score 30; DB 8; Length 666;
Best Local Similarity 54.5%; Pred. No. 2.2e+02;
RESULT 1183
ID AAZ16278 standard; cDNA; 758 BP.
DE Human gene expression product cDNA sequence SEQ ID NO:3748.
PN WO9938972-A2.
PD 05-AUG-1999.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 4.7%; Score 30; DB 2; Length 758;
Best Local Similarity 54.5%; Pred. No. 2.3e+02;
RESULT 1184
ID AAC48694 standard; DNA; 802 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 58418.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.7%; Score 30; DB 3; Length 802;
Best Local Similarity 51.5%; Pred. No. 2.3e+02;
RESULT 1185
ID AAC42553 standard; DNA; 804 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 35989.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.7%; Score 30; DB 3; Length 804;
Best Local Similarity 51.5%; Pred. No. 2.4e+02;
RESULT 1186
ID AAS28197 standard; DNA; 805 BP.
DE Genomic sequence #37 encoding for novel human respiratory antigen.
PN WO200155448-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 30; DB 4; Length 805;
Best Local Similarity 54.5%; Pred. No. 2.4e+02;
RESULT 1187
ID ADG41393 standard; DNA; 805 BP.
DE Human respiratory system associated genomic DNA seq id 631.
PN US2003215893-A1.
PD 20-NOV-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 30; DB 10; Length 805;
Best Local Similarity 54.5%; Pred. No. 2.4e+02;
RESULT 1188
ID ADI97167 standard; DNA; 805 BP.
DE Human respiratory system associated polypeptide-related DNA SeqID631.
PN US2003077704-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 4.7%; Score 30; DB 11; Length 805;
Best Local Similarity 54.5%; Pred. No. 2.4e+02;
RESULT 1189
ID AAA08036 standard; cDNA; 830 BP.
DE Human protein transport molecule (PTAM) encoding cDNA SEQ ID NO:10.
PN WO200012703-A2.
PD 09-MAR-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 4.7%; Score 30; DB 3; Length 830;
Best Local Similarity 55.9%; Pred. No. 2.4e+02;
RESULT 1190
ID AAS26215 standard; cDNA; 864 BP.
DE Human cDNA encoding a novel secreted protein, Seq ID 394.
PN WO200155322-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 30; DB 4; Length 864;
Best Local Similarity 55.9%; Pred. No. 2.4e+02;
RESULT 1191
ID ABX73556 standard; DNA; 864 BP.
DE Human novel polynucleotide #384.
PN US2002132753-A1.
PD 19-SEP-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 4.7%; Score 30; DB 8; Length 864;
Best Local Similarity 55.9%; Pred. No. 2.4e+02;
RESULT 1192
ID ABA18653 standard; DNA; 865 BP.
DE Human nervous system related polynucleotide SEQ ID NO 10984.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 30; DB 5; Length 865;
Best Local Similarity 52.4%; Pred. No. 2.4e+02;
RESULT 1193
ID AAC52848 standard; DNA; 915 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 72648.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.7%; Score 30; DB 3; Length 915;
Best Local Similarity 51.5%; Pred. No. 2.5e+02;
RESULT 1194
ID ABT23476 standard; DNA; 919 BP.
DE Immune-related mouse DNA SEQ ID No 72.
PN WO2003002599-A2.
PD 09-JAN-2003.
PA (FARB) BAYER AG.
Query Match 4.7%; Score 30; DB 8; Length 919;
Best Local Similarity 46.6%; Pred. No. 2.5e+02;
RESULT 1195
ID ABN98593 standard; DNA; 941 BP.
DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 361.
PN US2002023281-A1.
PD 21-FEB-2002.
PA (GORL/) GORLACH J.
PA (ANYY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T M.
PA (YUYY/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHEW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
PA (KRIC/) KRICKER M.
PA (SLAT/) SLATER T.
PA (DAVI/) DAVIS K R.
PA (ALLE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURB/) HURBAN P.
Query Match 4.7%; Score 30; DB 6; Length 941;
Best Local Similarity 51.5%; Pred. No. 2.5e+02;
RESULT 1196
ID ACD28659 standard; DNA; 957 BP.
DE DNA encoding Bacillus megaterium YkoM.
PN US2002182690-A1.
PD 05-DEC-2002.
PA (CANN/) CANNON M C.
PA (CANN/) CANNON F C.
PA (MCCO/) MCCOOL G J.
PA (VALE/) VALENTINE H E.
PA (GRUY/) GRUYS K J.
Query Match 4.7%; Score 30; DB 9; Length 957;
Best Local Similarity 52.4%; Pred. No. 2.6e+02;
RESULT 1197
ID AAH51405 standard; DNA; 1001 BP.
DE Human UGT1A7 related DNA containing a biallelic polymorphism SEQ ID 296.
PN WO200058508-A2.
PD 05-OCT-2000.
PA (GEST) GENSET.
Query Match 4.7%; Score 30; DB 3; Length 1001;
Best Local Similarity 48.8%; Pred. No. 2.6e+02;
RESULT 1198
ID ADQ81148 standard; DNA; 1001 BP.
DE Human phenotype associated polynucleotide baySNP56978 SEQ ID NO:236.
PN WO2004067774-A2.
PD 12-AUG-2004.
PA (FARB) BAYER HEALTHCARE AG.
Query Match 4.7%; Score 30; DB 13; Length 1001;
Best Local Similarity 54.5%; Pred. No. 2.6e+02;
RESULT 1199
ID ACA22530 standard; DNA; 1188 BP.
DE Prokaryotic essential gene #4187.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.7%; Score 30; DB 8; Length 1188;
Best Local Similarity 54.5%; Pred. No. 2.8e+02;
RESULT 1200
ID AAS36418 standard; DNA; 1234 BP.
DE Human cardiovascular system antigen genomic DNA SEQ ID No 1918.
PN WO200155321-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 30; DB 4; Length 1234;
Best Local Similarity 48.8%; Pred. No. 2.9e+02;
RESULT 1201
ID ADE47112 standard; DNA; 1234 BP.
DE Human cardiovascular system related genomic DNA #678.
PN US2003059908-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 30; DB 10; Length 1234;
Best Local Similarity 48.8%; Pred. No. 2.9e+02;
RESULT 1202
ID ADJ08530 standard; DNA; 1234 BP.
DE Human cardiovascular system associated polypeptide-related DNA SeqID1918.
PN US2004005575-A1.
PD 08-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 30; DB 13; Length 1234;
Best Local Similarity 48.8%; Pred. No. 2.9e+02;
RESULT 1203
ID ADQ24751 standard; DNA; 1265 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7571.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.7%; Score 30; DB 12; Length 1265;
Best Local Similarity 51.5%; Pred. No. 2.9e+02;
RESULT 1204

ID ADI45092 standard; cDNA; 1270 BP.
DE Rice isoprenoid biosynthesis-associated cDNA #12.
PN US2004010815-A1.
PD 15-JAN-2004.
PA (LANG/) LANGE B M.
PA (GHAS/) GHASSEMIAN M.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (MOUG/) MOUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
PA (ZHUT/) ZHU T.
Query Match 4.7%; Score 30; DB 12; Length 1270;
Best Local Similarity 52.4%; Pred. No. 2.9e+02;
RESULT 1205
ID AAC34495 standard; DNA; 1301 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 6849.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.7%; Score 30; DB 3; Length 1301;
Best Local Similarity 52.4%; Pred. No. 2.9e+02;
RESULT 1206
ID AAS46419 standard; DNA; 1452 BP.
DE Tumour suppressor gene derived chemically modified sequence #141.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 30; DB 4; Length 1452;
Best Local Similarity 54.5%; Pred. No. 3.1e+02;
RESULT 1207
ID ABL33220 standard; DNA; 1452 BP.
DE Human immune system associated gene SEQ ID NO: 1193.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 30; DB 6; Length 1452;
Best Local Similarity 54.5%; Pred. No. 3.1e+02;
RESULT 1208
ID AAD30172 standard; DNA; 1561 BP.
DE Human UDP-glucuronosyl transferase (UGT1) gene exon 5.
PN WO200206523-A2.
PD 24-JAN-2002.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Query Match 4.7%; Score 30; DB 6; Length 1561;
Best Local Similarity 48.8%; Pred. No. 3.2e+02;
RESULT 1209
ID ACA28033 standard; DNA; 1632 BP.
DE Prokaryotic essential gene #9690.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.7%; Score 30; DB 8; Length 1632;
Best Local Similarity 51.5%; Pred. No. 3.3e+02;
RESULT 1210
ID ABZ16090 standard; DNA; 1963 BP.
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 3895.
PN WO200216655-A2.
PD 28-FEB-2002.
PA (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 4.7%; Score 30; DB 6; Length 1963;
Best Local Similarity 48.3%; Pred. No. 3.6e+02;
RESULT 1211
ID ABT42879 standard; DNA; 1971 BP.
DE Human neuroblastoma-related DNA sequence, SEQ ID NO:160.
PN WO2002103017-A1.
PD 27-DEC-2002.
PA (CHIB-) CHIBA PREFECTURE.
PA (HISM) HISAMITSU PHARM CO LTD.
Query Match 4.7%; Score 30; DB 8; Length 1971;
Best Local Similarity 64.3%; Pred. No. 3.6e+02;
RESULT 1212
ID AAS62458 standard; cDNA; 2017 BP.
DE cDNA sequence #245 encoding novel human secreted protein.
PN WO200177291-A2.
PD 18-OCT-2001.
PA (GEMY) GENETICS INST INC.
Query Match 4.7%; Score 30; DB 6; Length 2017;
Best Local Similarity 55.9%; Pred. No. 3.6e+02;
RESULT 1213
ID ABV24289 standard; cDNA; 2021 BP.
DE Human prostate expression marker cDNA 24280.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.7%; Score 30; DB 5; Length 2021;
Best Local Similarity 48.8%; Pred. No. 3.6e+02;
RESULT 1214
ID AAC60002 standard; cDNA; 2414 BP.
DE Human secreted protein gene 37 SEQ ID NO:47.
PN WO200058356-A1.
PD 05-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 30; DB 3; Length 2414;
Best Local Similarity 52.4%; Pred. No. 3.9e+02;
RESULT 1215
ID ADS45428 standard; cDNA; 2454 BP.
DE Bacterial polynucleotide #171.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 4.7%; Score 30; DB 13; Length 2454;
Best Local Similarity 53.4%; Pred. No. 4e+02;
RESULT 1216
ID ADM72569 standard; DNA; 2585 BP.
DE Nucleotide sequence of UGT allele UGT1A9*1.
PN WO2004027088-A2.
PD 01-APR-2004.
PA (UYLA-) UNIV LAVAL.
Query Match 4.7%; Score 30; DB 12; Length 2585;
Best Local Similarity 48.8%; Pred. No. 4.1e+02;
RESULT 1217
ID ADM72571 standard; DNA; 2585 BP.
DE Nucleotide sequence of UGT allele UGT1A9*3.
PN WO2004027088-A2.
PD 01-APR-2004.
PA (UYLA-) UNIV LAVAL.
Query Match 4.7%; Score 30; DB 12; Length 2585;
Best Local Similarity 48.8%; Pred. No. 4.1e+02;
RESULT 1218
ID ADM72570 standard; DNA; 2585 BP.
DE Nucleotide sequence of UGT allele UGT1A9*2.
PN WO2004027088-A2.
PD 01-APR-2004.
PA (UYLA-) UNIV LAVAL.
Query Match 4.7%; Score 30; DB 12; Length 2585;
Best Local Similarity 48.8%; Pred. No. 4.1e+02;
RESULT 1219
ID AAK94632 standard; cDNA; 2645 BP.
DE Human full-length cDNA, SEQ ID NO: 3603.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 4.7%; Score 30; DB 4; Length 2645;
Best Local Similarity 48.8%; Pred. No. 4.1e+02;
RESULT 1220
ID ADL31570 standard; cDNA; 2645 BP.
DE Full length human cDNA clone SeqID 3603.

PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 4.7%; Score 30; DB 12; Length 2645;
Best Local Similarity 48.8%; Pred. No. 4.1e+02;
RESULT 1221
ID ADJ84391 standard; DNA; 2956 BP.
DE Human phenotype associated (PA) gene SEQ ID NO:112.
PN EP1394267-A1.
PD 03-MAR-2004.
PA (FARB) BAYER HEALTHCARE AG.
Query Match 4.7%; Score 30; DB 12; Length 2956;
Best Local Similarity 54.5%; Pred. No. 4.3e+02;
RESULT 1222
ID ABL04598 standard; cDNA; 3017 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 8276.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.7%; Score 30; DB 4; Length 3017;
Best Local Similarity 48.8%; Pred. No. 4.4e+02;
RESULT 1223
ID ADA31375 standard; DNA; 3162 BP.
DE DNA encoding Acinetobacter baumannii protein #2662.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.7%; Score 30; DB 9; Length 3162;
Best Local Similarity 50.0%; Pred. No. 4.5e+02;
RESULT 1224
ID ACA21169 standard; DNA; 3192 BP.
DE Prokaryotic essential gene #2826.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.7%; Score 30; DB 8; Length 3192;
Best Local Similarity 50.0%; Pred. No. 4.5e+02;
RESULT 1225
ID ABL28186 standard; DNA; 3263 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 36031.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.7%; Score 30; DB 4; Length 3263;
Best Local Similarity 57.4%; Pred. No. 4.5e+02;
RESULT 1226
ID ADF13361 standard; DNA; 3276 BP.
DE Human Xanthine dehydrogenase DNA, SEQ ID 55.
PN WO2003072813-A2.
PD 04-SEP-2003.
PA (FARB) BAYER AG.
Query Match 4.7%; Score 30; DB 10; Length 3276;
Best Local Similarity 54.5%; Pred. No. 4.5e+02;
RESULT 1227
ID ADA53403 standard; cDNA; 3301 BP.
DE Human coding sequence, SEQ ID 971.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 4.7%; Score 30; DB 10; Length 3301;
Best Local Similarity 67.7%; Pred. No. 4.5e+02;
RESULT 1228
ID ABL03652 standard; cDNA; 3387 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 5438.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.7%; Score 30; DB 4; Length 3387;
Best Local Similarity 48.8%; Pred. No. 4.6e+02;
RESULT 1229
ID AAA70225 standard; DNA; 4056 BP.
DE Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:358.
PN WO200025728-A2.
PD 11-MAY-2000.
PA (HOFF/) HOFFMAN S.
PA (CARU/) CARUCCI D.
PA (GARD/) GARDNER M.
PA (VENT/) VENTER J C.
Query Match 4.7%; Score 30; DB 3; Length 4056;
Best Local Similarity 50.0%; Pred. No. 5e+02;
RESULT 1230
ID AAQ27189 standard; DNA; 4673 BP.
DE P. yoelii SSP2 antigen.
PN WO9211868-A1.
PD 23-JUL-1992.
PA (USNA) US SEC OF NAVY.
Query Match 4.7%; Score 30; DB 2; Length 4673;
Best Local Similarity 49.4%; Pred. No. 5.3e+02;
RESULT 1231
ID AAK84720 standard; DNA; 4840 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39532.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 30; DB 4; Length 4840;
Best Local Similarity 47.0%; Pred. No. 5.4e+02;
RESULT 1232
ID AAS46785 standard; DNA; 5986 BP.
DE Tumour suppressor gene derived chemically modified sequence #510.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 30; DB 4; Length 5986;
Best Local Similarity 47.8%; Pred. No. 6e+02;
RESULT 1233
ID AAS46783 standard; DNA; 5986 BP.
DE Tumour suppressor gene derived chemically modified sequence #508.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 30; DB 4; Length 5986;
Best Local Similarity 47.8%; Pred. No. 6e+02;
RESULT 1234
ID ABL34095 standard; DNA; 5986 BP.
DE Human immune system associated gene SEQ ID NO: 2068.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 30; DB 6; Length 5986;
Best Local Similarity 47.8%; Pred. No. 6e+02;
RESULT 1235
ID AAS61459 standard; DNA; 5986 BP.
DE Human gene regulation-associated gene oligonucleotide #414.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 30; DB 6; Length 5986;
Best Local Similarity 47.8%; Pred. No. 6e+02;
RESULT 1236
ID ABK28373 standard; DNA; 6074 BP.
DE DNA transcription associated genomic DNA #124.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 30; DB 6; Length 6074;
Best Local Similarity 55.9%; Pred. No. 6e+02;
RESULT 1237
ID AAX24302 standard; DNA; 6476 BP.
DE Murine mWRN gene (WRN homologue).
PN WO9906543-A1.
PD 11-FEB-1999.
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
Query Match 4.7%; Score 30; DB 2; Length 6476;
Best Local Similarity 54.5%; Pred. No. 6.2e+02;
RESULT 1238

ID AAA50142 standard; DNA; 7916 BP.
DE Bacilus megaterium polyhydroxyalkanoate biosynthesis gene region.
PN WO200040730-A1.
PD 13-JUL-2000.
PA (UYMA-) UNIV MASSACHUSETTS.
Query Match 4.7%; Score 30; DB 3; Length 7916;
Best Local Similarity 52.4%; Pred. No. 6.8e+02;
RESULT 1239
ID ACD28644 standard; DNA; 7916 BP.
DE Bacillus megaterium DNA fragment containing pha genes.
PN US2002182690-A1.
PD 05-DEC-2002.
PA (CANN/) CANNON M C.
PA (CANN/) CANNON F C.
PA (MCCO/) MCCOOL G J.
PA (VALE/) VALENTINE H E.
PA (GRUY/) GRUYS K J.
Query Match 4.7%; Score 30; DB 9; Length 7916;
Best Local Similarity 52.4%; Pred. No. 6.8e+02;
RESULT 1240
ID ADL12831 standard; cDNA; 8411 BP.
DE Human steroid-induced C3A liver cell cDNA #560.
PN US6673549-B1.
PD 06-JAN-2004.
PA (INCY-) INCYTE CORP.
Query Match 4.7%; Score 30; DB 12; Length 8411;
Best Local Similarity 48.3%; Pred. No. 7e+02;
RESULT 1241
ID ADE77058 standard; cDNA; 8412 BP.
DE Human cDNA differentially expressed in a liver disorder #163.
PN US2003108871-A1.
PD 12-JUN-2003.
PA (KASE/) KASER M R.
Query Match 4.7%; Score 30; DB 12; Length 8412;
Best Local Similarity 48.3%; Pred. No. 7e+02;
RESULT 1242
ID AAL04905 standard; DNA; 9431 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 7593.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 30; DB 4; Length 9431;
Best Local Similarity 61.5%; Pred. No. 7.4e+02;
RESULT 1243
ID ABL97799 standard; DNA; 9431 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2451.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 30; DB 4; Length 9431;
Best Local Similarity 61.5%; Pred. No. 7.4e+02;
RESULT 1244
ID AAL04904 standard; DNA; 9434 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 7592.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 30; DB 4; Length 9434;
Best Local Similarity 61.5%; Pred. No. 7.4e+02;
RESULT 1245
ID ABL97798 standard; DNA; 9434 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2450.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 30; DB 4; Length 9434;
Best Local Similarity 61.5%; Pred. No. 7.4e+02;
RESULT 1246
ID AAS45389 standard; DNA; 15732 BP.
DE Chemically pretreated complementary DNA associated with cell cycle #47.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 30; DB 4; Length 15732;
Best Local Similarity 49.4%; Pred. No. 9.4e+02;
RESULT 1247
ID ABK28234 standard; DNA; 15732 BP.
DE DNA transcription associated complementary genomic DNA #54.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 30; DB 6; Length 15732;
Best Local Similarity 49.4%; Pred. No. 9.4e+02;
RESULT 1248
ID AAS18543 standard; DNA; 18887 BP.
DE DNA encoding UDP glycosyltransferase 1 (UGT1A1).
PN WO200179230-A2.
PD 25-OCT-2001.
PA (GENA-) GENAISSANCE PHARM INC.
Query Match 4.7%; Score 30; DB 6; Length 18887;
Best Local Similarity 48.8%; Pred. No. 1e+03;
RESULT 1249
ID AAK78483 standard; DNA; 19597 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33295.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 30; DB 4; Length 19597;
Best Local Similarity 51.5%; Pred. No. 1e+03;
RESULT 1250
ID ABL19989 standard; DNA; 20448 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 11440.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.7%; Score 30; DB 4; Length 20448;
Best Local Similarity 47.3%; Pred. No. 1.1e+03;
RESULT 1251
ID ABL19988 standard; DNA; 24971 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 11437.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.7%; Score 30; DB 4; Length 24971;
Best Local Similarity 47.3%; Pred. No. 1.2e+03;
RESULT 1252
ID AAL04473 standard; DNA; 32249 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 7161.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 30; DB 4; Length 32249;
Best Local Similarity 51.5%; Pred. No. 1.3e+03;
RESULT 1253
ID ACN44080 standard; DNA; 44972 BP.
DE Mouse genomic sequence mCG14116.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 4.7%; Score 30; DB 11; Length 44972;
Best Local Similarity 50.0%; Pred. No. 1.5e+03;
RESULT 1254
ID AAK75029 standard; DNA; 49777 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:29841.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 30; DB 4; Length 49777;
Best Local Similarity 51.5%; Pred. No. 1.6e+03;
RESULT 1255
ID AAK76214 standard; DNA; 49777 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:31026.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 30; DB 4; Length 49777;

Best Local Similarity 51.5%; Pred. No. 1.6e+03;
RESULT 1256
ID ACN43902 standard; DNA; 58329 BP.
DE Human genomic sequence hCG15849.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 4.7%; Score 30; DB 11; Length 58329;
Best Local Similarity 52.4%; Pred. No. 1.7e+03;
RESULT 1257
ID ADA02864 standard; DNA; 96596 BP.
DE Human ITPR1 carcinoma associated gene, SEQ ID NO:1382.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 4.7%; Score 30; DB 9; Length 96596;
Best Local Similarity 50.7%; Pred. No. 2.2e+03;
RESULT 1258
ID ADB72602 standard; DNA; 96596 BP.
DE Human ITPR1 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 4.7%; Score 30; DB 10; Length 96596;
Best Local Similarity 50.7%; Pred. No. 2.2e+03;
RESULT 1259
ID ADC85343 standard; DNA; 96596 BP.
DE Mouse Itpr1 coding sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 4.7%; Score 30; DB 10; Length 96596;
Best Local Similarity 50.7%; Pred. No. 2.2e+03;
RESULT 1260
ID ADM74459 standard; DNA; 96596 BP.
DE Human carcinoma associated (CA) nucleic acid #64.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.
PA (ENGE/) ENGELHARD E K.
Query Match 4.7%; Score 30; DB 12; Length 96596;
Best Local Similarity 50.7%; Pred. No. 2.2e+03;
RESULT 1261
ID ADQ59410 standard; DNA; 103689 BP.
DE Human cancer-associated (CA) gene sequence SEQ ID NO:46.
PN WO2004058288-A1.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 4.7%; Score 30; DB 12; Length 103689;
Best Local Similarity 52.4%; Pred. No. 2.2e+03;
RESULT 1262
Query Match 4.7%; Score 30; DB 13; Length 110000;
Best Local Similarity 55.9%; Pred. No. 2.3e+03;
RESULT 1263
Query Match 4.7%; Score 30; DB 13; Length 110000;
Best Local Similarity 45.9%; Pred. No. 2.3e+03;
RESULT 1264
ID ABD33624 standard; DNA; 133787 BP.
DE Human cancer-associated (CA) gene HD07-127.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 4.7%; Score 30; DB 13; Length 133787;
Best Local Similarity 52.4%; Pred. No. 2.5e+03;
RESULT 1265
ID ADQ97146 standard; DNA; 348101 BP.
DE Human cancer associated sequence HD08-007, SEQ ID 122.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 4.7%; Score 30; DB 12; Length 348101;
Best Local Similarity 64.3%; Pred. No. 3.5e+03;
RESULT 1266
ID ADF58356 standard; cDNA; 204 BP.
DE Human polynucleotide sequence SEQ ID NO:723.
PN WO2003080795-A2.
PD 02-OCT-2003.
PA (HYSE-) HYSEQ INC.
Query Match 4.7%; Score 29.8; DB 10; Length 204;
Best Local Similarity 49.7%; Pred. No. 1.4e+02;
RESULT 1267
ID AAT03342 standard; DNA; 261 BP.
DE CD46 PCR product.
PN WO9523512-A1.
PD 08-SEP-1995.
PA (ALEX-) ALEXION PHARM INC.
Query Match 4.7%; Score 29.8; DB 2; Length 261;
Best Local Similarity 54.0%; Pred. No. 1.6e+02;
RESULT 1268
ID AAS32493 standard; DNA; 294 BP.
DE Human genomic DNA for novel endocrine antigen, SEQ ID No 447.
PN WO200155319-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 29.8; DB 4; Length 294;
Best Local Similarity 56.7%; Pred. No. 1.7e+02;
RESULT 1269
ID ACH31608 standard; cDNA; 345 BP.
DE Human bone marrow cDNA #899.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 4.7%; Score 29.8; DB 9; Length 345;
Best Local Similarity 58.4%; Pred. No. 1.8e+02;
RESULT 1270
ID AAC53132 standard; DNA; 482 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 73488.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.7%; Score 29.8; DB 3; Length 482;
Best Local Similarity 63.0%; Pred. No. 2.1e+02;
RESULT 1271
ID ADS71875 standard; cDNA; 539 BP.
DE Human kidney tumour specific cDNA, SEQ ID 472.
PN US2003109434-A1.
PD 12-JUN-2003.
PA (CORI-) CORIXA CORP.
Query Match 4.7%; Score 29.8; DB 7; Length 539;
Best Local Similarity 54.0%; Pred. No. 2.2e+02;
RESULT 1272
ID ADQ49807 standard; DNA; 597 BP.
DE Novel canine microarray-related DNA sequence SeqID1109.
PN WO2004063324-A2.
PD 29-JUL-2004.
PA (GENE-) GENE LOGIC INC.
PA (PFIZ) PFIZER PROD INC.
Query Match 4.7%; Score 29.8; DB 13; Length 597;
Best Local Similarity 49.3%; Pred. No. 2.4e+02;
RESULT 1273
ID AAC43018 standard; DNA; 645 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 37726.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.7%; Score 29.8; DB 3; Length 645;
Best Local Similarity 52.0%; Pred. No. 2.4e+02;
RESULT 1274
ID ABX66540 standard; DNA; 682 BP.
DE Helicobacter pylori selected interacting domain (SID) DNA #1139.
PN WO200266501-A2.
PD 29-AUG-2002.
PA (HYBR-) HYBRIGENICS.
PA (INSP) INST PASTEUR.

Query Match 4.7%; Score 29.8; DB 6; Length 682;
Best Local Similarity 45.2%; Pred. No. 2.5e+02;
RESULT 1275
ID ADD27484 standard; DNA; 798 BP.
DE Human adipocyte Selected Interacting Domain (SID) prey protein DNA #948.
PN WO200290544-A2.
PD 14-NOV-2002.
PA (HYBR-) HYBRIGENICS.
PA (LYNX-) LYNX THERAPEUTICS INC.
Query Match 4.7%; Score 29.8; DB 10; Length 798;
Best Local Similarity 54.0%; Pred. No. 2.7e+02;
RESULT 1276
ID ABQ68410 standard; DNA; 878 BP.
DE Listeria monocytogenes 4b contig DNA sequence #1176.
PN WO200228891-A2.
PD 11-APR-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 4.7%; Score 29.8; DB 6; Length 878;
Best Local Similarity 55.2%; Pred. No. 2.8e+02;
RESULT 1277
ID ACA34722 standard; DNA; 927 BP.
DE Prokaryotic essential gene #16379.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.7%; Score 29.8; DB 8; Length 927;
Best Local Similarity 45.2%; Pred. No. 2.9e+02;
RESULT 1278
ID AAQ14918 standard; DNA; 1389 BP.
DE CD46 clone pm5.3.
PN WO9118097-A.
PD 28-NOV-1991.
PA (UYME) UNIV MELBOURNE.
Query Match 4.7%; Score 29.8; DB 2; Length 1389;
Best Local Similarity 54.0%; Pred. No. 3.5e+02;
RESULT 1279
ID AAV60073 standard; DNA; 1422 BP.
DE Immunoreactive lambda 11 clone designated Lisa3.
PN US5814617-A.
PD 29-SEP-1998.
PA (USNA) US SEC OF NAVY.
Query Match 4.7%; Score 29.8; DB 2; Length 1422;
Best Local Similarity 48.5%; Pred. No. 3.5e+02;
RESULT 1280
ID AAQ14917 standard; DNA; 1431 BP.
DE CD46 clone pm5.10.
PN WO9118097-A.
PD 28-NOV-1991.
PA (UYME) UNIV MELBOURNE.
Query Match 4.7%; Score 29.8; DB 2; Length 1431;
Best Local Similarity 54.0%; Pred. No. 3.5e+02;
RESULT 1281
ID AAQ99106 standard; cDNA to mRNA; 1530 BP.
DE Human MCP (CD46) full-length cDNA.
PN WO9523856-A1.
PD 08-SEP-1995.
PA (ALEX-) ALEXION PHARM INC.
Query Match 4.7%; Score 29.8; DB 2; Length 1530;
Best Local Similarity 54.0%; Pred. No. 3.7e+02;
RESULT 1282
ID AAT03339 standard; cDNA to mRNA; 1530 BP.
DE Human CD46 cDNA.
PN WO9523512-A1.
PD 08-SEP-1995.
PA (ALEX-) ALEXION PHARM INC.
Query Match 4.7%; Score 29.8; DB 2; Length 1530;
Best Local Similarity 54.0%; Pred. No. 3.7e+02;
RESULT 1283
ID ABL04627 standard; cDNA; 1531 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 8363.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.7%; Score 29.8; DB 4; Length 1531;
Best Local Similarity 51.1%; Pred. No. 3.7e+02;
RESULT 1284
ID AAQ10864 standard; cDNA; 1546 BP.
DE Sequence encoding human membrane cofactor protein isoform with CYT2 C-
DE terminus.
PN WO9102002-A.
PD 21-FEB-1991.
PA (UNIW) UNIV WASHINGTON.
Query Match 4.7%; Score 29.8; DB 2; Length 1546;
Best Local Similarity 54.0%; Pred. No. 3.7e+02;
RESULT 1285
ID AAL51161 standard; cDNA; 1648 BP.
DE Nucleotide reductase 16-61 coding sequence.
PN CN1343778-A.
PD 10-APR-2002.
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
Query Match 4.7%; Score 29.8; DB 6; Length 1648;
Best Local Similarity 51.9%; Pred. No. 3.8e+02;
RESULT 1286
ID AAN50411 standard; DNA; 1707 BP.
DE Secretion enhancing sequence.
PN JP60058076-A.
PD 04-APR-1985.
PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
PA (NIIT) JAPAN MIN INT TRADE & IND.
Query Match 4.7%; Score 29.8; DB 1; Length 1707;
Best Local Similarity 55.2%; Pred. No. 3.8e+02;
RESULT 1287
ID AAC49693 standard; DNA; 1824 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 62090.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.7%; Score 29.8; DB 3; Length 1824;
Best Local Similarity 63.0%; Pred. No. 4e+02;
RESULT 1288
ID ADA71727 standard; DNA; 2000 BP.
DE Rice gene, SEQ ID 5052.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 4.7%; Score 29.8; DB 8; Length 2000;
Best Local Similarity 58.4%; Pred. No. 4.1e+02;
RESULT 1289
ID ACC60655 standard; DNA; 2000 BP.
DE Gene sequence #SEQ ID 92.
PN EP1258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZOME AG.
Query Match 4.7%; Score 29.8; DB 10; Length 2000;
Best Local Similarity 58.4%; Pred. No. 4.1e+02;
RESULT 1290
ID ADK63569 standard; DNA; 2000 BP.
DE Disease treating protein complex-derived gene #869.
PN EP1338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match 4.7%; Score 29.8; DB 10; Length 2000;
Best Local Similarity 58.4%; Pred. No. 4.1e+02;
RESULT 1291
ID ADK64149 standard; DNA; 2000 BP.
DE Disease treating protein complex-derived gene #1301.
PN EP1338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match 4.7%; Score 29.8; DB 10; Length 2000;
Best Local Similarity 58.4%; Pred. No. 4.1e+02;
RESULT 1292
ID ADL45830 standard; DNA; 2139 BP.
DE Human ovarian cancer DNA marker #19720.
PN WO200170979-A2.
PD 27-SEP-2001.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.7%; Score 29.8; DB 5; Length 2139;
Best Local Similarity 49.1%; Pred. No. 4.3e+02;
RESULT 1293
ID ACN41919 standard; cDNA; 2265 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:794.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 4.7%; Score 29.8; DB 13; Length 2265;
Best Local Similarity 54.0%; Pred. No. 4.4e+02;
RESULT 1294
ID ACN44937 standard; cDNA; 2399 BP.
DE Mouse mRNA sequence mCT5149.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 4.7%; Score 29.8; DB 11; Length 2399;
Best Local Similarity 48.0%; Pred. No. 4.5e+02;
RESULT 1295
ID AAX20301 standard; DNA; 2401 BP.
DE Borrelia burgdorferi polynucleotide sequence #54.
PN WO9858943-A1.
PD 30-DEC-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (MEDI-) MEDIMMUNE INC.
Query Match 4.7%; Score 29.8; DB 2; Length 2401;
Best Local Similarity 63.0%; Pred. No. 4.5e+02;
RESULT 1296
ID AAH15133 standard; cDNA; 2506 BP.
DE Human cDNA sequence SEQ ID NO:13185.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 4.7%; Score 29.8; DB 4; Length 2506;
Best Local Similarity 63.0%; Pred. No. 4.6e+02;
RESULT 1297
ID ADF76350 standard; cDNA; 2506 BP.
DE Novel human secreted and transmembrane protein cDNA SeqID 23.
PN WO2003072035-A2.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 29.8; DB 10; Length 2506;
Best Local Similarity 63.0%; Pred. No. 4.6e+02;
RESULT 1298
ID AAZ77559 standard; cDNA; 2627 BP.
DE Human ovarian tumor cDNA library derived EST fragment 110.
PN DE19817557-A1.
PD 21-OCT-1999.
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
Query Match 4.7%; Score 29.8; DB 2; Length 2627;
Best Local Similarity 54.0%; Pred. No. 4.7e+02;
RESULT 1299
ID ABQ70786 standard; DNA; 3037 BP.
DE Listeria monocytogenes 4b contig DNA sequence #728.
PN WO200228891-A2.
PD 11-APR-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 4.7%; Score 29.8; DB 6; Length 3037;
Best Local Similarity 55.2%; Pred. No. 5e+02;
RESULT 1300
ID AAF58337 standard; cDNA; 3206 BP.
DE Human GTP-binding associated protein #37 coding sequence.
PN WO200105970-A2.
PD 25-JAN-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 4.7%; Score 29.8; DB 4; Length 3206;
Best Local Similarity 63.0%; Pred. No. 5.2e+02;
RESULT 1301
ID ABK84595 standard; cDNA; 3225 BP.
DE Human cDNA differentially expressed in granulocytic cells #1166.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 4.7%; Score 29.8; DB 6; Length 3225;
Best Local Similarity 54.0%; Pred. No. 5.2e+02;
RESULT 1302
ID AAH34933 standard; cDNA; 3302 BP.
DE Human colon cancer antigen encoding cDNA SEQ ID NO:2015.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 29.8; DB 4; Length 3302;
Best Local Similarity 54.0%; Pred. No. 5.2e+02;
RESULT 1303
ID AAF18270 standard; DNA; 3308 BP.
DE Lung cancer associated polynucleotide sequence SEQ ID 289.
PN WO200055180-A2.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 4.7%; Score 29.8; DB 3; Length 3308;
Best Local Similarity 54.0%; Pred. No. 5.2e+02;
RESULT 1304
ID ABV76204 standard; DNA; 3385 BP.
DE Human nicotinamide N-methyltransferase gene.
PN WO200290512-A2.
PD 14-NOV-2002.
PA (GENA-) GENAISSANCE PHARM INC.
Query Match 4.7%; Score 29.8; DB 8; Length 3385;
Best Local Similarity 46.8%; Pred. No. 5.3e+02;
RESULT 1305
ID ACA27903 standard; DNA; 3726 BP.
DE Prokaryotic essential gene #9560.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.7%; Score 29.8; DB 8; Length 3726;
Best Local Similarity 56.7%; Pred. No. 5.5e+02;
RESULT 1306
ID AAL03716 standard; DNA; 3866 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 6404.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 29.8; DB 4; Length 3866;
Best Local Similarity 51.9%; Pred. No. 5.6e+02;
RESULT 1307
ID ABA07899 standard; DNA; 3866 BP.
DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 694.
PN WO200155325-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 29.8; DB 4; Length 3866;
Best Local Similarity 51.9%; Pred. No. 5.6e+02;
RESULT 1308
ID ADR06706 standard; cDNA; 3873 BP.
DE Full length human cDNA useful for treating neurological disease Seq 212.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 4.7%; Score 29.8; DB 13; Length 3873;
Best Local Similarity 52.9%; Pred. No. 5.6e+02;
RESULT 1309
ID ADE53995 standard; cDNA; 4435 BP.
DE Human prostate cancer cDNA #342.
PN US2003190640-A1.
PD 09-OCT-2003.
PA (FARI/) FARIS M.
PA (PEAR/) PEARSON C I.
Query Match 4.7%; Score 29.8; DB 10; Length 4435;
Best Local Similarity 46.8%; Pred. No. 6e+02;
RESULT 1310
ID ADQ96329 standard; cDNA; 5164 BP.
DE T cell activation associated cDNA #254.

PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAHI KASEI PHARMA CORP.
Query Match 4.7%; Score 29.8; DB 12; Length 5164;
Best Local Similarity 49.1%; Pred. No. 6.4e+02;
RESULT 1311
ID ABL32799 standard; DNA; 5193 BP.
DE Human immune system associated gene SEQ ID NO: 772.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 29.8; DB 6; Length 5193;
Best Local Similarity 56.7%; Pred. No. 6.5e+02;
RESULT 1312
ID ADF81602 standard; DNA; 5597 BP.
DE Leukaemia-related DNA sequence #2158.
PN WO2003039443-A2.
PD 15-MAY-2003.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAFE/) HAFERLACH T.
PA (SCHO/) SCHOCH C.
PA (KERN/) KERN W.
Query Match 4.7%; Score 29.8; DB 10; Length 5597;
Best Local Similarity 50.4%; Pred. No. 6.7e+02;
RESULT 1313
ID ADF82126 standard; DNA; 5880 BP.
DE Leukaemia-related DNA sequence #2682.
PN WO2003039443-A2.
PD 15-MAY-2003.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAFE/) HAFERLACH T.
PA (SCHO/) SCHOCH C.
PA (KERN/) KERN W.
Query Match 4.7%; Score 29.8; DB 10; Length 5880;
Best Local Similarity 46.7%; Pred. No. 6.8e+02;
RESULT 1314
ID AAK85188 standard; DNA; 5974 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40000.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 29.8; DB 4; Length 5974;
Best Local Similarity 55.2%; Pred. No. 6.9e+02;
RESULT 1315
ID ADJ12467 standard; DNA; 6171 BP.
DE DNA fragment of a BAC clone that encodes a human secreted protein Seq321.
PN US2004010132-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (BREW/) BREWER L A.
PA (DUAN/) DUAN R D.
PA (RUBE/) RUBEN S M.
PA (FLOR/) FLORENCE K A.
PA (GREE/) GREENE J M.
PA (YOUN/) YOUNG P E.
PA (FERR/) FERRIE A M.
PA (YUGG/) YU G.
PA (FLOR/) FLORENCE C.
PA (EBNE/) EBNER R.
PA (OLSE/) OLSEN H.
Query Match 4.7%; Score 29.8; DB 12; Length 6171;
Best Local Similarity 51.9%; Pred. No. 7e+02;
RESULT 1316
ID ADA19460 standard; DNA; 6307 BP.
DE Mouse LAT Y136F gene SEQ ID NO:1.
PN WO2003068968-A2.
PD 21-AUG-2003.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
Query Match 4.7%; Score 29.8; DB 9; Length 6307;
Best Local Similarity 56.7%; Pred. No. 7.1e+02;
RESULT 1317
ID AAK85189 standard; DNA; 7223 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40001.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 29.8; DB 4; Length 7223;
Best Local Similarity 55.2%; Pred. No. 7.5e+02;
RESULT 1318
ID ABL06304 standard; cDNA; 9012 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 13394.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.7%; Score 29.8; DB 4; Length 9012;
Best Local Similarity 48.0%; Pred. No. 8.3e+02;
RESULT 1319
ID ABL32362 standard; DNA; 15674 BP.
DE Human immune system associated gene SEQ ID NO: 335.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 29.8; DB 6; Length 15674;
Best Local Similarity 55.2%; Pred. No. 1.1e+03;
RESULT 1320
ID ABL34476 standard; DNA; 15674 BP.
DE Human metastasis associated gene SEQ ID NO: 29.
PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 29.8; DB 6; Length 15674;
Best Local Similarity 55.2%; Pred. No. 1.1e+03;
RESULT 1321
ID ABL70513 standard; DNA; 15674 BP.
DE Chemically treated cell signalling DNA sequence#202.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 29.8; DB 6; Length 15674;
Best Local Similarity 55.2%; Pred. No. 1.1e+03;
RESULT 1322
ID ADS99737 standard; DNA; 15674 BP.
DE Bisulphite treated human gene associated with metastasis #15.
PN US2003148327-A1.
PD 07-AUG-2003.
PA (OLEK/) OLEK A.
PA (PIEP/) PIEPENBROCK C.
PA (BERL/) BERLIN K.
Query Match 4.7%; Score 29.8; DB 7; Length 15674;
Best Local Similarity 55.2%; Pred. No. 1.1e+03;
RESULT 1323
ID ABL33206 standard; DNA; 15767 BP.
DE Human immune system associated gene SEQ ID NO: 1179.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 29.8; DB 6; Length 15767;
Best Local Similarity 66.2%; Pred. No. 1.1e+03;
RESULT 1324
ID ABL34552 standard; DNA; 15767 BP.
DE Human metastasis associated gene SEQ ID NO: 105.
PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 29.8; DB 6; Length 15767;
Best Local Similarity 66.2%; Pred. No. 1.1e+03;
RESULT 1325
ID ADS99813 standard; DNA; 15767 BP.
DE Bisulphite treated human gene associated with metastasis #53.
PN US2003148327-A1.
PD 07-AUG-2003.
PA (OLEK/) OLEK A.
PA (PIEP/) PIEPENBROCK C.
PA (BERL/) BERLIN K.

Query Match 4.7%; Score 29.8; DB 7; Length 15767;
Best Local Similarity 66.2%; Pred. No. 1.1e+03;
RESULT 1326
ID ABD33133 standard; DNA; 21986 BP.
DE Human cancer-associated (CA) gene HD07-015.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 4.7%; Score 29.8; DB 13; Length 21986;
Best Local Similarity 58.4%; Pred. No. 1.3e+03;
RESULT 1327
ID ACC00503 standard; DNA; 23434 BP.
DE Human histone deacetylase HDAC10 genomic DNA sequence, SEQ ID NO:4.
PN WO2003014340-A2.
PD 20-FEB-2003.
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS PHARMA GMBH.
Query Match 4.7%; Score 29.8; DB 8; Length 23434;
Best Local Similarity 66.2%; Pred. No. 1.3e+03;
RESULT 1328
ID ABL08132 standard; cDNA; 23710 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 18878.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.7%; Score 29.8; DB 4; Length 23710;
Best Local Similarity 54.0%; Pred. No. 1.3e+03;
RESULT 1329
ID ACN44720 standard; DNA; 32359 BP.
DE Mouse genomic sequence mCG2706.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 4.7%; Score 29.8; DB 11; Length 32359;
Best Local Similarity 66.2%; Pred. No. 1.5e+03;
RESULT 1330
ID ABK31511 standard; DNA; 47108 BP.
DE Signal transduction associated gene modified complementary DNA #177.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 29.8; DB 6; Length 47108;
Best Local Similarity 47.6%; Pred. No. 1.8e+03;
RESULT 1331
ID ACN44936 standard; DNA; 50460 BP.
DE Mouse genomic sequence mCG5738.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 4.7%; Score 29.8; DB 11; Length 50460;
Best Local Similarity 48.0%; Pred. No. 1.8e+03;
RESULT 1332
ID ABL16442 standard; DNA; 80251 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 799.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.7%; Score 29.8; DB 4; Length 80251;
Best Local Similarity 51.1%; Pred. No. 2.3e+03;
RESULT 1333
ID ABL16448 standard; DNA; 80251 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 817.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.7%; Score 29.8; DB 4; Length 80251;
Best Local Similarity 51.1%; Pred. No. 2.3e+03;
RESULT 1334
ID ACN44000 standard; DNA; 90026 BP.
DE Mouse genomic sequence mCG12663.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 4.7%; Score 29.8; DB 11; Length 90026;
Best Local Similarity 54.0%; Pred. No. 2.4e+03;
RESULT 1335
ID ABD33549 standard; DNA; 99291 BP.
DE Human cancer-associated (CA) gene HD07-109.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 4.7%; Score 29.8; DB 13; Length 99291;
Best Local Similarity 60.5%; Pred. No. 2.5e+03;
RESULT 1336
ID ACN44734 standard; DNA; 102980 BP.
DE Human genomic sequence hCG27644.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 4.7%; Score 29.8; DB 11; Length 102980;
Best Local Similarity 51.9%; Pred. No. 2.5e+03;
RESULT 1337
Query Match 4.7%; Score 29.8; DB 2; Length 110000;
Best Local Similarity 57.6%; Pred. No. 2.6e+03;
RESULT 1338
ID ABA03041 standard; DNA; 2944528 BP.
DE Listeria monocytogenes EGD-e genome sequence.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 4.7%; Score 29.8; DB 6; Length 110000;
Best Local Similarity 55.2%; Pred. No. 2.6e+03;
RESULT 1339
ID ACN43860 standard; DNA; 113633 BP.
DE Mouse genomic sequence mCG10208.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 4.7%; Score 29.8; DB 11; Length 113633;
Best Local Similarity 56.7%; Pred. No. 2.6e+03;
RESULT 1340
ID ACN44626 standard; DNA; 175077 BP.
DE Human genomic sequence hCG19724.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 4.7%; Score 29.8; DB 11; Length 175077;
Best Local Similarity 51.9%; Pred. No. 3.2e+03;
RESULT 1341
ID ADQ97831 standard; DNA; 199868 BP.
DE Mouse cancer associated sequence MD11-008, SEQ ID 808.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 4.7%; Score 29.8; DB 12; Length 199868;
Best Local Similarity 51.9%; Pred. No. 3.3e+03;
RESULT 1342
ID ABZ80229 standard; DNA; 249999 BP.
DE Human tramdorin gene region genomic DNA SEQ ID NO:26.
PN WO2003016502-A2.
PD 27-FEB-2003.
PA (MCLA-) MCLAUGHLIN RES INST.
Query Match 4.7%; Score 29.8; DB 8; Length 249999;
Best Local Similarity 56.7%; Pred. No. 3.6e+03;
RESULT 1343
ID ABD32730 standard; DNA; 260803 BP.
DE Human cancer-associated genomic DNA HD15-016.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 4.7%; Score 29.8; DB 13; Length 260803;
Best Local Similarity 56.7%; Pred. No. 3.7e+03;
RESULT 1344
ID ADK61432 standard; DNA; 298 BP.
DE Ovarian cancer-related DNA #587 with altered ovarian cancer expression.
PN WO2003068054-A2.

PD 21-AUG-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
Query Match 4.6%; Score 29.6; DB 10; Length 298;
Best Local Similarity 51.5%; Pred. No. 2e+02;
RESULT 1345
ID ABV11025 standard; cDNA; 410 BP.
DE Human prostate expression marker cDNA 11016.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.6%; Score 29.6; DB 5; Length 410;
Best Local Similarity 53.4%; Pred. No. 2.3e+02;
RESULT 1346
ID ACN89285 standard; DNA; 429 BP.
DE Breast cancer related marker, seq id 10435.
PN US2003099974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 4.6%; Score 29.6; DB 11; Length 429;
Best Local Similarity 68.3%; Pred. No. 2.3e+02;
RESULT 1347
ID ABV32173 standard; cDNA; 449 BP.
DE Human prostate expression marker cDNA 32164.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.6%; Score 29.6; DB 5; Length 449;
Best Local Similarity 53.4%; Pred. No. 2.4e+02;
RESULT 1348
ID ABV41105 standard; cDNA; 449 BP.
DE Human prostate expression marker cDNA 41096.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.6%; Score 29.6; DB 5; Length 449;
Best Local Similarity 53.4%; Pred. No. 2.4e+02;
RESULT 1349
ID AAI11134 standard; DNA; 476 BP.
DE Probe #1067 for gene expression analysis in human cervical cell sample.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 4.6%; Score 29.6; DB 4; Length 476;
Best Local Similarity 48.8%; Pred. No. 2.4e+02;
RESULT 1350
ID ABA52793 standard; DNA; 476 BP.
DE Human foetal liver single exon nucleic acid probe #1098.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 4.6%; Score 29.6; DB 4; Length 476;
Best Local Similarity 48.8%; Pred. No. 2.4e+02;
RESULT 1351
ID AAI32399 standard; DNA; 476 BP.
DE Probe #1085 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 4.6%; Score 29.6; DB 4; Length 476;
Best Local Similarity 48.8%; Pred. No. 2.4e+02;
RESULT 1352
ID ABA42366 standard; DNA; 476 BP.
DE Human breast cell single exon nucleic acid probe #1061.
PN WO200157271-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 4.6%; Score 29.6; DB 4; Length 476;
Best Local Similarity 48.8%; Pred. No. 2.4e+02;
RESULT 1353
ID ABA22578 standard; DNA; 476 BP.
DE Probe #1044 for gene expression analysis in human heart cell sample.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 4.6%; Score 29.6; DB 4; Length 476;
Best Local Similarity 48.8%; Pred. No. 2.4e+02;
RESULT 1354
ID AAK01047 standard; DNA; 476 BP.
DE Human brain expressed single exon probe SEQ ID NO: 1038.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 4.6%; Score 29.6; DB 4; Length 476;
Best Local Similarity 48.8%; Pred. No. 2.4e+02;
RESULT 1355
ID ABS26097 standard; DNA; 476 BP.
DE Human liver single exon probe, SEQ ID No 1087.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 4.6%; Score 29.6; DB 4; Length 476;
Best Local Similarity 48.8%; Pred. No. 2.4e+02;
RESULT 1356
ID AAI01052 standard; DNA; 476 BP.
DE Probe #1043 used to measure gene expression in human breast sample.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 4.6%; Score 29.6; DB 5; Length 476;
Best Local Similarity 48.8%; Pred. No. 2.4e+02;
RESULT 1357
ID ABS01095 standard; DNA; 476 BP.
DE Human genome-derived single exon probe from lung SEQ ID No 1086.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 4.6%; Score 29.6; DB 6; Length 476;
Best Local Similarity 48.8%; Pred. No. 2.4e+02;
RESULT 1358
ID ADL39536 standard; DNA; 490 BP.
DE Human ovarian cancer DNA marker #13426.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.6%; Score 29.6; DB 5; Length 490;
Best Local Similarity 59.5%; Pred. No. 2.5e+02;
RESULT 1359
ID ADE57765 standard; DNA; 571 BP.
DE Human gene AV703731, SEQ ID NO 3630.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 4.6%; Score 29.6; DB 10; Length 571;
Best Local Similarity 48.8%; Pred. No. 2.7e+02;
RESULT 1360
ID ADE57761 standard; DNA; 571 BP.
DE Human gene AV703731, SEQ ID NO 3626.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 4.6%; Score 29.6; DB 10; Length 571;
Best Local Similarity 48.8%; Pred. No. 2.7e+02;
RESULT 1361
ID ADE57769 standard; DNA; 571 BP.
DE Human gene AV703731, SEQ ID NO 3634.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 4.6%; Score 29.6; DB 10; Length 571;
Best Local Similarity 48.8%; Pred. No. 2.7e+02;
RESULT 1362
ID ADE57773 standard; DNA; 571 BP.

DE Human gene AV703731, SEQ ID NO 3638.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 4.6%; Score 29.6; DB 10; Length 571;
Best Local Similarity 48.8%; Pred. No. 2.7e+02;
RESULT 1363
ID AAI96371 standard; cDNA; 763 BP.
DE Human neuroblastoma expressed polynucleotide SEQ ID NO 2446.
PN WO200166719-A1.
PD 13-SEP-2001.
PA (CHIB-) CHIBA PREFECTURE.
PA (HISM) HISAMITSU PHARM CO LTD.
Query Match 4.6%; Score 29.6; DB 4; Length 763;
Best Local Similarity 47.1%; Pred. No. 3e+02;
RESULT 1364
ID ADH82490 standard; DNA; 777 BP.
DE Enterococcus faecalis polynucleotide #375.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 4.6%; Score 29.6; DB 10; Length 777;
Best Local Similarity 49.4%; Pred. No. 3.1e+02;
RESULT 1365
ID ADR61214 standard; cDNA; 803 BP.
DE Cotton cDNA sequence, SEQ ID 1995.
PN US2004181830-A1.
PD 16-SEP-2004.
PA (KOVA/) KOVALIC D K.
PA (ZHOU/) ZHOU Y.
PA (CAOY/) CAO Y.
Query Match 4.6%; Score 29.6; DB 13; Length 803;
Best Local Similarity 51.5%; Pred. No. 3.1e+02;
RESULT 1366
ID ADN13964 standard; cDNA; 870 BP.
DE Human prostate/colon/lung/breast cancer-related cDNA 1479, SEQ:1479.
PN WO2004039943-A2.
PD 13-MAY-2004.
PA (CHIR) CHIRON CORP.
Query Match 4.6%; Score 29.6; DB 12; Length 870;
Best Local Similarity 51.5%; Pred. No. 3.2e+02;
RESULT 1367
ID AAH51408 standard; DNA; 1001 BP.
DE Human UGT1A7 related DNA containing a biallelic polymorphism SEQ ID 299.
PN WO200058508-A2.
PD 05-OCT-2000.
PA (GEST) GENSET.
Query Match 4.6%; Score 29.6; DB 3; Length 1001;
Best Local Similarity 48.2%; Pred. No. 3.5e+02;
RESULT 1368
ID ABN93451 standard; cDNA; 1318 BP.
DE Human gene GS913839 coding sequence from chromosome 9q31-34 #3.
PN WO200071710-A2.
PD 30-NOV-2000.
PA (AVET) AVENTIS PHARMA SA.
Query Match 4.6%; Score 29.6; DB 4; Length 1318;
Best Local Similarity 57.6%; Pred. No. 3.9e+02;
RESULT 1369
ID AAZ96342 standard; DNA; 1477 BP.
DE S. pneumoniae derived DNA from ORF #170.
PN WO9806734-A1.
PD 19-FEB-1998.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 4.6%; Score 29.6; DB 2; Length 1477;
Best Local Similarity 56.0%; Pred. No. 4.1e+02;
RESULT 1370
ID ACA37143 standard; DNA; 1515 BP.
DE Prokaryotic essential gene #18800.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.6%; Score 29.6; DB 8; Length 1515;
Best Local Similarity 57.6%; Pred. No. 4.2e+02;
RESULT 1371
ID ADI43018 standard; DNA; 1571 BP.
DE Plant transcription factor polynucleotide #969.
PN US2004019927-A1.
PD 29-JAN-2004.
PA (SHER/) SHERMAN B K.
PA (RIEC/) RIECHMANN J L.
PA (JIAN/) JIANG C.
PA (HEAR/) HEARD J E.
PA (HAAK/) HAAKE V.
PA (CREE/) CREELMAN R A.
PA (RATC/) RATCLIFFE O.
PA (ADAM/) ADAM L J.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J.
PA (BROU/) BROUN P E.
PA (PILG/) PILGRIM M L.
PA (DUBE/) DUBELL A N.
PA (PINE/) PINEDA O.
PA (YUGG/) YU G.
Query Match 4.6%; Score 29.6; DB 12; Length 1571;
Best Local Similarity 61.8%; Pred. No. 4.3e+02;
RESULT 1372
ID ADO03156 standard; cDNA; 1571 BP.
DE Corn orthologue of Thalecress transcription factor, cDNA #160.
PN US2004045049-A1.
PD 04-MAR-2004.
PA (ZHAN/) ZHANG J.
PA (FROM/) FROMM M E.
PA (HEAR/) HEARD J E.
PA (RIEC/) RIECHMANN J L.
PA (ADAM/) ADAM L J.
PA (BROU/) BROUN P E.
PA (PINE/) PINEDA O.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J S.
PA (YUGG/) YU G.
PA (JIAN/) JIANG C.
PA (SAMA/) SAMAHA R S.
PA (PILG/) PILGRIM M L.
PA (CREE/) CREELMAN R A.
PA (DUBE/) DUBELL A N.
PA (RATC/) RATCLIFFE O.
PA (KUMI/) KUMIMOTO R.
PA (SHER/) SHERMAN B K.
Query Match 4.6%; Score 29.6; DB 12; Length 1571;
Best Local Similarity 61.8%; Pred. No. 4.3e+02;
RESULT 1373
ID ADC91460 standard; DNA; 1692 BP.
DE E. faecium DNA sequence SEQ ID 1087.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.6%; Score 29.6; DB 10; Length 1692;
Best Local Similarity 49.4%; Pred. No. 4.4e+02;
RESULT 1374
ID AAH15126 standard; cDNA; 1736 BP.
DE Human cDNA sequence SEQ ID NO:13174.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 4.6%; Score 29.6; DB 4; Length 1736;
Best Local Similarity 46.9%; Pred. No. 4.5e+02;
RESULT 1375
ID AAS74524 standard; cDNA; 1972 BP.
DE DNA encoding novel human diagnostic protein #10328.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.6%; Score 29.6; DB 5; Length 1972;
Best Local Similarity 57.6%; Pred. No. 4.7e+02;

RESULT 1376
ID AAC59339 standard; cDNA; 2405 BP.
DE Human secreted protein cDNA #5.
PN WO200056881-A1.
PD 28-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 4.6%; Score 29.6; DB 3; Length 2405;
Best Local Similarity 54.6%; Pred. No. 5.2e+02;
RESULT 1377
ID ABL01577 standard; cDNA; 2483 BP.
DE Human secreted protein encoding polynucleotide SEQ ID NO 22.
PN WO200183510-A1.
PD 08-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.6%; Score 29.6; DB 6; Length 2483;
Best Local Similarity 54.6%; Pred. No. 5.3e+02;
RESULT 1378
ID AAN81459 standard; DNA; 2520 BP.
DE C3 mutant gene encoding herbicide resistant form of ALS.
PN EP257993-A.
PD 02-MAR-1988.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 4.6%; Score 29.6; DB 1; Length 2520;
Best Local Similarity 54.6%; Pred. No. 5.3e+02;
RESULT 1379
ID AAQ11495 standard; DNA; 2520 BP.
DE Tobacco SURA-C3 mutant.
PN US5013659-A.
PD 07-MAY-1991.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 4.6%; Score 29.6; DB 2; Length 2520;
Best Local Similarity 54.6%; Pred. No. 5.3e+02;
RESULT 1380
ID AAQ28388 standard; DNA; 2520 BP.
DE Gene from the ALS C3 mutant of tobacco.
PN US5141870-A.
PD 25-AUG-1992.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 4.6%; Score 29.6; DB 2; Length 2520;
Best Local Similarity 54.6%; Pred. No. 5.3e+02;
RESULT 1381
ID AAQ81182 standard; DNA; 2520 BP.
DE ALS SURA-C3 (P197E) mutant gene.
PN US5378824-A.
PD 03-JAN-1995.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 4.6%; Score 29.6; DB 2; Length 2520;
Best Local Similarity 54.6%; Pred. No. 5.3e+02;
RESULT 1382
ID AAT33353 standard; DNA; 2520 BP.
DE Tobacco herbicide-resistant acetolactate synthase SURA-C3 gene.
PN EP730030-A1.
PD 04-SEP-1996.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 4.6%; Score 29.6; DB 2; Length 2520;
Best Local Similarity 54.6%; Pred. No. 5.3e+02;
RESULT 1383
ID AAT72862 standard; DNA; 2520 BP.
DE Tobacco C3 gene encoding herbicide resistant acetolactate synthase.
PN US5605011-A.
PD 25-FEB-1997.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 4.6%; Score 29.6; DB 2; Length 2520;
Best Local Similarity 54.6%; Pred. No. 5.3e+02;
RESULT 1384
ID AAX13335 standard; DNA; 2927 BP.
DE Enterococcus faecalis genome contig SEQ ID NO:398.
PN WO9850555-A2.
PD 12-NOV-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.6%; Score 29.6; DB 2; Length 2927;
Best Local Similarity 49.4%; Pred. No. 5.7e+02;

RESULT 1385
ID ABS99130 standard; DNA; 2927 BP.
DE Enterococcus faecalis contig sequence #398.
PN US2002120116-A1.
PD 29-AUG-2002.
PA (KUNS/) KUNSCH C A.
PA (DILL/) DILLON P J.
PA (BARA/) BARASH S.
Query Match 4.6%; Score 29.6; DB 6; Length 2927;
Best Local Similarity 49.4%; Pred. No. 5.7e+02;
RESULT 1386
ID ABL23940 standard; DNA; 3166 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 23293.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.6%; Score 29.6; DB 4; Length 3166;
Best Local Similarity 57.6%; Pred. No. 5.9e+02;
RESULT 1387
ID AAC91216 standard; DNA; 3291 BP.
DE Human GAR transformylase gene SEQ ID NO: 12.
PN WO200071754-A1.
PD 30-NOV-2000.
PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
Query Match 4.6%; Score 29.6; DB 5; Length 3291;
Best Local Similarity 51.5%; Pred. No. 6e+02;
RESULT 1388
ID ABL65868 standard; DNA; 3291 BP.
DE Lung cancer related gene sequence SEQ ID NO:4205.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 4.6%; Score 29.6; DB 6; Length 3291;
Best Local Similarity 51.5%; Pred. No. 6e+02;
RESULT 1389
ID ABL67257 standard; DNA; 3291 BP.
DE Thyroid cancer related gene sequence SEQ ID NO:5594.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 4.6%; Score 29.6; DB 6; Length 3291;
Best Local Similarity 51.5%; Pred. No. 6e+02;
RESULT 1390
ID ABL87915 standard; DNA; 3291 BP.
DE Human ovarian cancer related DNA clone SEQ ID NO:10893.
PN WO200192581-A2.
PD 06-DEC-2001.
PA (CORI-) CORIXA CORP.
Query Match 4.6%; Score 29.6; DB 6; Length 3291;
Best Local Similarity 51.5%; Pred. No. 6e+02;
RESULT 1391
ID ADK61431 standard; DNA; 3291 BP.
DE Ovarian cancer-related DNA #586 with altered ovarian cancer expression.
PN WO2003068054-A2.
PD 21-AUG-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
Query Match 4.6%; Score 29.6; DB 10; Length 3291;
Best Local Similarity 51.5%; Pred. No. 6e+02;
RESULT 1392
ID ADF55414 standard; DNA; 3515 BP.
DE Human DNA encoding a novel polypeptide #27.
PN JP2003245081-A.
PD 02-SEP-2003.
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.
Query Match 4.6%; Score 29.6; DB 10; Length 3515;
Best Local Similarity 57.6%; Pred. No. 6.2e+02;
RESULT 1393
ID ABV25489 standard; cDNA; 3586 BP.
DE Human prostate expression marker cDNA 25480.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Query Match 4.6%; Score 29.6; DB 5; Length 3586;
Best Local Similarity 51.5%; Pred. No. 6.3e+02;
RESULT 1394
ID ADQ22842 standard; DNA; 3956 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5662.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.6%; Score 29.6; DB 12; Length 3956;
Best Local Similarity 51.5%; Pred. No. 6.6e+02;
RESULT 1395
ID ABQ75511 standard; DNA; 5732 BP.
DE Murine PTP-lambda gene sequence SEQ ID NO:1.
PN WO200245493-A2.
PD 13-JUN-2002.
PA (DELT-) DELTAGEN INC.
Query Match 4.6%; Score 29.6; DB 6; Length 5732;
Best Local Similarity 57.6%; Pred. No. 7.8e+02;
RESULT 1396
ID ADB79776 standard; DNA; 5732 BP.
DE Rat putative receptor tyrosine phosphatase coding sequence, SEQ ID 16.
PN EP1279744-A2.
PD 29-JAN-2003.
PA (WARN) WARNER LAMBERT CO.
Query Match 4.6%; Score 29.6; DB 10; Length 5732;
Best Local Similarity 57.6%; Pred. No. 7.8e+02;
RESULT 1397
ID AAV15004 standard; DNA; 5769 BP.
DE Receptor protein tyrosine phosphatase lambda polypeptide coding sequence.
PN WO9744458-A1.
PD 27-NOV-1997.
PA (GETH) GENENTECH INC.
Query Match 4.6%; Score 29.6; DB 2; Length 5769;
Best Local Similarity 57.6%; Pred. No. 7.8e+02;
RESULT 1398
ID ABK31164 standard; DNA; 6133 BP.
DE Signal transduction associated gene modified DNA #4.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.6%; Score 29.6; DB 6; Length 6133;
Best Local Similarity 56.0%; Pred. No. 8e+02;
RESULT 1399
ID ABL70503 standard; DNA; 6133 BP.
DE Chemically treated cell signalling DNA sequence#197.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.6%; Score 29.6; DB 6; Length 6133;
Best Local Similarity 56.0%; Pred. No. 8e+02;
RESULT 1400
ID AAS61051 standard; DNA; 6133 BP.
DE Human gene regulation-associated gene oligonucleotide #6.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.6%; Score 29.6; DB 6; Length 6133;
Best Local Similarity 56.0%; Pred. No. 8e+02;
RESULT 1401
ID ABN79986 standard; DNA; 6133 BP.
DE Human chemically modified disease associated gene SEQ ID NO 3.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.6%; Score 29.6; DB 6; Length 6133;
Best Local Similarity 56.0%; Pred. No. 8e+02;
RESULT 1402
ID AAX02986 standard; DNA; 6210 BP.
DE Human IL-1ra BAC contiguous DNA sequence 31.
PN WO9906426-A1.
PD 11-FEB-1999.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match 4.6%; Score 29.6; DB 2; Length 6210;
Best Local Similarity 51.5%; Pred. No. 8.1e+02;
RESULT 1403
ID ABL07524 standard; cDNA; 6915 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 17054.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.6%; Score 29.6; DB 4; Length 6915;
Best Local Similarity 54.6%; Pred. No. 8.5e+02;
RESULT 1404
ID ABL04174 standard; cDNA; 7714 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 7004.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.6%; Score 29.6; DB 4; Length 7714;
Best Local Similarity 47.8%; Pred. No. 8.9e+02;
RESULT 1405
ID AAX76578 standard; cDNA; 7885 BP.
DE Human pancreas-specific tumour suppressor TSA305 gene SEQ ID NO:3.
PN WO9928457-A1.
PD 10-JUN-1999.
PA (SAKA) OTSUKA PHARM CO LTD.
Query Match 4.6%; Score 29.6; DB 2; Length 7885;
Best Local Similarity 50.7%; Pred. No. 9e+02;
RESULT 1406
ID ABK89799 standard; DNA; 8367 BP.
DE Anther specific cotton gene CoFS.
PN WO200257470-A1.
PD 25-JUL-2002.
PA (MOLE-) INST MOLECULAR AGROBIOLOGY.
Query Match 4.6%; Score 29.6; DB 6; Length 8367;
Best Local Similarity 46.9%; Pred. No. 9.3e+02;
RESULT 1407
ID ABL49301 standard; DNA; 10467 BP.
DE Human polynucleotide associated with DNA replication SEQ ID NO 1.
PN WO200177377-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.6%; Score 29.6; DB 6; Length 10467;
Best Local Similarity 50.0%; Pred. No. 1e+03;
RESULT 1408
ID ABL14976 standard; cDNA; 12714 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 39410.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.6%; Score 29.6; DB 4; Length 12714;
Best Local Similarity 52.3%; Pred. No. 1.1e+03;
RESULT 1409
ID AAV21211 standard; DNA; 16550 BP.
DE Methanococcus jannaschii small circular extrachromosomal element.
PN WO9807830-A2.
PD 26-FEB-1998.
PA (GENO-) INST GENOMIC RES.
PA (UNII) UNIV ILLINOIS FOUND.
PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
Query Match 4.6%; Score 29.6; DB 2; Length 16550;
Best Local Similarity 51.5%; Pred. No. 1.3e+03;
RESULT 1410
ID ADB16930 standard; DNA; 17386 BP.
DE Human DYXC1 DNA, chromosomal gene region nucleotides 200001-217386.
PN WO2003068814-A1.
PD 21-AUG-2003.
PA (LICN) LICENTIA LTD.
Query Match 4.6%; Score 29.6; DB 9; Length 17386;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
RESULT 1411
ID ADE36585 standard; DNA; 26639 BP.
DE Mouse mCG2257 gene genomic DNA sequence SEQ ID NO:1.
PN WO2003080639-A1.
PD 02-OCT-2003.
PA (SAGR-) SAGRES DISCOVERY.

Query Match 4.6%; Score 29.6; DB 10; Length 26639;
Best Local Similarity 54.6%; Pred. No. 1.6e+03;
RESULT 1412
ID ADA03059 standard; DNA; 26642 BP.
DE Mouse Kcnj9 carcinoma associated gene, SEQ ID NO:1577.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 4.6%; Score 29.6; DB 9; Length 26642;
Best Local Similarity 54.6%; Pred. No. 1.6e+03;
RESULT 1413
ID ADA66343 standard; DNA; 26642 BP.
DE Mouse Kcnj9 gene genomic DNA sequence.
PN WO2003053224-A2.
PD 03-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 4.6%; Score 29.6; DB 9; Length 26642;
Best Local Similarity 54.6%; Pred. No. 1.6e+03;
RESULT 1414
ID ADB72797 standard; DNA; 26642 BP.
DE Mouse Kcnj9 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 4.6%; Score 29.6; DB 10; Length 26642;
Best Local Similarity 54.6%; Pred. No. 1.6e+03;
RESULT 1415
ID ADL27137 standard; DNA; 26642 BP.
DE Mouse genomic sequence for Kcnj9.
PN US2003216558-A1.
PD 20-NOV-2003.
PA (MORR/) MORRIS D W.
PA (ENGE/) ENGELHARD E K.
Query Match 4.6%; Score 29.6; DB 11; Length 26642;
Best Local Similarity 54.6%; Pred. No. 1.6e+03;
RESULT 1416
ID ABD33593 standard; DNA; 27901 BP.
DE Murine cancer-associated (CA) gene MD07-120.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 4.6%; Score 29.6; DB 13; Length 27901;
Best Local Similarity 54.6%; Pred. No. 1.6e+03;
RESULT 1417
ID ABL55857 standard; DNA; 34337 BP.
DE Human GABA transporter protein gene.
PN US2002031800-A1.
PD 14-MAR-2002.
PA (LIZZ/) LI Z.
PA (CHAT/) CHATURVEDI K.
PA (ZHUS/) ZHU S.
PA (WOOD/) WOODAGE T.
PA (GUEG/) GUEGLER K.
PA (WEBS/) WEBSTER M.
PA (DFRA/) DI FRANCESCO V.
PA (BEAS/) BEASLEY E M.
Query Match 4.6%; Score 29.6; DB 6; Length 34337;
Best Local Similarity 54.6%; Pred. No. 1.8e+03;
RESULT 1418
ID ADG88376 standard; DNA; 34337 BP.
DE Human transporter gene.
PN US2003157649-A1.
PD 21-AUG-2003.
PA (APPL-) APPLERA CORP.
Query Match 4.6%; Score 29.6; DB 10; Length 34337;
Best Local Similarity 54.6%; Pred. No. 1.8e+03;
RESULT 1419
ID ABL34196 standard; DNA; 37973 BP.
DE Human immune system associated gene SEQ ID NO: 2169.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.6%; Score 29.6; DB 6; Length 37973;
Best Local Similarity 51.5%; Pred. No. 1.9e+03;
RESULT 1420
ID AAK77833 standard; DNA; 44354 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32645.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.6%; Score 29.6; DB 4; Length 44354;
Best Local Similarity 51.5%; Pred. No. 2e+03;
RESULT 1421
ID AAK77836 standard; DNA; 44354 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32648.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.6%; Score 29.6; DB 4; Length 44354;
Best Local Similarity 51.5%; Pred. No. 2e+03;
RESULT 1422
ID AAK77837 standard; DNA; 44354 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32649.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.6%; Score 29.6; DB 4; Length 44354;
Best Local Similarity 51.5%; Pred. No. 2e+03;
RESULT 1423
ID ACN44528 standard; DNA; 49806 BP.
DE Mouse genomic sequence mCG20647.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 4.6%; Score 29.6; DB 11; Length 49806;
Best Local Similarity 57.6%; Pred. No. 2.1e+03;
RESULT 1424
Query Match 4.6%; Score 29.6; DB 12; Length 55211;
Best Local Similarity 59.5%; Pred. No. 2.2e+03;
RESULT 1425
Query Match 4.6%; Score 29.6; DB 10; Length 65186;
Best Local Similarity 59.5%; Pred. No. 2.4e+03;
RESULT 1426
Query Match 4.6%; Score 29.6; DB 12; Length 84973;
Best Local Similarity 52.4%; Pred. No. 2.7e+03;
RESULT 1427
Query Match 4.6%; Score 29.6; DB 12; Length 90183;
Best Local Similarity 50.7%; Pred. No. 2.8e+03;
RESULT 1428
ID ADJ33491 standard; DNA; 94001 BP.
DE Human LAR related nucleotide sequence SEQ ID NO:20.
PN WO2004010956-A2.
PD 05-FEB-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 4.6%; Score 29.6; DB 13; Length 94001;
Best Local Similarity 53.4%; Pred. No. 2.8e+03;
RESULT 1429
ID ACN44740 standard; DNA; 101241 BP.
DE Mouse genomic sequence mCG3043.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 4.6%; Score 29.6; DB 11; Length 101241;
Best Local Similarity 49.4%; Pred. No. 2.9e+03;
RESULT 1430
Query Match 4.6%; Score 29.6; DB 6; Length 110000;
Best Local Similarity 52.4%; Pred. No. 3e+03;
RESULT 1431
Query Match 4.6%; Score 29.6; DB 6; Length 110000;
Best Local Similarity 54.6%; Pred. No. 3e+03;
RESULT 1432
ID ABQ69245 standard; DNA; 3011208 BP.
DE Listeria innocua DNA sequence #684.
PN WO200228891-A2.
PD 11-APR-2002.
PA (INSP) INST PASTEUR.

PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 4.6%; Score 29.6; DB 6; Length 110000;
Best Local Similarity 54.6%; Pred. No. 3e+03;
RESULT 1433
Query Match 4.6%; Score 29.6; DB 6; Length 110000;
Best Local Similarity 54.6%; Pred. No. 3e+03;
RESULT 1434
Query Match 4.6%; Score 29.6; DB 13; Length 110000;
Best Local Similarity 61.8%; Pred. No. 3e+03;
RESULT 1435
ID ABT17385 standard; DNA; 118951 BP.
DE Human IG gene related nucleic acid SEQ ID No 11.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 4.6%; Score 29.6; DB 8; Length 118951;
Best Local Similarity 48.3%; Pred. No. 3.1e+03;
RESULT 1436
ID ACN45052 standard; DNA; 119414 BP.
DE Mouse genomic sequence mCG7348.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 4.6%; Score 29.6; DB 11; Length 119414;
Best Local Similarity 52.4%; Pred. No. 3.1e+03;
RESULT 1437
ID ADE43582 standard; DNA; 128034 BP.
DE Polymorphic human IDE genomic sequence, SEQ ID 187.
PN WO2003054143-A2.
PD 03-JUL-2003.
PA (NEUR-) NEUROGENETICS INC.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 4.6%; Score 29.6; DB 10; Length 128034;
Best Local Similarity 61.8%; Pred. No. 3.2e+03;
RESULT 1438
ID ADE43581 standard; DNA; 128034 BP.
DE Human IDE genomic sequence, SEQ ID 186.
PN WO2003054143-A2.
PD 03-JUL-2003.
PA (NEUR-) NEUROGENETICS INC.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 4.6%; Score 29.6; DB 10; Length 128034;
Best Local Similarity 61.8%; Pred. No. 3.2e+03;
RESULT 1439
ID ADH54059 standard; DNA; 128034 BP.
DE Human IDE gene DNA sequence SeqID186.
PN US2003224380-A1.
PD 04-DEC-2003.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 4.6%; Score 29.6; DB 12; Length 128034;
Best Local Similarity 61.8%; Pred. No. 3.2e+03;
RESULT 1440
ID ADH54060 standard; DNA; 128034 BP.
DE Human IDE gene variant DNA sequence SeqID187.
PN US2003224380-A1.
PD 04-DEC-2003.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 4.6%; Score 29.6; DB 12; Length 128034;
Best Local Similarity 61.8%; Pred. No. 3.2e+03;
RESULT 1441
ID AAD55694 standard; DNA; 175561 BP.
DE Human THBS4 reference gene (GI 14916146).
PN WO2003020120-A2.
PD 13-MAR-2003.
PA (VITI-) VITIVITY INC.
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
Query Match 4.6%; Score 29.6; DB 8; Length 175561;
Best Local Similarity 57.6%; Pred. No. 3.6e+03;
RESULT 1442
ID ADL08129 standard; DNA; 175561 BP.
DE Human gene associated with low HDL-C THBS4.
PN US2004043389-A1.
PD 04-MAR-2004.

PA (VITI-) VITIVITY INC.
Query Match 4.6%; Score 29.6; DB 12; Length 175561;
Best Local Similarity 57.6%; Pred. No. 3.6e+03;
RESULT 1443
ID ADF69677 standard; DNA; 181257 BP.
DE Human SLC5A8 gene SEQ ID NO:2.
PN WO2003104427-A2.
PD 18-DEC-2003.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
Query Match 4.6%; Score 29.6; DB 12; Length 181257;
Best Local Similarity 46.9%; Pred. No. 3.7e+03;
RESULT 1444
ID ADE43315 standard; DNA; 202100 BP.
DE Human IDE/ KNSL1 genomic sequence, SEQ ID 484.
PN WO2003054143-A2.
PD 03-JUL-2003.
PA (NEUR-) NEUROGENETICS INC.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 4.6%; Score 29.6; DB 10; Length 202100;
Best Local Similarity 61.8%; Pred. No. 3.8e+03;
RESULT 1445
ID ADH54357 standard; DNA; 202100 BP.
DE Human IDE/KNSL1 gene DNA sequence SeqID484.
PN US2003224380-A1.
PD 04-DEC-2003.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 4.6%; Score 29.6; DB 12; Length 202100;
Best Local Similarity 61.8%; Pred. No. 3.8e+03;
RESULT 1446
ID ABX16034 standard; DNA; 203654 BP.
DE Human gene encoding calcium channel transporter family member.
PN US2002142938-A1.
PD 03-OCT-2002.
PA (YANC/) YAN C.
PA (KETC/) KETCHUM K A.
PA (DFRA/) DI FRANCESCO V.
PA (BEAS/) BEASLEY E M.
Query Match 4.6%; Score 29.6; DB 10; Length 203654;
Best Local Similarity 50.0%; Pred. No. 3.8e+03;
RESULT 1447
ID ABQ67193 standard; DNA; 213251 BP.
DE Listeria innocua contig DNA sequence #6.
PN WO200228891-A2.
PD 11-APR-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 4.6%; Score 29.6; DB 6; Length 213251;
Best Local Similarity 54.6%; Pred. No. 3.9e+03;
RESULT 1448
ID ACN44202 standard; DNA; 321491 BP.
DE Human genomic sequence hCG18268.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 4.6%; Score 29.6; DB 11; Length 321491;
Best Local Similarity 64.7%; Pred. No. 4.4e+03;
RESULT 1449
ID AAV89307 standard; cDNA; 301 BP.
DE EST clone CN343.
PN WO9845436-A2.
PD 15-OCT-1998.
PA (GEMY) GENETICS INST INC.
Query Match 4.6%; Score 29.4; DB 2; Length 301;
Best Local Similarity 56.8%; Pred. No. 2.3e+02;
RESULT 1450
ID ABN20600 standard; cDNA; 341 BP.
DE Human ORFX polynucleotide sequence SEQ ID NO:9677.
PN WO200192523-A2.
PD 06-DEC-2001.
PA (CURA-) CURAGEN CORP.
Query Match 4.6%; Score 29.4; DB 6; Length 341;
Best Local Similarity 54.8%; Pred. No. 2.4e+02;
RESULT 1451

ID ACH18489 standard; cDNA; 396 BP.
DE Human adult heart cDNA #2803.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 4.6%; Score 29.4; DB 9; Length 396;
Best Local Similarity 50.3%; Pred. No. 2.6e+02;
RESULT 1452
ID ABN90666 standard; DNA; 543 BP.
DE Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:129.
PN US6380370-B1.
PD 30-APR-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.6%; Score 29.4; DB 6; Length 543;
Best Local Similarity 50.3%; Pred. No. 3e+02;
RESULT 1453
ID ADS03840 standard; DNA; 543 BP.
DE Staphylococcus epidermis polynucleotide seqid 3135.
PN US2004147734-A1.
PD 29-JUL-2004.
PA (DOUC/) DOUCETTE-STAMM L.
PA (BUSH/) BUSH D.
Query Match 4.6%; Score 29.4; DB 13; Length 543;
Best Local Similarity 50.3%; Pred. No. 3e+02;
RESULT 1454
ID ACD95810 standard; cDNA; 557 BP.
DE Human colon cancer cell expressed cDNA #4222.
PN US2002155438-A1.
PD 24-OCT-2002.
PA (SIMP/) SIMPSON A J G.
PA (NETO/) NETO E D.
PA (BREN/) BRENTANI R R.
Query Match 4.6%; Score 29.4; DB 10; Length 557;
Best Local Similarity 56.8%; Pred. No. 3e+02;
RESULT 1455
ID AAH08761 standard; cDNA; 564 BP.
DE Human cDNA clone (3'-primer) SEQ ID NO:5596.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 4.6%; Score 29.4; DB 4; Length 564;
Best Local Similarity 53.6%; Pred. No. 3e+02;
RESULT 1456
ID ADH70191 standard; DNA; 650 BP.
DE Human Vbeta gene family microsatellite sequence #25.
PN US2002150891-A1.
PD 17-OCT-2002.
PA (HOOD/) HOOD L E.
PA (ROWE/) ROWEN L.
Query Match 4.6%; Score 29.4; DB 12; Length 650;
Best Local Similarity 49.1%; Pred. No. 3.3e+02;
RESULT 1457
ID ACA32954 standard; DNA; 663 BP.
DE Prokaryotic essential gene #14611.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.6%; Score 29.4; DB 8; Length 663;
Best Local Similarity 52.9%; Pred. No. 3.3e+02;
RESULT 1458
ID AAC48728 standard; DNA; 666 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 58545.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.6%; Score 29.4; DB 3; Length 666;
Best Local Similarity 48.5%; Pred. No. 3.3e+02;
RESULT 1459
ID ABQ28068 standard; DNA; 712 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 14659.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.6%; Score 29.4; DB 6; Length 712;
Best Local Similarity 56.8%; Pred. No. 3.4e+02;
RESULT 1460
ID ABQ28069 standard; DNA; 712 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 14660.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.6%; Score 29.4; DB 6; Length 712;
Best Local Similarity 56.8%; Pred. No. 3.4e+02;
RESULT 1461
ID AAA35172 standard; DNA; 715 BP.
DE Human adenosine receptor related polynucleotide 2nd SEQ ID NO:46.
PN WO200009525-A2.
PD 24-FEB-2000.
PA (UYEC-) UNIV EAST CAROLINA.
Query Match 4.6%; Score 29.4; DB 3; Length 715;
Best Local Similarity 52.9%; Pred. No. 3.4e+02;
RESULT 1462
ID AAF21294 standard; DNA; 715 BP.
DE Human low adenosine antisense oligonucleotide related sequence #2861.
PN WO200062736-A2.
PD 26-OCT-2000.
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
Query Match 4.6%; Score 29.4; DB 3; Length 715;
Best Local Similarity 52.9%; Pred. No. 3.4e+02;
RESULT 1463
ID ABZ96988 standard; DNA; 715 BP.
DE Human nucleic acid sequence.
PN WO200285308-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Query Match 4.6%; Score 29.4; DB 10; Length 715;
Best Local Similarity 52.9%; Pred. No. 3.4e+02;
RESULT 1464
ID ABD20837 standard; DNA; 715 BP.
DE Human pulmonary and inflammatory target DNA #448.
PN WO200285309-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Query Match 4.6%; Score 29.4; DB 11; Length 715;
Best Local Similarity 52.9%; Pred. No. 3.4e+02;
RESULT 1465
ID AAA35171 standard; DNA; 718 BP.
DE Human adenosine receptor related polynucleotide 2nd SEQ ID NO:45.
PN WO200009525-A2.
PD 24-FEB-2000.
PA (UYEC-) UNIV EAST CAROLINA.
Query Match 4.6%; Score 29.4; DB 3; Length 718;
Best Local Similarity 52.9%; Pred. No. 3.4e+02;
RESULT 1466
ID AAF21293 standard; DNA; 718 BP.
DE Human low adenosine antisense oligonucleotide related sequence #2860.
PN WO200062736-A2.
PD 26-OCT-2000.
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
Query Match 4.6%; Score 29.4; DB 3; Length 718;
Best Local Similarity 52.9%; Pred. No. 3.4e+02;
RESULT 1467
ID ABZ96987 standard; DNA; 718 BP.
DE Human nucleic acid sequence.
PN WO200285308-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Query Match 4.6%; Score 29.4; DB 10; Length 718;
Best Local Similarity 52.9%; Pred. No. 3.4e+02;
RESULT 1468
ID ABD20836 standard; DNA; 718 BP.

DE Human pulmonary and inflammatory target DNA #447.
PN WO200285309-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Query Match 4.6%; Score 29.4; DB 11; Length 718;
Best Local Similarity 52.9%; Pred. No. 3.4e+02;
RESULT 1469
ID ADG33035 standard; DNA; 726 BP.
DE Human DNA differentially expressed in patients with SLE SeqID359.
PN WO2003090694-A2.
PD 06-NOV-2003.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match 4.6%; Score 29.4; DB 10; Length 726;
Best Local Similarity 52.9%; Pred. No. 3.4e+02;
RESULT 1470
ID ABV16074 standard; cDNA; 843 BP.
DE Human prostate expression marker cDNA 16065.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.6%; Score 29.4; DB 5; Length 843;
Best Local Similarity 42.9%; Pred. No. 3.7e+02;
RESULT 1471
ID AAX30767 standard; DNA; 845 BP.
DE Streptococcus pneumoniae genomic DNA sequence SEQ ID NO:44.
PN WO9737026-A1.
PD 09-OCT-1997.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 4.6%; Score 29.4; DB 2; Length 845;
Best Local Similarity 49.1%; Pred. No. 3.7e+02;
RESULT 1472
ID ADS47382 standard; cDNA; 846 BP.
DE Bacterial polynucleotide #2125.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 4.6%; Score 29.4; DB 13; Length 846;
Best Local Similarity 49.1%; Pred. No. 3.7e+02;
RESULT 1473
ID ACN81296 standard; DNA; 873 BP.
DE Breast cancer related marker, seq id 2446.
PN US2003099974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 4.6%; Score 29.4; DB 11; Length 873;
Best Local Similarity 50.4%; Pred. No. 3.7e+02;
RESULT 1474
ID AAL22690 standard; cDNA; 878 BP.
DE Human breast cancer expressed polynucleotide 15147.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.6%; Score 29.4; DB 4; Length 878;
Best Local Similarity 52.9%; Pred. No. 3.7e+02;
RESULT 1475
ID AAX03593 standard; cDNA; 939 BP.
DE cDNA encoding a lectin derived progenitor cell preservation factor.
PN WO9859038-A1.
PD 30-DEC-1998.
PA (IMCL-) IMCLONE SYSTEMS INC.
PA (REGC) UNIV CALIFORNIA.
Query Match 4.6%; Score 29.4; DB 2; Length 939;
Best Local Similarity 52.0%; Pred. No. 3.9e+02;
RESULT 1476
ID AAH42287 standard; cDNA; 939 BP.
DE Nucleotide sequence of a hyacinth bean FRIL polypeptide.
PN WO200149851-A1.
PD 12-JUL-2001.
PA (PHYL-) PHYLOGIX LLC.
Query Match 4.6%; Score 29.4; DB 5; Length 939;
Best Local Similarity 52.0%; Pred. No. 3.9e+02;
RESULT 1477
ID ABZ58204 standard; cDNA; 939 BP.
DE Hyacinth bean FRIL nucleic acid.
PN WO2003004616-A2.
PD 16-JAN-2003.
PA (PHYL-) PHYLOGIX INC.
Query Match 4.6%; Score 29.4; DB 10; Length 939;
Best Local Similarity 52.0%; Pred. No. 3.9e+02;
RESULT 1478
ID AAQ10542 standard; DNA; 949 BP.
DE E.coli peptidyl-prolyl cis-trans isomerase-beta gene.
PN EP413440-A.
PD 20-FEB-1991.
PA (TOFU) TONEN CORP.
Query Match 4.6%; Score 29.4; DB 2; Length 949;
Best Local Similarity 49.1%; Pred. No. 3.9e+02;
RESULT 1479
ID AAQ86973 standard; DNA; 949 BP.
DE Clone contg. E. coli PPIase-beta gene.
PN EP647714-A1.
PD 12-APR-1995.
PA (TOFU) TONEN CORP.
Query Match 4.6%; Score 29.4; DB 2; Length 949;
Best Local Similarity 49.1%; Pred. No. 3.9e+02;
RESULT 1480
ID AAQ86966 standard; DNA; 949 BP.
DE Clone contg. E. coli PPIase-beta gene.
PN EP647713-A1.
PD 12-APR-1995.
PA (TOFU) TONEN CORP.
Query Match 4.6%; Score 29.4; DB 2; Length 949;
Best Local Similarity 49.1%; Pred. No. 3.9e+02;
RESULT 1481
ID AAC56057 standard; DNA; 988 BP.
DE Eucalyptus grandis transcription factor DNA sequence #188.
PN WO200053724-A2.
PD 14-SEP-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Query Match 4.6%; Score 29.4; DB 3; Length 988;
Best Local Similarity 63.4%; Pred. No. 4e+02;
RESULT 1482
ID AAH42288 standard; DNA; 1005 BP.
DE Nucleotide sequence of a hyacinth bean FRIL N-terminal sequence.
PN WO200149851-A1.
PD 12-JUL-2001.
PA (PHYL-) PHYLOGIX LLC.
Query Match 4.6%; Score 29.4; DB 5; Length 1005;
Best Local Similarity 52.0%; Pred. No. 4e+02;
RESULT 1483
ID AAH42295 standard; DNA; 1005 BP.
DE DNA encoding alpha-amylase inhibitor signal peptide and FRIL fusion.
PN WO200149851-A1.
PD 12-JUL-2001.
PA (PHYL-) PHYLOGIX LLC.
Query Match 4.6%; Score 29.4; DB 5; Length 1005;
Best Local Similarity 52.0%; Pred. No. 4e+02;
RESULT 1484
ID ABZ58205 standard; cDNA; 1005 BP.
DE Hyacinth bean FRIL nucleic acid.
PN WO2003004616-A2.
PD 16-JAN-2003.
PA (PHYL-) PHYLOGIX INC.
Query Match 4.6%; Score 29.4; DB 10; Length 1005;
Best Local Similarity 52.0%; Pred. No. 4e+02;
RESULT 1485
ID AAC43285 standard; DNA; 1131 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 38706.
PN EP1033405-A2.
PD 06-SEP-2000.

Query Match 4.6%; Score 29.4; DB 3; Length 1131;
Best Local Similarity 56.8%; Pred. No. 4.2e+02;
RESULT 1486
ID AAV26608 standard; cDNA; 1309 BP.
DE Cell division cycle protein HCDCB cDNA.
PN WO9811220-A2.
PD 19-MAR-1998.
PA (INCY-) INCYTE PHARM INC.
Query Match 4.6%; Score 29.4; DB 2; Length 1309;
Best Local Similarity 57.3%; Pred. No. 4.5e+02;
RESULT 1487
ID ACC79305 standard; cDNA; 1408 BP.
DE Human aprataxin (APTX) encoding cDNA SEQ ID NO:1.
PN EP1293570-A2.
PD 19-MAR-2003.
PA (UYNI-) UNIV NIIGATA.
Query Match 4.6%; Score 29.4; DB 10; Length 1408;
Best Local Similarity 54.1%; Pred. No. 4.7e+02;
RESULT 1488
ID AAC45815 standard; DNA; 1434 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 47862.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.6%; Score 29.4; DB 3; Length 1434;
Best Local Similarity 55.3%; Pred. No. 4.7e+02;
RESULT 1489
ID AAA35173 standard; DNA; 1452 BP.
DE Human adenosine receptor related polynucleotide 2nd SEQ ID NO:47.
PN WO200009525-A2.
PD 24-FEB-2000.
PA (UYEC-) UNIV EAST CAROLINA.
Query Match 4.6%; Score 29.4; DB 3; Length 1452;
Best Local Similarity 52.9%; Pred. No. 4.7e+02;
RESULT 1490
ID AAF21295 standard; DNA; 1452 BP.
DE Human low adenosine antisense oligonucleotide related sequence #2862.
PN WO200062736-A2.
PD 26-OCT-2000.
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
Query Match 4.6%; Score 29.4; DB 3; Length 1452;
Best Local Similarity 52.9%; Pred. No. 4.7e+02;
RESULT 1491
ID ABA92863 standard; DNA; 1452 BP.
DE Human eosinophil cationic protein (ECP) encoding DNA SEQ ID NO:1.
PN WO200185766-A2.
PD 15-NOV-2001.
PA (INNO-) INNOVENTUS UPPSALA LIFE SCI AB.
Query Match 4.6%; Score 29.4; DB 6; Length 1452;
Best Local Similarity 52.9%; Pred. No. 4.7e+02;
RESULT 1492
ID ABV75345 standard; cDNA; 1452 BP.
DE Human eosinophil cationic protein (ECP) encoding cDNA.
PN WO200289829-A2.
PD 14-NOV-2002.
PA (INNO-) INNOVENTUS PROJECT AB.
Query Match 4.6%; Score 29.4; DB 8; Length 1452;
Best Local Similarity 52.9%; Pred. No. 4.7e+02;
RESULT 1493
ID ABZ96989 standard; DNA; 1452 BP.
DE Human nucleic acid sequence.
PN WO200285308-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Query Match 4.6%; Score 29.4; DB 10; Length 1452;
Best Local Similarity 52.9%; Pred. No. 4.7e+02;
RESULT 1494
ID ABD20838 standard; DNA; 1452 BP.
DE Human pulmonary and inflammatory target DNA #449.
PN WO200285309-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Query Match 4.6%; Score 29.4; DB 11; Length 1452;
Best Local Similarity 52.9%; Pred. No. 4.7e+02;
RESULT 1495
ID AAD08292 standard; cDNA; 1566 BP.
DE Human secreted protein-encoding gene 10 cDNA clone HBINS58, SEQ ID NO:20.
PN WO200136440-A1.
PD 25-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.6%; Score 29.4; DB 4; Length 1566;
Best Local Similarity 46.0%; Pred. No. 4.9e+02;
RESULT 1496
ID ADA40269 standard; cDNA; 1566 BP.
DE Human secreted protein encoding cDNA.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.6%; Score 29.4; DB 8; Length 1566;
Best Local Similarity 46.0%; Pred. No. 4.9e+02;
RESULT 1497
ID ACC50689 standard; cDNA; 1566 BP.
DE Human secreted protein coding sequence, SEQ ID 356.
PN WO200295010-A2.
PD 28-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.6%; Score 29.4; DB 8; Length 1566;
Best Local Similarity 46.0%; Pred. No. 4.9e+02;
RESULT 1498
ID ABZ71376 standard; cDNA; 1566 BP.
DE Secreted protein-encoding gene 16 cDNA clone HBINS58, SEQ ID NO:197.
PN WO200276488-A1.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.6%; Score 29.4; DB 8; Length 1566;
Best Local Similarity 46.0%; Pred. No. 4.9e+02;
RESULT 1499
ID ADB91324 standard; cDNA; 1566 BP.
DE Human secreted protein cDNA #SEQ ID 270.
PN WO2003004622-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.6%; Score 29.4; DB 9; Length 1566;
Best Local Similarity 46.0%; Pred. No. 4.9e+02;
RESULT 1500
ID ADC73792 standard; DNA; 1566 BP.
DE Human secreted protein-related DNA - SEQ ID 425.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.6%; Score 29.4; DB 10; Length 1566;
Best Local Similarity 46.0%; Pred. No. 4.9e+02;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 24, 2005, 19:08:56 ; Search time 366.66 Seconds
(without alignments)
10300.558 Million cell updates/sec

Perfect score: 639
Sequence: 1 atgttgtggctgctcttttt.....tattaatgatgccttcatga 639

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5384158 seqs, 2955248155 residues

Total number of hits satisfying chosen parameters: 10768316

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
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3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
27	639	100.0	1346	10	US-09-997-428-386	Sequence 386, App
518	639	100.0	1346	19	US-10-931-886-481	Sequence 481, App
519	628	98.3	1312	16	US-10-133-013-205	Sequence 205, App
520	628	98.3	1432	14	US-10-097-065-17	Sequence 17, Appl
521	628	98.3	1432	17	US-10-372-876-17	Sequence 17, Appl
522	627.6	98.2	1447	10	US-09-892-877-22	Sequence 22, Appl
523	627.6	98.2	1447	10	US-09-948-783-22	Sequence 22, Appl
524	626	98.0	848	10	US-09-903-190-27	Sequence 27, Appl
525	626	98.0	848	15	US-10-319-763-27	Sequence 27, Appl
526	616	96.4	1356	14	US-10-097-065-122	Sequence 122, App
527	616	96.4	1356	17	US-10-372-876-122	Sequence 122, App
528	485.6	76.0	1181	17	US-10-152-319A-1744	Sequence 1744, Ap
529	310.6	48.6	532	9	US-09-728-445-570	Sequence 570, App
530	232.6	36.4	355	9	US-09-867-701-1636	Sequence 1636, Ap
c 531	197.4	30.9	213	9	US-09-864-761-23160	Sequence 23160, A
c 532	188.2	29.5	464	9	US-09-864-761-6445	Sequence 6445, Ap
533	144.2	22.6	2415	9	US-09-978-385-3	Sequence 3, Appli
534	138.4	21.7	620	13	US-10-027-632-228334	Sequence 228334,
535	138.4	21.7	620	17	US-10-027-632-228334	Sequence 228334,
536	125.6	19.7	2415	9	US-09-978-385-7	Sequence 7, Appli
537	125	19.6	3324	14	US-10-116-802-172	Sequence 172, App
538	125	19.6	3325	13	US-10-114-893-85	Sequence 85, Appl
539	125	19.6	3334	9	US-09-978-385-1	Sequence 1, Appli
540	125	19.6	3396	11	US-09-999-781-1	Sequence 1, Appli
541	125	19.6	3396	14	US-10-158-847-141	Sequence 141, App
542	125	19.6	3396	15	US-10-158-825-141	Sequence 141, App
543	125	19.6	3396	18	US-10-158-825-141	Sequence 141, App
544	125	19.6	3405	15	US-10-005-956-569	Sequence 569, App
545	125	19.6	3405	15	US-10-005-956-842	Sequence 842, App
992	119.8	18.7	3732	19	US-10-931-886-71	Sequence 71, Appl
993	117	18.3	2911	9	US-09-969-384-12	Sequence 12, Appl
994	117	18.3	2920	9	US-09-969-384-2	Sequence 2, Appli
995	117	18.3	2920	14	US-10-158-847-137	Sequence 137, App
996	117	18.3	2920	15	US-10-158-825-137	Sequence 137, App
997	117	18.3	2920	18	US-10-158-825-137	Sequence 137, App
998	111.4	17.4	2638	9	US-09-978-385-5	Sequence 5, Appli
999	108.2	16.9	2638	9	US-09-978-385-8	Sequence 8, Appli
1000	96.8	15.1	561	11	US-09-969-034-1556	Sequence 1556, Ap
1001	60	9.4	60	10	US-09-908-975-8765	Sequence 8765, Ap
c1002	54	8.5	11288	9	US-09-947-925A-4	Sequence 4, Appli
c1003	54	8.5	11288	9	US-09-822-634-1	Sequence 1, Appli
c1004	54	8.5	15056	9	US-09-392-822-4	Sequence 4, Appli
c1005	54	8.5	15056	10	US-09-814-357-14	Sequence 14, Appl
c1006	54	8.5	15056	10	US-09-814-351-14	Sequence 14, Appl
c1007	54	8.5	15056	14	US-10-045-116-25	Sequence 25, Appl
c1008	54	8.5	15056	15	US-10-226-820-10	Sequence 10, Appl
1009	48	7.5	65	10	US-09-908-975-25999	Sequence 25999, A
1010	45.8	7.2	531	10	US-09-814-353-18996	Sequence 18996, A
c1011	40.2	6.3	160820	18	US-10-473-939-5	Sequence 5, Appli
c1012	39.8	6.2	67810	13	US-10-087-192-1738	Sequence 1738, Ap
1013	38.4	6.0	3477	18	US-10-437-963-14564	Sequence 14564, A
c1014	38.4	6.0	3639	18	US-10-437-963-14560	Sequence 14560, A
c1015	37.8	5.9	2336	18	US-10-723-860-6198	Sequence 6198, Ap
1016	37.6	5.9	3785	17	US-10-424-599-86277	Sequence 86277, A
1017	37	5.8	3404	18	US-10-723-860-8117	Sequence 8117, Ap
1018	36.8	5.8	581	13	US-10-027-632-270905	Sequence 270905,
1019	36.8	5.8	581	17	US-10-027-632-270905	Sequence 270905,
1020	36.6	5.7	599	16	US-10-029-386-506	Sequence 506, App
c1021	36.6	5.7	8483	17	US-10-415-508-3	Sequence 3, Appli
1022	36.4	5.7	558	9	US-09-736-457-554	Sequence 554, App
1023	36.4	5.7	558	9	US-09-902-941-554	Sequence 554, App
1024	36.4	5.7	558	9	US-09-849-626-554	Sequence 554, App
1025	36.4	5.7	558	10	US-09-476-300-554	Sequence 554, App
1026	36.4	5.7	558	14	US-10-017-754-554	Sequence 554, App
1027	36.4	5.7	558	16	US-10-113-872-554	Sequence 554, App
1028	36.4	5.7	558	17	US-10-283-017-554	Sequence 554, App
1029	36.4	5.7	616	18	US-10-357-930-58020	Sequence 58020, A
1030	36	5.6	546	13	US-10-027-632-193402	Sequence 193402,
1031	36	5.6	546	17	US-10-027-632-193402	Sequence 193402,
1032	36	5.6	88445	18	US-10-322-281-724	Sequence 724, App
c1033	35.8	5.6	682	13	US-10-027-632-289222	Sequence 289222,
c1034	35.8	5.6	682	17	US-10-027-632-289222	Sequence 289222,
1035	35.8	5.6	2625	15	US-10-163-818-1	Sequence 1, Appli
1036	35.8	5.6	2625	16	US-10-269-909-6	Sequence 6, Appli
1037	35.8	5.6	2625	17	US-10-172-118-670	Sequence 670, App
1038	35.8	5.6	2625	17	US-10-457-257-1	Sequence 1, Appli
1039	35.8	5.6	2625	17	US-10-342-887-670	Sequence 670, App
1040	35.8	5.6	2625	18	US-10-678-160A-19	Sequence 19, Appl
1041	35.8	5.6	2625	19	US-10-941-442-1	Sequence 1, Appli
1042	35.8	5.6	3403	13	US-10-044-090-597	Sequence 597, App
1043	35.8	5.6	3403	15	US-10-084-817-136	Sequence 136, App
1044	35.8	5.6	3661	17	US-10-440-464-151	Sequence 151, App
1045	35.8	5.6	3661	17	US-10-240-425-1210	Sequence 1210, Ap
c1046	35.6	5.6	339234	18	US-10-322-696-73	Sequence 73, Appl
1047	35.4	5.5	624	13	US-10-027-632-187865	Sequence 187865,

1048	35.4	5.5	624	17	US-10-027-632-187865	Sequence 187865,
c1049	35.4	5.5	121410	19	US-10-741-600-17733	Sequence 17733, A
c1050	35.2	5.5	29993	18	US-10-482-823-3	Sequence 3, Appli
c1051	35.2	5.5	38342	17	US-10-221-714A-472	Sequence 472, App
1052	35	5.5	653122	13	US-10-087-192-226	Sequence 226, App
1053	34.8	5.4	94463	18	US-10-719-993-6944	Sequence 6944, Ap
1054	34.4	5.4	546025	18	US-10-719-993-6862	Sequence 6862, Ap
1055	34.2	5.4	426	10	US-09-814-353-6334	Sequence 6334, Ap
1056	34.2	5.4	426	10	US-09-814-353-12612	Sequence 12612, A
c1057	34.2	5.4	1290	17	US-10-282-122A-36317	Sequence 36317, A
c1058	34.2	5.4	1311	18	US-10-437-963-20021	Sequence 20021, A
c1059	34.2	5.4	2026	18	US-10-437-963-90691	Sequence 90691, A
1060	34	5.3	822	17	US-10-104-047-1202	Sequence 1202, Ap
1061	34	5.3	7161	18	US-10-723-860-5828	Sequence 5828, Ap
c1062	34	5.3	166472	19	US-10-741-600-17788	Sequence 17788, A
c1063	34	5.3	174703	13	US-10-087-192-1336	Sequence 1336, Ap
1064	33.8	5.3	428	17	US-10-242-535A-45633	Sequence 45633, A
1065	33.8	5.3	428	17	US-10-085-783A-45633	Sequence 45633, A
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1067	33.8	5.3	657	13	US-10-027-632-255368	Sequence 255368,
1068	33.8	5.3	657	17	US-10-027-632-255368	Sequence 255368,
c1069	33.8	5.3	1982	9	US-09-864-761-2855	Sequence 2855, Ap
c1070	33.8	5.3	4846	17	US-10-062-674-1880	Sequence 1880, Ap
c1071	33.8	5.3	96898	17	US-10-417-476-3	Sequence 3, Appli
1072	33.6	5.3	384	9	US-09-960-352-37	Sequence 37, Appl
c1073	33.6	5.3	476	18	US-10-357-930-6220	Sequence 6220, Ap
1074	33.6	5.3	694	18	US-10-437-963-100927	Sequence 100927,
c1075	33.6	5.3	898	18	US-10-425-115-142066	Sequence 142066,
c1076	33.6	5.3	3579	18	US-10-437-963-100925	Sequence 100925,
1077	33.6	5.3	5337	14	US-10-239-676-138	Sequence 138, App
c1078	33.4	5.2	2514	17	US-10-282-122A-40536	Sequence 40536, A
1079	33.4	5.2	7778	8	US-08-781-986A-48	Sequence 48, Appl
1080	33.4	5.2	7778	17	US-10-329-624-48	Sequence 48, Appl
c1081	33.4	5.2	11337	9	US-09-764-877-2651	Sequence 2651, Ap
c1082	33.4	5.2	11337	17	US-10-242-515-2651	Sequence 2651, Ap
1083	33.4	5.2	717651	18	US-10-719-993-6817	Sequence 6817, Ap
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c1085	33.2	5.2	453	11	US-09-938-842A-4309	Sequence 4309, Ap
1086	33.2	5.2	3867	9	US-09-919-497-5	Sequence 5, Appli
1087	33.2	5.2	3867	15	US-10-101-510-485	Sequence 485, App
1088	33.2	5.2	3867	17	US-10-440-464-152	Sequence 152, App
1089	33.2	5.2	3867	17	US-10-240-425-1211	Sequence 1211, Ap
1090	33.2	5.2	3948	18	US-10-723-860-5413	Sequence 5413, Ap
1091	33.2	5.2	70601	17	US-10-085-117-82	Sequence 82, Appl
c1092	33	5.2	362	18	US-10-357-930-15389	Sequence 15389, A
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c1094	33	5.2	390	18	US-10-357-930-45261	Sequence 45261, A
c1095	33	5.2	511	17	US-10-424-599-56759	Sequence 56759, A
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1098	33	5.2	2000	11	US-09-938-842A-2796	Sequence 2796, Ap
1099	33	5.2	5101	9	US-09-070-927A-516	Sequence 516, App
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c1101	33	5.2	15732	14	US-10-239-676-96	Sequence 96, Appl
c1102	33	5.2	15732	15	US-10-240-453-108	Sequence 108, App
1103	33	5.2	79831	13	US-10-087-192-139	Sequence 139, App
1104	32.8	5.1	477	15	US-10-301-997-81	Sequence 81, Appl
1105	32.8	5.1	477	18	US-10-818-509-81	Sequence 81, Appl
c1106	32.8	5.1	2893	17	US-10-108-260A-490	Sequence 490, App
c1107	32.8	5.1	21126	9	US-09-070-927A-23	Sequence 23, Appl
c1108	32.8	5.1	289730	18	US-10-719-993-6780	Sequence 6780, Ap
c1109	32.6	5.1	12822	9	US-09-764-847-1579	Sequence 1579, Ap
c1110	32.6	5.1	12822	14	US-10-092-154-1579	Sequence 1579, Ap
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c1117	32.4	5.1	5992	17	US-10-221-613-167	Sequence 167, App
1118	32.4	5.1	12733	15	US-10-311-455-64	Sequence 64, Appl
1119	32.4	5.1	394468	19	US-10-741-600-17952	Sequence 17952, A
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1121	32.2	5.0	551	18	US-10-425-115-102356	Sequence 102356,
1122	32.2	5.0	599	13	US-10-027-632-270093	Sequence 270093,
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1125	32.2	5.0	639	13	US-10-027-632-182322	Sequence 182322,
1126	32.2	5.0	639	17	US-10-027-632-182321	Sequence 182321,
1127	32.2	5.0	639	17	US-10-027-632-182322	Sequence 182322,
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1131	32.2	5.0	15598	17	US-10-329-624-82	Sequence 82, Appl
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c1134	32	5.0	564	13	US-10-027-632-188082	Sequence 188082,
c1135	32	5.0	564	17	US-10-027-632-188081	Sequence 188081,
c1136	32	5.0	564	17	US-10-027-632-188082	Sequence 188082,
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1139	32	5.0	1431	11	US-09-938-842A-3843	Sequence 3843, Ap
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c1141	32	5.0	17234	18	US-10-433-793-48	Sequence 48, Appl
c1142	32	5.0	43360	14	US-10-114-170-206	Sequence 206, App
c1143	32	5.0	45325	14	US-10-114-170-261	Sequence 261, App
c1144	32	5.0	47601	13	US-10-087-192-187	Sequence 187, App
1145	32	5.0	66126	18	US-10-322-281-423	Sequence 423, App
1146	32	5.0	100944	18	US-10-322-696-4	Sequence 4, Appli
c1147	32	5.0	101438	18	US-10-331-053-81	Sequence 81, Appl
c1148	32	5.0	117754	13	US-10-087-192-28	Sequence 28, Appl
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c1150	32	5.0	195917	18	US-10-723-860-3426	Sequence 3426, Ap
c1151	32	5.0	3673778	16	US-10-312-841-1	Sequence 1, Appli
1152	31.8	5.0	315	17	US-10-388-934-627	Sequence 627, App
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c1157	31.8	5.0	559	17	US-10-027-632-316080	Sequence 316080,
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c1159	31.8	5.0	617	18	US-10-742-656-9	Sequence 9, Appli
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c1161	31.8	5.0	630	13	US-10-027-632-211879	Sequence 211879,
c1162	31.8	5.0	630	17	US-10-027-632-211878	Sequence 211878,
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1166	31.8	5.0	1091	13	US-10-027-632-117398	Sequence 117398,
1167	31.8	5.0	1091	17	US-10-027-632-117398	Sequence 117398,
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1169	31.8	5.0	1121	17	US-10-388-934-626	Sequence 626, App
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c1172	31.8	5.0	2000	11	US-09-938-842A-4671	Sequence 4671, Ap
c1173	31.8	5.0	2000	17	US-10-260-238-1625	Sequence 1625, Ap
c1174	31.8	5.0	2655	17	US-10-282-122A-10255	Sequence 10255, A
1175	31.8	5.0	3720	18	US-10-473-126-291	Sequence 291, App
c1176	31.8	5.0	5700	19	US-10-857-625-33	Sequence 33, Appl
c1177	31.8	5.0	6730	8	US-08-781-986A-51	Sequence 51, Appl
c1178	31.8	5.0	6730	17	US-10-329-624-51	Sequence 51, Appl
c1179	31.8	5.0	12278	17	US-10-398-221-3886	Sequence 3886, Ap
c1180	31.8	5.0	20158	18	US-10-719-993-6760	Sequence 6760, Ap
c1181	31.8	5.0	175561	14	US-10-017-721-3	Sequence 3, Appli
c1182	31.8	5.0	175561	17	US-10-235-192A-48	Sequence 48, Appl
c1183	31.8	5.0	567564	18	US-10-699-156-3	Sequence 3, Appli
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1186	31.6	4.9	863	18	US-10-425-115-184509	Sequence 184509,
1187	31.6	4.9	3891	17	US-10-282-122A-35508	Sequence 35508, A
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1189	31.6	4.9	7604	18	US-10-802-034-1	Sequence 1, Appli
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c1191	31.6	4.9	8996	15	US-10-240-453-310	Sequence 310, App
1192	31.6	4.9	640681	9	US-09-790-988-1	Sequence 1, Appli
c1193	31.6	4.9	1691139	14	US-10-067-514-1	Sequence 1, Appli
c1194	31.6	4.9	1691139	17	US-10-419-723-1	Sequence 1, Appli
1195	31.4	4.9	178	18	US-10-437-963-77155	Sequence 77155, A

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1197	31.4	4.9	438	10	US-09-918-995-35152	Sequence 35152, A
1198	31.4	4.9	469	9	US-09-770-444-234	Sequence 234, App
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1214	31.4	4.9	690	13	US-10-027-632-11494	Sequence 11494, A
1215	31.4	4.9	690	17	US-10-027-632-11492	Sequence 11492, A
1216	31.4	4.9	690	17	US-10-027-632-11493	Sequence 11493, A
1217	31.4	4.9	690	17	US-10-027-632-11494	Sequence 11494, A
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1220	31.4	4.9	843	17	US-10-221-278-134	Sequence 134, App
1221	31.4	4.9	865	17	US-10-291-172-510	Sequence 510, App
1222	31.4	4.9	865	17	US-10-221-278-510	Sequence 510, App
1223	31.4	4.9	955	15	US-10-119-926-93	Sequence 93, Appl
c1224	31.4	4.9	2642	17	US-10-104-047-692	Sequence 692, App
1225	31.4	4.9	2972	18	US-10-723-860-7757	Sequence 7757, Ap
c1226	31.4	4.9	3954	18	US-10-602-494-259	Sequence 259, App
c1227	31.4	4.9	5860	17	US-10-221-613-336	Sequence 336, App
c1228	31.4	4.9	43709	18	US-10-322-696-118	Sequence 118, App
c1229	31.4	4.9	86500	18	US-10-719-993-6771	Sequence 6771, Ap
c1230	31.4	4.9	238484	13	US-10-087-192-544	Sequence 544, App
c1231	31.2	4.9	452	18	US-10-674-124A-14799	Sequence 14799, A
1232	31.2	4.9	528	17	US-10-282-122A-21197	Sequence 21197, A
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1238	31.2	4.9	1001	17	US-10-294-934-298	Sequence 298, App
c1239	31.2	4.9	1179	13	US-10-027-632-263173	Sequence 263173,
c1240	31.2	4.9	1179	17	US-10-027-632-263173	Sequence 263173,
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1244	31.2	4.9	1909	13	US-10-027-632-97874	Sequence 97874, A
1245	31.2	4.9	1909	17	US-10-027-632-97872	Sequence 97872, A
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1251	31.2	4.9	7837	17	US-10-041-018-2	Sequence 2, Appli
1252	31.2	4.9	12571	9	US-09-965-553-20	Sequence 20, Appl
1253	31.2	4.9	12571	17	US-10-615-005-20	Sequence 20, Appl
1254	31.2	4.9	12571	17	US-10-395-607-20	Sequence 20, Appl
1255	31.2	4.9	12571	18	US-10-799-870-20	Sequence 20, Appl
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1257	31.2	4.9	55544	13	US-10-087-192-811	Sequence 811, App
1258	31.2	4.9	122859	13	US-10-087-192-37	Sequence 37, Appl
c1259	31.2	4.9	144179	13	US-10-087-192-511	Sequence 511, App
1260	31.2	4.9	357652	18	US-10-322-696-34	Sequence 34, Appl
c1261	31.2	4.9	358246	17	US-10-292-798-1095	Sequence 1095, Ap
1262	31.2	4.9	1790242	18	US-10-719-993-6940	Sequence 6940, Ap
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1266	31	4.9	442	13	US-10-027-632-294020	Sequence 294020,
1267	31	4.9	442	17	US-10-027-632-36029	Sequence 36029, A
1268	31	4.9	442	17	US-10-027-632-294020	Sequence 294020,
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1274	31	4.9	542	17	US-10-027-632-181029	Sequence 181029,
1275	31	4.9	542	17	US-10-027-632-181030	Sequence 181030,
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1277	31	4.9	559	17	US-10-027-632-271467	Sequence 271467,
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1279	31	4.9	608	13	US-10-027-632-207341	Sequence 207341,
1280	31	4.9	608	17	US-10-027-632-207340	Sequence 207340,
1281	31	4.9	608	17	US-10-027-632-207341	Sequence 207341,
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c1283	31	4.9	611	17	US-10-027-632-188828	Sequence 188828,
1284	31	4.9	612	15	US-10-128-714-1158	Sequence 1158, Ap
1285	31	4.9	612	15	US-10-128-714-2158	Sequence 2158, Ap
c1286	31	4.9	626	8	US-08-781-986A-1046	Sequence 1046, Ap
c1287	31	4.9	626	17	US-10-329-624-1046	Sequence 1046, Ap
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c1289	31	4.9	707	17	US-10-027-632-17424	Sequence 17424, A
1290	31	4.9	846	15	US-10-128-714-7158	Sequence 7158, Ap
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1292	31	4.9	990	17	US-10-369-493-45010	Sequence 45010, A
c1293	31	4.9	1018	13	US-10-027-632-119602	Sequence 119602,
c1294	31	4.9	1018	17	US-10-027-632-119602	Sequence 119602,
c1295	31	4.9	1069	17	US-10-424-599-121380	Sequence 121380,
1296	31	4.9	1087	15	US-10-128-714-6158	Sequence 6158, Ap
1297	31	4.9	1424	18	US-10-437-963-50393	Sequence 50393, A
1298	31	4.9	2453	18	US-10-437-963-16680	Sequence 16680, A
1299	31	4.9	2612	15	US-10-128-714-158	Sequence 158, App
1300	31	4.9	3087	15	US-10-128-714-5158	Sequence 5158, Ap
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c1302	31	4.9	7246	16	US-10-085-959-181	Sequence 181, App
c1303	31	4.9	7268	15	US-10-238-075-597	Sequence 597, App
c1304	31	4.9	50000	19	US-10-706-635-25	Sequence 25, Appl
c1305	31	4.9	326014	9	US-09-731-231A-3	Sequence 3, Appli
c1306	31	4.9	326014	18	US-10-751-985-3	Sequence 3, Appli
1307	31	4.9	347001	18	US-10-319-908-16	Sequence 16, Appl
1308	31	4.9	418550	17	US-10-292-798-1463	Sequence 1463, Ap
c1309	31	4.9	3673778	16	US-10-312-841-2	Sequence 2, Appli
c1310	30.8	4.8	300	18	US-10-674-124A-321	Sequence 321, App
1311	30.8	4.8	393	18	US-10-425-115-116404	Sequence 116404,
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Maximum Match 100%
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SUMMARIES

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4	639	100.0	1346	6	AX464348	AX464348 Sequence
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6	628	98.3	666	6	AX083382	AX083382 Sequence
7	628	98.3	1347	6	AX083392	AX083392 Sequence
8	628	98.3	1377	9	BC050606	BC050606 Homo sapi
9	628	98.3	1440	9	BC015099	BC015099 Homo sapi
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64	157.4	24.6	226820	2	AC118872	AC118872 Rattus no
65	152.2	23.8	112893	10	AL732294	AL732294 Mouse DNA
66	152.2	23.8	234105	10	AC091606	AC091606 Mus Muscu
67	144.2	22.6	2415	6	AX047760	AX047760 Sequence
68	126.8	19.8	1877	5	BC065470	BC065470 Danio rer
69	125.6	19.7	2415	6	AX047764	AX047764 Sequence
70	125	19.6	2415	6	AR135178	AR135178 Sequence
71	125	19.6	2415	6	BD274685	BD274685 Angiotens
72	125	19.6	2415	6	E43987	E43987 ACE-analogo
73	125	19.6	2415	6	AR382342	AR382342 Sequence
74	125	19.6	2415	6	AX418984	AX418984 Sequence
75	125	19.6	2418	6	E39033	E39033 MPROT15 pol
76	125	19.6	2418	9	AY623811	AY623811 Homo sapi
77	125	19.6	2599	6	E43988	E43988 ACE-analogo
78	125	19.6	3325	9	AF291820	AF291820 Homo sapi
79	125	19.6	3334	6	AX047758	AX047758 Sequence
80	125	19.6	3339	9	BC048094	BC048094 Homo sapi
81	125	19.6	3341	9	HSM800880	AL110224 Homo sapi
82	125	19.6	3348	9	BC039902	BC039902 Homo sapi
83	125	19.6	3375	9	BC059378	BC059378 Homo sapi
84	125	19.6	3396	6	AR135177	AR135177 Sequence
85	125	19.6	3396	6	BD274684	BD274684 Angiotens
86	125	19.6	3396	6	AR353104	AR353104 Sequence
87	125	19.6	3396	6	AR382341	AR382341 Sequence
88	125	19.6	3396	6	AX418982	AX418982 Sequence
89	125	19.6	3396	6	AX431513	AX431513 Sequence
90	125	19.6	3405	6	CQ754222	CQ754222 Sequence
91	125	19.6	3405	9	AF241254	AF241254 Homo sapi
92	123.4	19.3	2599	9	AB046569	AB046569 Homo sapi

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	94	119.8	18.7	3732	6	AX463938
	95	119.8	18.7	3732	9	AY358714
	96	118	18.5	1879	5	BC053284
	97	117	18.3	2920	6	AR353103
	98	111.4	17.4	2638	6	AX047762
	99	109.6	17.2	2760	10	AB053181
	100	108.6	17.0	1993	10	AB053182
	101	108.2	16.9	2638	6	AX047765
	102	108.2	16.9	2739	6	CQ754224
	103	108.2	16.9	2739	10	BC026801
	104	96.8	15.1	2134	6	CQ714933
	105	96.8	15.1	2262	6	E39034
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	114	60	9.4	60	6	CQ539130
	115	60	9.4	82453	9	AC004558
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	131	52.2	8.2	1155	5	BX934887
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	134	48	7.5	65	6	CQ556364
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	136	46	7.2	642	9	HSA342764
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	138	45	7.0	43581	9	AC005337
	139	43	6.7	51	6	AX159686
	140	42.6	6.7	2862	9	HUMHPI
	141	41.6	6.5	237658	2	AC094219
	142	41.6	6.5	274059	2	AC123367
	143	41.4	6.5	51	6	AX159685
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	145	41.4	6.5	151763	2	AC011715
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	154	39.8	6.2	135506	9	AC009950
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c	160	39.6	6.2	168812	9	AC011327
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AR528488 Sequence
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AR353103 Sequence
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AX159685 Sequence
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AP003549 Homo sapi
AC101962 Mus muscu
AC018840 Homo sapi
AC093185 Papio anu
AC011327 Homo sapi
CR735106 Danio rer
AC023514 Homo sapi
AC092529 Papio anu
AC018493 Homo sapi
AC066606 Homo sapi

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	171	39	6.1	173149	2	AL391218
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	174	39	6.1	207240	10	AC145744
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	187	38	5.9	81491	2	AC117319_3
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	197	37.6	5.9	159983	2	BX936352
	198	37.6	5.9	173103	9	AL512658
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	201	37.6	5.9	180179	2	AC018881
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	224	37	5.8	110000	2	PFMAL7P1_07
	225	37	5.8	125020	9	AF429315
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	229	37	5.8	225782	2	AC109529
	230	37	5.8	231840	5	AL954746
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	232	36.8	5.8	53242	2	AC136291
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	234	36.8	5.8	110000	2	AC140833_3
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	237	36.8	5.8	130932	9	AC092658
	238	36.8	5.8	132254	3	AC116330

AC067736 Homo sapi
BX004850 Zebrafish
AX655393 Sequence
AC020551 Homo sapi
AC117256 Mus muscu
AL391218 Homo sapi
AC068622 Homo sapi
AL590128 Human DNA
AC145744 Mus muscu
AC140279 Mus muscu
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AF002983 Xenopus l
AC021130 Homo sapi
AP002801 Homo sapi
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AC005308 Plasmodiu
AC103043 Rattus no
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AC130544 Mus muscu
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AC133114 Rattus no
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c 240	36.8	5.8	161523	9	AC012186	AC012186 Homo sapi
241	36.8	5.8	168194	9	AC040934	AC040934 Homo sapi
c 242	36.8	5.8	170563	9	AC092368	AC092368 Homo sapi
243	36.8	5.8	188383	2	AC053489	AC053489 Homo sapi
c 244	36.8	5.8	190266	2	AC141222	AC141222 Rattus no
245	36.8	5.8	194994	2	AC020609	AC020609 Homo sapi
246	36.8	5.8	206023	2	AC146657	AC146657 Otolemur
c 247	36.8	5.8	216680	2	AC021211	AC021211 Homo sapi
248	36.8	5.8	252366	2	AC096178	AC096178 Rattus no
c 249	36.8	5.8	264340	2	AC112537	AC112537 Rattus no
c 250	36.8	5.8	275547	2	AC128056	AC128056 Rattus no
251	36.6	5.7	3422	5	BC077316	BC077316 Xenopus l
252	36.6	5.7	84912	9	AL137840	AL137840 Human DNA
253	36.6	5.7	99030	5	BX572083	BX572083 Zebrafish
254	36.6	5.7	110000	2	BX001063_0	BX001063 Mus muscu
c 255	36.6	5.7	122557	9	HS229A8	Z86090 Human DNA s
256	36.6	5.7	144274	5	BX537138	BX537138 Zebrafish
257	36.6	5.7	153153	2	BX324227	BX324227 Danio rer
258	36.6	5.7	157955	10	AL807388	AL807388 Mouse DNA
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260	36.4	5.7	558	6	AR272825	AR272825 Sequence
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263	36.4	5.7	558	6	AR440531	AR440531 Sequence
264	36.4	5.7	558	6	AR472689	AR472689 Sequence
265	36.4	5.7	558	6	AR543342	AR543342 Sequence
266	36.4	5.7	558	6	AX062927	AX062927 Sequence
267	36.4	5.7	558	6	AX367844	AX367844 Sequence
268	36.4	5.7	616	6	CQ526153	CQ526153 Sequence
c 269	36.4	5.7	2491	9	AK125384	AK125384 Homo sapi
c 270	36.4	5.7	2784	9	AK095608	AK095608 Homo sapi
271	36.4	5.7	4030	10	AB029486	AB029486 Rattus no
272	36.4	5.7	4382	10	BC078640	BC078640 Mus muscu
273	36.4	5.7	54264	9	AC097529	AC097529 Homo sapi
274	36.4	5.7	57214	2	AC025653	AC025653 Homo sapi
275	36.4	5.7	67962	2	AL928684	AL928684 Homo sapi
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277	36.4	5.7	117480	10	BX255878	BX255878 Mouse DNA
278	36.4	5.7	118577	9	AC079997	AC079997 Homo sapi
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280	36.4	5.7	139336	2	AC148383	AC148383 Taeniopyg
281	36.4	5.7	139890	2	AC148440	AC148440 Taeniopyg
282	36.4	5.7	140808	2	AC021858	AC021858 Homo sapi
283	36.4	5.7	143928	2	AC148381	AC148381 Taeniopyg
c 284	36.4	5.7	160678	9	AC022536	AC022536 Homo sapi
c 285	36.4	5.7	165730	2	AC061988	AC061988 Homo sapi
286	36.4	5.7	168586	9	AC011497	AC011497 Homo sapi
287	36.4	5.7	170916	10	AC122060	AC122060 Mus muscu
c 288	36.4	5.7	184430	10	AC115811	AC115811 Mus muscu
289	36.4	5.7	185373	2	AC102079	AC102079 Mus muscu
c 290	36.4	5.7	190015	2	AC140056	AC140056 Rattus no
291	36.4	5.7	201360	2	AC107634	AC107634 Mus muscu
c 292	36.4	5.7	213729	2	AC150816	AC150816 Callithri
c 293	36.4	5.7	229782	2	AC111350	AC111350 Rattus no
c 294	36.4	5.7	251905	2	AC093682	AC093682 Homo sapi
295	36.2	5.7	2710	10	BC021887	BC021887 Mus muscu
296	36.2	5.7	110000	8	CR382125_07	Continuation (8 of
c 297	36.2	5.7	117406	9	AC010792	AC010792 Homo sapi
298	36.2	5.7	145172	9	AC104361	AC104361 Homo sapi
299	36.2	5.7	166370	2	AC036218	AC036218 Homo sapi
300	36.2	5.7	168080	9	AC073172	AC073172 Homo sapi
301	36.2	5.7	171671	2	AC115059	AC115059 Mus muscu
c 302	36.2	5.7	201397	9	AC091628	AC091628 Homo sapi
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c 304	36.2	5.7	220931	2	AC116066	AC116066 Rattus no
305	36.2	5.7	223409	9	BS000028	BS000028 Pan trogl
c 306	36.2	5.7	233303	2	AC114025	AC114025 Rattus no
307	36.2	5.7	236508	2	AC094222	AC094222 Rattus no
308	36.2	5.7	238394	2	AC133351	AC133351 Rattus no
309	36.2	5.7	244962	2	AC098272	AC098272 Rattus no
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c 311	36.2	5.7	259028	2	AC103238	AC103238 Rattus no
312	36.2	5.7	262363	2	AC131868	AC131868 Rattus no
c 313	36.2	5.7	284337	2	AC119016	AC119016 Rattus no
c 314	36	5.6	10852	1	MTU19363	U19363 Methanobact
315	36	5.6	11037	1	AE000883	AE000883 Methanoba
316	36	5.6	32488	3	AF100307	AF100307 Caenorhab
c 317	36	5.6	65394	2	AC117645	AC117645 Mus muscu
318	36	5.6	72461	9	AC073322	AC073322 Homo sapi
319	36	5.6	110000	2	AC129041_2	Continuation (3 of
320	36	5.6	126873	10	AC133171	AC133171 Mus muscu
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c 322	36	5.6	145806	2	BS000644	BS000644 Pan trogl
323	36	5.6	150988	2	AC141178	AC141178 Rattus no
c 324	36	5.6	153572	5	BX323992	BX323992 Zebrafish
325	36	5.6	157393	2	AC036212	AC036212 Homo sapi
326	36	5.6	165349	2	AC093665	AC093665 Homo sapi
327	36	5.6	171032	2	AC116242	AC116242 Rattus no
328	36	5.6	172200	2	AC147197	AC147197 Sus scrof
c 329	36	5.6	172780	10	AL805960	AL805960 Mouse DNA
330	36	5.6	173518	9	AC146450	AC146450 Pan trogl
331	36	5.6	177468	5	AL953916	AL953916 Zebrafish
332	36	5.6	179560	2	AC149106	AC149106 Papio anu
333	36	5.6	180836	2	AC025241	AC025241 Homo sapi
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335	36	5.6	189846	10	AC147234	AC147234 Mus muscu
336	36	5.6	192074	9	AC147133	AC147133 Pan trogl
c 337	36	5.6	192713	2	AC116253	AC116253 Rattus no
338	36	5.6	198894	10	AC134611	AC134611 Mus muscu
339	36	5.6	215102	2	CNS01DW3	AL136327 Homo sapi
340	36	5.6	217879	2	BS000646	BS000646 Pan trogl
341	36	5.6	225071	2	AC120955	AC120955 Rattus no
342	36	5.6	227178	2	AC107537	AC107537 Rattus no
343	36	5.6	246367	2	AC130871	AC130871 Rattus no
344	36	5.6	247515	2	AC116080	AC116080 Rattus no
345	36	5.6	278216	2	AC120814	AC120814 Rattus no
c 346	36	5.6	285659	2	AC128227	AC128227 Rattus no
347	35.8	5.6	2625	6	A83536	A83536 Sequence 1
348	35.8	5.6	2625	6	BD193369	BD193369 Cadherin-
349	35.8	5.6	2625	6	CQ824166	CQ824166 Sequence
350	35.8	5.6	2625	6	I34433	I34433 Sequence 57
351	35.8	5.6	2625	6	I46831	I46831 Sequence 51
352	35.8	5.6	2625	6	I55100	I55100 Sequence 57
353	35.8	5.6	2625	6	AX093786	AX093786 Sequence
354	35.8	5.6	2625	9	HUMCA11A	L34056 Homo sapien
355	35.8	5.6	2627	6	CQ722548	CQ722548 Sequence
356	35.8	5.6	3440	9	BC013609	BC013609 Homo sapi
357	35.8	5.6	3661	9	HUMOSF4A	D21254 Human mRNA
358	35.8	5.6	3712	6	AR034822	AR034822 Sequence
359	35.8	5.6	3712	6	E07382	E07382 cDNA encodi
c 360	35.8	5.6	75001	2	AC018581	AC018581 Homo sapi
c 361	35.8	5.6	131345	9	AC069023	AC069023 Homo sapi
c 362	35.8	5.6	137473	2	AC015944	AC015944 Homo sapi
c 363	35.8	5.6	167943	9	HS267M20	AL031053 Human DNA
c 364	35.8	5.6	168513	2	AC011982	AC011982 Homo sapi
365	35.8	5.6	173117	2	AL157885	AL157885 Homo sapi
366	35.8	5.6	201008	2	AC120584	AC120584 Rattus no
367	35.8	5.6	202967	2	AC107746	AC107746 Mus muscu
c 368	35.8	5.6	219310	2	AC111337	AC111337 Rattus no
c 369	35.8	5.6	227168	2	AC137448	AC137448 Rattus no
370	35.8	5.6	254733	3	AC117075	AC117075 Dictyoste
371	35.8	5.6	258927	2	AC106569	AC106569 Rattus no
c 372	35.8	5.6	349381	10	BX883052	BX883052 Rattus no
373	35.6	5.6	73794	2	AC101544	AC101544 Mus muscu
c 374	35.6	5.6	110000	2	AC111775_2	Continuation (3 of
c 375	35.6	5.6	118869	9	AC004903	AC004903 Homo sapi
376	35.6	5.6	137065	2	CR847942	CR847942 Danio rer
377	35.6	5.6	143565	2	AC023195	AC023195 Homo sapi
378	35.6	5.6	150830	2	CR628382	CR628382 Danio rer
379	35.6	5.6	159029	2	AC077691	AC077691 Mus muscu
380	35.6	5.6	160091	2	CR749182	CR749182 Danio rer
381	35.6	5.6	163117	10	AC131921	AC131921 Mus muscu
382	35.6	5.6	169142	2	BX119972	BX119972 Danio rer
c 383	35.6	5.6	172776	2	CR847498	CR847498 Danio rer
c 384	35.6	5.6	177849	2	BX927353	BX927353 Danio rer

	385	35.6	5.6	187304	10	AC131039 AC131039 Mus muscu
	386	35.6	5.6	188815	2	AC130245 AC130245 Rattus no
	387	35.6	5.6	190712	10	AC116997 AC116997 Mus muscu
c	388	35.6	5.6	190999	2	AC103899 AC103899 Bos tauru
	389	35.6	5.6	203266	9	CNS0000D AL049833 Human chr
	390	35.6	5.6	203638	2	AC135953 AC135953 Macaca mu
	391	35.6	5.6	204008	2	AC094417 AC094417 Rattus no
	392	35.6	5.6	205450	2	BX927330 BX927330 Danio rer
	393	35.6	5.6	234400	10	AC134468 AC134468 Mus muscu
	394	35.6	5.6	244237	2	AC096482 AC096482 Rattus no
c	395	35.6	5.6	249450	2	AC108355 AC108355 Rattus no
c	396	35.6	5.6	251100	2	AC127656 AC127656 Rattus no
c	397	35.6	5.6	254464	2	AC130856 AC130856 Rattus no
c	398	35.6	5.6	256437	5	BX664629 BX664629 Zebrafish
	399	35.4	5.5	1022	9	HSCD11S2 AF060370 Homo sapi
c	400	35.4	5.5	2744	9	AK126164 AK126164 Homo sapi
c	401	35.4	5.5	65870	2	AC132912 AC132912 Homo sapi
c	402	35.4	5.5	68352	8	T15F17 AF262042 Arabidops
	403	35.4	5.5	85579	9	AC004744 AC004744 Homo sapi
	404	35.4	5.5	104309	9	AL138717 AL138717 Human DNA
c	405	35.4	5.5	116966	8	AB046433 AB046433 Arabidops
c	406	35.4	5.5	142441	2	HSJ344H20 AL132710 Homo sapi
c	407	35.4	5.5	152696	5	BX294371 BX294371 Zebrafish
c	408	35.4	5.5	153588	9	AC010533 AC010533 Homo sapi
c	409	35.4	5.5	153728	10	AC093449 AC093449 Mus muscu
c	410	35.4	5.5	159645	2	AC092026 AC092026 Homo sapi
c	411	35.4	5.5	167511	2	AC083802 AC083802 Homo sapi
c	412	35.4	5.5	174414	5	AL954772 AL954772 Zebrafish
	413	35.4	5.5	174696	9	AC097533 AC097533 Homo sapi
	414	35.4	5.5	175651	9	AC145783 AC145783 Pan trogl
c	415	35.4	5.5	179988	10	AC110243 AC110243 Mus muscu
	416	35.4	5.5	186835	9	AC145378 AC145378 Pan trogl
c	417	35.4	5.5	189894	2	AC068656 AC068656 Homo sapi
	418	35.4	5.5	194225	2	AC124696 AC124696 Mus muscu
c	419	35.4	5.5	194690	9	AC025763 AC025763 Homo sapi
c	420	35.4	5.5	197632	10	AL672039 AL672039 Mouse DNA
	421	35.4	5.5	207443	2	CR589950 CR589950 Danio rer
	422	35.4	5.5	215416	10	AC129537 AC129537 Mus muscu
	423	35.4	5.5	216571	2	AC106506 AC106506 Rattus no
	424	35.4	5.5	221140	2	AC118076 AC118076 Rattus no
c	425	35.4	5.5	237271	2	AC106162 AC106162 Rattus no
	426	35.4	5.5	250318	2	AC109983 AC109983 Rattus no
c	427	35.4	5.5	250517	2	AC094734 AC094734 Rattus no
c	428	35.4	5.5	259175	2	AC106521 AC106521 Rattus no
	429	35.4	5.5	269126	2	AC096191 AC096191 Rattus no
	430	35.4	5.5	300050	1	AP004599 AP004599 Oceanobac
c	431	35.2	5.5	352	6	AX900887 AX900887 Sequence
c	432	35.2	5.5	352	6	BD036420 BD036420 Sequence
	433	35.2	5.5	1141	6	AX083744 AX083744 Sequence
c	434	35.2	5.5	15389	1	AF026147 AF026147 Bacillus
c	435	35.2	5.5	29993	6	AX825169 AX825169 Sequence
	436	35.2	5.5	32960	3	CET27E7 Z82284 Caenorhabdi
c	437	35.2	5.5	38342	6	AX251504 AX251504 Sequence
c	438	35.2	5.5	38342	6	AX344503 AX344503 Sequence
	439	35.2	5.5	69269	2	AC101436 AC101436 Mus muscu
	440	35.2	5.5	102425	9	AC011363 AC011363 Homo sapi
c	441	35.2	5.5	118661	2	AC139854 AC139854 Medicago
c	442	35.2	5.5	125020	9	AF429315 AF429315 Homo sapi
c	443	35.2	5.5	126062	8	AP006135 AP006135 Lotus cor
	444	35.2	5.5	127666	2	AC105069 AC105069 Mus muscu
	445	35.2	5.5	133563	2	AC099481 AC099481 Homo sapi
c	446	35.2	5.5	139762	10	AC122497 AC122497 Mus muscu
c	447	35.2	5.5	164658	2	AC142488 AC142488 Rattus no
	448	35.2	5.5	186258	10	AC138460 AC138460 Mus muscu
	449	35.2	5.5	192961	1	BSUB0011 Z99114 Bacillus su
	450	35.2	5.5	195349	2	AC006705 AC006705 Caenorhab
	451	35.2	5.5	200923	9	AC091928 AC091928 Homo sapi
	452	35.2	5.5	207441	5	AC145958 AC145958 Gallus ga
c	453	35.2	5.5	210223	10	AC122183 AC122183 Mus muscu
	454	35.2	5.5	213033	2	AC138246 AC138246 Mus muscu
c	455	35.2	5.5	218761	2	BX897744 BX897744 Danio rer
	456	35.2	5.5	234203	2	AC121311 AC121311 Mus muscu
c	457	35.2	5.5	241204	2	AC099185 AC099185 Rattus no
	458	35.2	5.5	246635	2	AC094740 AC094740 Rattus no
c	459	35.2	5.5	249251	10	AC134585 AC134585 Mus muscu
c	460	35.2	5.5	255087	2	AC124887 AC124887 Rattus no
c	461	35.2	5.5	279685	2	AC095731 AC095731 Rattus no
c	462	35.2	5.5	311677	2	AC118899 AC118899 Rattus no
	463	35	5.5	1659	3	AK113405 AK113405 Ciona int
c	464	35	5.5	2490	8	BT003013 BT003013 Arabidops
c	465	35	5.5	2856	8	AY125524 AY125524 Arabidops
c	466	35	5.5	3249	10	BC057361 BC057361 Mus muscu
c	467	35	5.5	3249	10	BC058733 BC058733 Mus muscu
c	468	35	5.5	14287	3	AC115588 AC115588 Dictyoste
c	469	35	5.5	42171	2	AC149389 AC149389 Phakopsor
c	470	35	5.5	52717	8	AB019227 AB019227 Arabidops
c	471	35	5.5	104295	9	AC117502 AC117502 Homo sapi
	472	35	5.5	107736	5	BX936376 BX936376 Zebrafish
c	473	35	5.5	110000	2	PFMAL13_07 Continuation (8 of
	474	35	5.5	128294	8	AC135225 AC135225 Oryza sat
c	475	35	5.5	131796	9	AC097632 AC097632 Homo sapi
	476	35	5.5	132097	2	AC131378 AC131378 Strongylo
	477	35	5.5	134347	9	AL356295 AL356295 Human DNA
c	478	35	5.5	134867	2	AC013788 AC013788 Homo sapi
c	479	35	5.5	137580	8	AF377947 AF377947 Oryza sat
c	480	35	5.5	145467	2	BX649627 BX649627 Danio rer
c	481	35	5.5	147449	2	CR626923 CR626923 Danio rer
	482	35	5.5	147917	2	AC122455 AC122455 Mus muscu
c	483	35	5.5	149096	2	AC025083 AC025083 Homo sapi
c	484	35	5.5	149202	2	AC022160 AC022160 Homo sapi
c	485	35	5.5	149820	2	CR382286 CR382286 Danio rer
	486	35	5.5	154434	5	BX649404 BX649404 Zebrafish
c	487	35	5.5	156382	10	AC093448 AC093448 Mus muscu
c	488	35	5.5	158472	9	AC110612 AC110612 Homo sapi
	489	35	5.5	158908	5	BX511176 BX511176 Zebrafish
c	490	35	5.5	159442	5	AL954768 AL954768 Zebrafish
c	491	35	5.5	163476	2	BX950866 BX950866 Danio rer
c	492	35	5.5	164677	2	BX908774 BX908774 Danio rer
	493	35	5.5	167658	2	AC139358 AC139358 Mus muscu
c	494	35	5.5	168332	2	BX321886 BX321886 Danio rer
	495	35	5.5	170227	2	AC019161 AC019161 Homo sapi
	496	35	5.5	173359	2	AC021536 AC021536 Homo sapi
c	497	35	5.5	176056	10	AC073437 AC073437 Mus muscu
c	498	35	5.5	177130	3	AC092219 AC092219 Drosophil
c	499	35	5.5	178013	5	BX005166 BX005166 Zebrafish
	500	35	5.5	178238	4	AC092519 AC092519 Felis cat
	501	35	5.5	179529	2	AC020004 AC020004 Drosophil
	502	35	5.5	180038	2	AC137950 AC137950 Mus muscu
c	503	35	5.5	180126	2	AC022074 AC022074 Homo sapi
c	504	35	5.5	182934	5	BX000690 BX000690 Zebrafish
c	505	35	5.5	186713	2	AC123644 AC123644 Mus muscu
	506	35	5.5	192484	10	AC134906 AC134906 Mus muscu
	507	35	5.5	194715	9	AC078989 AC078989 Homo sapi
c	508	35	5.5	196421	10	AL672100 AL672100 Mouse DNA
	509	35	5.5	202686	5	AC146539 AC146539 Gasterost
	510	35	5.5	203390	10	AC121940 AC121940 Mus muscu
c	511	35	5.5	207672	3	AC005834 AC005834 Drosophil
c	512	35	5.5	232065	2	AC069425 AC069425 Homo sapi
	513	35	5.5	243789	10	AL672082 AL672082 Mouse DNA
	514	35	5.5	246163	2	AC121623 AC121623 Rattus no
	515	35	5.5	268661	3	AE003618 AE003618 Drosophil
	516	35	5.5	281000	3	TBBCHR1A2 AL929604 Trypanoso
c	517	35	5.5	315176	2	AC078956 AC078956 Homo sapi
	518	35	5.5	320170	2	CR792440 CR792440 Danio rer
	519	35	5.5	334462	6	AX773937 AX773937 Sequence
c	520	34.8	5.4	652	6	A68693 A68693 Sequence 7
	521	34.8	5.4	978	6	AX047948 AX047948 Sequence
	522	34.8	5.4	4602	9	AK128194 AK128194 Homo sapi
c	523	34.8	5.4	18246	14	AF212302 AF212302 Nipah vir
c	524	34.8	5.4	18246	14	AY029767 AY029767 Nipah vir
c	525	34.8	5.4	18246	14	AY029768 AY029768 Nipah vir
c	526	34.8	5.4	18246	14	NVI564621 AJ564621 Nipah vir
c	527	34.8	5.4	18246	14	NVI564622 AJ564622 Nipah vir
c	528	34.8	5.4	18246	14	NVI564623 AJ564623 Nipah vir
	529	34.8	5.4	61547	2	AC105025 AC105025 Homo sapi
	530	34.8	5.4	76988	9	AC006578 AC006578 Homo sapi

c 531	34.8	5.4	83007	8	AC123575	AC123575 Medicago
532	34.8	5.4	110000	2	AL359978_1	Continuation (2 of
533	34.8	5.4	111051	9	AL353806	AL353806 Human DNA
c 534	34.8	5.4	115339	8	AP003940	AP003940 Oryza sat
c 535	34.8	5.4	129438	10	AL929132	AL929132 Mouse DNA
536	34.8	5.4	147762	5	CR388421	CR388421 Zebrafish
c 537	34.8	5.4	154354	2	RN470J21	AL627239 Rattus no
c 538	34.8	5.4	156916	9	AC068278	AC068278 Homo sapi
539	34.8	5.4	158573	2	AC078823	AC078823 Homo sapi
c 540	34.8	5.4	159386	2	CR751548	CR751548 Danio rer
541	34.8	5.4	173535	2	AC120202	AC120202 Papio anu
542	34.8	5.4	182666	5	AL929172	AL929172 Zebrafish
c 543	34.8	5.4	185300	9	AP000962	AP000962 Homo sapi
c 544	34.8	5.4	188417	9	AC025205	AC025205 Homo sapi
545	34.8	5.4	206537	10	AC134578	AC134578 Mus muscu
c 546	34.8	5.4	212813	10	AC118210	AC118210 Mus muscu
547	34.8	5.4	221548	10	AC132142	AC132142 Mus muscu
c 548	34.8	5.4	223646	5	BX511306	BX511306 Zebrafish
c 549	34.8	5.4	224095	2	CR392350	CR392350 Danio rer
c 550	34.8	5.4	228140	2	AC122736	AC122736 Mus muscu
551	34.8	5.4	228821	2	AC098626	AC098626 Rattus no
552	34.8	5.4	231028	2	AC105707	AC105707 Rattus no
553	34.8	5.4	240178	2	AC094173	AC094173 Rattus no
554	34.8	5.4	242445	2	AC105670	AC105670 Rattus no
555	34.8	5.4	250361	2	AC105656	AC105656 Rattus no
556	34.8	5.4	255841	2	AC140260	AC140260 Mus muscu
c 557	34.8	5.4	287626	2	AC111963	AC111963 Rattus no
558	34.8	5.4	288136	2	AC120489	AC120489 Rattus no
c 559	34.8	5.4	296666	2	AC112983	AC112983 Mus muscu
c 560	34.8	5.4	340000	9	AP001667	AP001667 Homo sapi
c 561	34.6	5.4	2031	10	BC048915	BC048915 Mus muscu
c 562	34.6	5.4	3291	10	AB038519	AB038519 Mus muscu
c 563	34.6	5.4	3344	10	BC057936	BC057936 Mus muscu
c 564	34.6	5.4	68556	9	AL590027	AL590027 Human DNA
c 565	34.6	5.4	76587	9	AL390954	AL390954 Human DNA
566	34.6	5.4	89196	9	AC012619	AC012619 Homo sapi
c 567	34.6	5.4	102546	5	BX470088	BX470088 Zebrafish
c 568	34.6	5.4	102798	2	AL138730	AL138730 Homo sapi
569	34.6	5.4	110000	2	AC092450_3	Continuation (4 of
c 570	34.6	5.4	110000	2	AC092450_4	Continuation (5 of
571	34.6	5.4	110000	3	AC116305_2	Continuation (3 of
c 572	34.6	5.4	113164	2	AC136925	AC136925 Oryza sat
c 573	34.6	5.4	117296	9	AC092865	AC092865 Homo sapi
574	34.6	5.4	117347	2	CR388377	CR388377 Homo sapi
575	34.6	5.4	130377	2	AC122130	AC122130 Homo sapi
c 576	34.6	5.4	132290	9	AL627402	AL627402 Human DNA
c 577	34.6	5.4	133974	2	AC108894	AC108894 Bos tauru
c 578	34.6	5.4	135714	9	AL160037	AL160037 Human DNA
579	34.6	5.4	137586	9	AC106775	AC106775 Homo sapi
580	34.6	5.4	143093	9	AL442635	AL442635 Human DNA
c 581	34.6	5.4	143717	2	AC083933	AC083933 Homo sapi
c 582	34.6	5.4	144391	2	AC055823	AC055823 Homo sapi
583	34.6	5.4	144735	2	AL161458	AL161458 Homo sapi
584	34.6	5.4	148481	2	AC122139	AC122139 Homo sapi
585	34.6	5.4	150027	2	AC015596	AC015596 Homo sapi
c 586	34.6	5.4	150594	2	AC108889	AC108889 Bos tauru
587	34.6	5.4	151198	9	AC024730	AC024730 Homo sapi
c 588	34.6	5.4	153339	2	AC143280	AC143280 Macaca mu
589	34.6	5.4	153477	2	AC006278	AC006278 Plasmodiu
c 590	34.6	5.4	153563	2	CR628371	CR628371 Danio rer
591	34.6	5.4	154054	2	AC020919	AC020919 Homo sapi
592	34.6	5.4	155044	2	CR450771	CR450771 Danio rer
c 593	34.6	5.4	158066	9	AC107307	AC107307 Homo sapi
c 594	34.6	5.4	159716	2	AC025807	AC025807 Homo sapi
595	34.6	5.4	162325	2	CR774195	CR774195 Danio rer
596	34.6	5.4	167311	9	AC073895	AC073895 Homo sapi
c 597	34.6	5.4	167478	9	AL445235	AL445235 Human DNA
598	34.6	5.4	168665	5	AC146870	AC146870 Xenopus t
c 599	34.6	5.4	170329	2	AC069424	AC069424 Homo sapi
c 600	34.6	5.4	170776	9	AL139087	AL139087 Human DNA
601	34.6	5.4	170970	2	AC021564	AC021564 Homo sapi
c 602	34.6	5.4	171370	9	AC004021	AC004021 Human PAC
603	34.6	5.4	171637	2	AC116691	AC116691 Mus muscu
c 604	34.6	5.4	172021	2	AC024666	AC024666 Homo sapi
c 605	34.6	5.4	172577	2	AL365174	AL365174 Homo sapi
606	34.6	5.4	174128	9	AL137139	AL137139 Human DNA
c 607	34.6	5.4	174698	9	AC092962	AC092962 Homo sapi
c 608	34.6	5.4	174830	9	AL805977	AL805977 Human DNA
609	34.6	5.4	175838	2	AC116356	AC116356 Homo sapi
610	34.6	5.4	178233	8	AC134256	AC134256 Oryza sat
c 611	34.6	5.4	178985	9	AC015524	AC015524 Homo sapi
c 612	34.6	5.4	180091	2	AC117141	AC117141 Rattus no
613	34.6	5.4	180347	9	AC009415	AC009415 Homo sapi
614	34.6	5.4	182311	10	AC114677	AC114677 Mus muscu
c 615	34.6	5.4	183580	9	AL160253	AL160253 Human DNA
616	34.6	5.4	188209	2	AC099649	AC099649 Homo sapi
c 617	34.6	5.4	190119	2	AC136412	AC136412 Rattus no
618	34.6	5.4	192480	10	AL807832	AL807832 Mouse DNA
c 619	34.6	5.4	193180	2	AC112588	AC112588 Rattus no
620	34.6	5.4	199117	10	AC112257	AC112257 Mus muscu
c 621	34.6	5.4	201156	2	AC021757	AC021757 Homo sapi
622	34.6	5.4	204769	2	AC150377	AC150377 Callithri
623	34.6	5.4	212019	2	AL929453	AL929453 Danio rer
c 624	34.6	5.4	222879	5	BX324175	BX324175 Zebrafish
c 625	34.6	5.4	242449	10	AC102618	AC102618 Mus muscu
626	34.6	5.4	251551	3	AE014844	AE014844 Plasmodiu
c 627	34.6	5.4	255815	2	AC098130	AC098130 Rattus no
628	34.6	5.4	262565	2	BX914199	BX914199 Danio rer
c 629	34.6	5.4	264095	9	AC008500	AC008500 Homo sapi
630	34.6	5.4	286449	2	AC126168	AC126168 Rattus no
631	34.6	5.4	295808	2	AC151867	AC151867 Callithri
632	34.6	5.4	336376	2	AC106127	AC106127 Rattus no
633	34.4	5.4	564	11	BV042314	BV042314 S212P6036
634	34.4	5.4	758	5	BX931879	BX931879 Gallus ga
c 635	34.4	5.4	1645	9	AK091983	AK091983 Homo sapi
c 636	34.4	5.4	1971	2	AC019478	AC019478 Drosophil
c 637	34.4	5.4	13405	8	SOYACCA	L48995 Glycine max
c 638	34.4	5.4	40545	9	AL500524	AL500524 Human DNA
c 639	34.4	5.4	98404	2	AL355676	AL355676 Homo sapi
640	34.4	5.4	110000	2	AC098269_2	Continuation (3 of
641	34.4	5.4	110000	2	AC098269_3	Continuation (4 of
642	34.4	5.4	110000	2	AC109525_0	AC109525 Rattus no
643	34.4	5.4	134167	9	AC064814	AC064814 Homo sapi
644	34.4	5.4	135334	8	AC146554	AC146554 Medicago
c 645	34.4	5.4	139401	2	BX957315	BX957315 Danio rer
c 646	34.4	5.4	142617	2	AC150014	AC150014 Atelerix
c 647	34.4	5.4	158622	2	CR384060	CR384060 Danio rer
c 648	34.4	5.4	158972	2	CR752649	CR752649 Danio rer
c 649	34.4	5.4	159509	8	AP004225	AP004225 Oryza sat
650	34.4	5.4	163119	10	AL824713	AL824713 Mouse DNA
c 651	34.4	5.4	163339	2	AC149785	AC149785 Otolemur
652	34.4	5.4	169567	10	AC122508	AC122508 Mus muscu
653	34.4	5.4	170695	2	AC068545	AC068545 Homo sapi
c 654	34.4	5.4	171627	2	AC126924	AC126924 Sus scrof
655	34.4	5.4	172206	9	AC007619	AC007619 Homo sapi
c 656	34.4	5.4	172642	8	AP004258	AP004258 Oryza sat
657	34.4	5.4	174696	2	AC125165	AC125165 Mus muscu
c 658	34.4	5.4	176384	2	AC150507	AC150507 Bos tauru
c 659	34.4	5.4	178778	2	AC105810	AC105810 Rattus no
660	34.4	5.4	180555	2	AC148143	AC148143 Sus scrof
c 661	34.4	5.4	181531	9	AC007690	AC007690 Homo sapi
c 662	34.4	5.4	182553	2	AC149646	AC149646 Bos tauru
c 663	34.4	5.4	188344	2	AC131617	AC131617 Homo sapi
664	34.4	5.4	189639	9	AC010997	AC010997 Homo sapi
c 665	34.4	5.4	196468	10	AC111065	AC111065 Mus muscu
666	34.4	5.4	201188	5	AC145974	AC145974 Gallus ga
c 667	34.4	5.4	211815	2	CR753872	CR753872 Danio rer
c 668	34.4	5.4	213290	5	BX005237	BX005237 Zebrafish
669	34.4	5.4	219047	2	AC136822	AC136822 Rattus no
c 670	34.4	5.4	229333	2	AC102082	AC102082 Mus muscu
671	34.4	5.4	230115	2	AC095927	AC095927 Rattus no
672	34.4	5.4	232974	2	AC114193	AC114193 Rattus no
673	34.4	5.4	244692	2	AC108646	AC108646 Rattus no
674	34.4	5.4	258025	2	AC107254	AC107254 Rattus no
c 675	34.4	5.4	258594	2	AC115393	AC115393 Rattus no
c 676	34.4	5.4	275024	2	CR384078	CR384078 Danio rer

c 677	34.4	5.4	283666	2	AC127794	AC127794 Rattus no
678	34.4	5.4	288186	2	AC107100	AC107100 Rattus no
c 679	34.4	5.4	293726	2	AC135123	AC135123 Rattus no
680	34.4	5.4	303671	1	AE015937	AE015937 Clostridi
c 681	34.4	5.4	338858	2	AC130501	AC130501 Rattus no
682	34.4	5.4	348753	2	AC109063	AC109063 Rattus no
c 683	34.2	5.4	374	3	AF356331	AF356331 Taenia so
684	34.2	5.4	426	6	CQ399263	CQ399263 Sequence
685	34.2	5.4	426	6	CQ405541	CQ405541 Sequence
686	34.2	5.4	630	11	BV063787	BV063787 S212P6018
c 687	34.2	5.4	1399	8	AK068641	AK068641 Oryza sat
c 688	34.2	5.4	2296	8	AK068118	AK068118 Oryza sat
c 689	34.2	5.4	2566	8	AK122122	AK122122 Oryza sat
690	34.2	5.4	11767	1	AE015036	AE015036 Streptoco
c 691	34.2	5.4	42421	3	U80836	U80836 Caenorhabdi
692	34.2	5.4	55870	9	AL645585	AL645585 Human DNA
693	34.2	5.4	71506	2	AC151318	AC151318 Xenopus t
694	34.2	5.4	71903	9	AL607035	AL607035 Human DNA
695	34.2	5.4	75849	2	AC101259	AC101259 Mus muscu
c 696	34.2	5.4	87894	2	AC125031	AC125031 Mus muscu
697	34.2	5.4	100564	8	AC149266	AC149266 Solanum d
698	34.2	5.4	107044	9	AC011375	AC011375 Homo sapi
699	34.2	5.4	119923	2	AC013943	AC013943 Drosophil
c 700	34.2	5.4	123219	6	AX195073	AX195073 Sequence
c 701	34.2	5.4	134305	2	AC068743	AC068743 Homo sapi
c 702	34.2	5.4	145231	10	AC119969	AC119969 Mus muscu
703	34.2	5.4	157122	2	AC149241	AC149241 Macaca mu
c 704	34.2	5.4	158365	2	AC150811	AC150811 Callithri
c 705	34.2	5.4	160055	2	AC144744	AC144744 Danio rer
c 706	34.2	5.4	160943	9	AC116317	AC116317 Homo sapi
c 707	34.2	5.4	164354	9	AC022721	AC022721 Homo sapi
708	34.2	5.4	164971	3	AC016792	AC016792 Drosophil
709	34.2	5.4	166543	9	AP000742	AP000742 Homo sapi
c 710	34.2	5.4	179954	9	AC007271	AC007271 Homo sapi
c 711	34.2	5.4	180221	9	AC007277	AC007277 Homo sapi
712	34.2	5.4	181300	9	AP001376	AP001376 Homo sapi
c 713	34.2	5.4	183477	2	BX957239	BX957239 Danio rer
c 714	34.2	5.4	184040	2	AC102842	AC102842 Mus muscu
715	34.2	5.4	184729	9	AC097521	AC097521 Homo sapi
c 716	34.2	5.4	187735	2	AC101837	AC101837 Mus muscu
c 717	34.2	5.4	191975	10	AC147045	AC147045 Mus muscu
c 718	34.2	5.4	195141	2	AC149627	AC149627 Papio anu
719	34.2	5.4	196195	10	AC122383	AC122383 Mus muscu
720	34.2	5.4	199730	2	AC083940	AC083940 Homo sapi
c 721	34.2	5.4	200000	2	AC004689	AC004689 Homo sapi
c 722	34.2	5.4	205069	9	AC068205	AC068205 Homo sapi
723	34.2	5.4	206691	2	AC128760	AC128760 Rattus no
724	34.2	5.4	210000	2	AC004599	AC004599 Homo sapi
725	34.2	5.4	211682	5	AL772198	AL772198 Zebrafish
c 726	34.2	5.4	216522	5	AC147448	AC147448 Gallus ga
c 727	34.2	5.4	219044	2	AC098090	AC098090 Rattus no
c 728	34.2	5.4	220678	3	AE003704	AE003704 Drosophil
c 729	34.2	5.4	221723	10	AL844582	AL844582 Mouse DNA
c 730	34.2	5.4	221755	5	BX119909	BX119909 Zebrafish
731	34.2	5.4	224657	2	AC119194	AC119194 Mus muscu
732	34.2	5.4	230701	10	AL713871	AL713871 Mouse DNA
733	34.2	5.4	231218	2	AC105673	AC105673 Rattus no
c 734	34.2	5.4	239216	2	BX546443	BX546443 Danio rer
735	34.2	5.4	240137	2	AC115875	AC115875 Mus muscu
c 736	34.2	5.4	241394	2	AC132789	AC132789 Rattus no
737	34.2	5.4	246367	2	AC112005	AC112005 Rattus no
738	34.2	5.4	247349	10	AC113206	AC113206 Mus muscu
c 739	34.2	5.4	251412	2	AC136586	AC136586 Rattus no
c 740	34.2	5.4	253050	1	AP000984	AP000984 Sulfolobu
c 741	34.2	5.4	259818	2	AC114852	AC114852 Rattus no
742	34.2	5.4	260955	2	AC095410	AC095410 Rattus no
c 743	34.2	5.4	274498	2	AC006765	AC006765 Caenorhab
744	34.2	5.4	281307	2	AC106352	AC106352 Rattus no
745	34.2	5.4	284046	2	AC130575	AC130575 Rattus no
c 746	34.2	5.4	294771	2	AC096201	AC096201 Rattus no
c 747	34	5.3	447	3	AF029116	AF029116 Sathon fa
c 748	34	5.3	616	11	G93032	G93032 S208P6186FE
749	34	5.3	822	6	AX747677	AX747677 Sequence
750	34	5.3	822	9	AK092699	AK092699 Homo sapi
c 751	34	5.3	4257	9	HSM803631	AL832324 Homo sapi
c 752	34	5.3	10912	1	AE010833	AE010833 Methanosa
753	34	5.3	11211	6	CQ727446	CQ727446 Sequence
c 754	34	5.3	32467	9	BS000053	BS000053 Pan trogl
755	34	5.3	48733	9	AC109488	AC109488 Homo sapi
c 756	34	5.3	64467	9	AC010344	AC010344 Homo sapi
757	34	5.3	108301	9	HS348I23	AL035090 Human DNA
758	34	5.3	110000	2	AC151769_2	Continuation (3 of
759	34	5.3	118773	8	AF541963	AF541963 Glycine m
760	34	5.3	134469	2	AC140085	AC140085 Cercopith
761	34	5.3	139440	2	AC137926	AC137926 Brassica
c 762	34	5.3	143728	10	AL645476	AL645476 Mouse DNA
c 763	34	5.3	145502	2	AC102464	AC102464 Mus muscu
c 764	34	5.3	150695	10	AL672056	AL672056 Mouse DNA
c 765	34	5.3	151722	10	AC116578	AC116578 Mus muscu
c 766	34	5.3	153924	2	AC149744	AC149744 Bos tauru
c 767	34	5.3	155090	2	BX950193	BX950193 Danio rer
c 768	34	5.3	156008	9	AL353093	AL353093 Human DNA
c 769	34	5.3	159043	9	AC027359	AC027359 Homo sapi
c 770	34	5.3	161478	2	AC148042	AC148042 Cercopith
c 771	34	5.3	165582	2	AC142536	AC142536 Homo sapi
c 772	34	5.3	166185	5	BX649507	BX649507 Zebrafish
773	34	5.3	168421	5	AL954311	AL954311 Zebrafish
774	34	5.3	169147	2	AC129989	AC129989 Rattus no
c 775	34	5.3	173744	9	AC107892	AC107892 Homo sapi
c 776	34	5.3	176584	9	AC103686	AC103686 Homo sapi
777	34	5.3	176945	2	AC147931	AC147931 Cercopith
778	34	5.3	177647	9	AC091969	AC091969 Homo sapi
c 779	34	5.3	178405	5	BX005017	BX005017 Zebrafish
780	34	5.3	178832	5	BX511212	BX511212 Zebrafish
c 781	34	5.3	180399	2	AP001144	AP001144 Homo sapi
782	34	5.3	182016	9	AF228660	AF228660 Homo sapi
c 783	34	5.3	182041	9	AC090921	AC090921 Homo sapi
c 784	34	5.3	182616	10	AC133494	AC133494 Mus muscu
785	34	5.3	185548	2	AP001018	AP001018 Homo sapi
786	34	5.3	186846	9	AC091046	AC091046 Homo sapi
787	34	5.3	187059	9	AY316117	AY316117 Homo sapi
c 788	34	5.3	187691	5	BX324194	BX324194 Zebrafish
c 789	34	5.3	188618	5	BX936428	BX936428 Zebrafish
790	34	5.3	189391	2	AC019151	AC019151 Homo sapi
791	34	5.3	191011	2	AC036138	AC036138 Homo sapi
792	34	5.3	195874	9	AP000789	AP000789 Homo sapi
793	34	5.3	198523	10	AL845158	AL845158 Mouse DNA
794	34	5.3	201092	2	AC099614	AC099614 Mus muscu
c 795	34	5.3	201103	2	AC115842	AC115842 Mus muscu
c 796	34	5.3	201725	2	AL591706	AL591706 Homo sapi
c 797	34	5.3	201851	2	AC121647	AC121647 Rattus no
798	34	5.3	203737	10	AC116461	AC116461 Mus muscu
799	34	5.3	204325	2	BX284609	BX284609 Mus muscu
800	34	5.3	208909	5	BX004975	BX004975 Zebrafish
801	34	5.3	227923	2	AC099077	AC099077 Rattus no
c 802	34	5.3	229150	2	AC131842	AC131842 Rattus no
c 803	34	5.3	240752	2	AC098049	AC098049 Rattus no
c 804	34	5.3	247296	2	AC127145	AC127145 Rattus no
c 805	34	5.3	252567	2	AC106154	AC106154 Rattus no
806	34	5.3	255411	2	AC118315	AC118315 Rattus no
c 807	34	5.3	256777	2	AC110239	AC110239 Mus muscu
c 808	34	5.3	308929	1	AE017145	AE017145 Helicobac
c 809	34	5.3	331094	2	AC113834	AC113834 Rattus no
c 810	34	5.3	347050	3	PFA929351	AL929351 Plasmodiu
811	33.8	5.3	428	6	CQ700707	CQ700707 Sequence
812	33.8	5.3	1233	4	AY568570S4	AY568573 Bos tauru
c 813	33.8	5.3	1982	6	CQ067037	CQ067037 Sequence
c 814	33.8	5.3	1982	6	CQ094089	CQ094089 Sequence
c 815	33.8	5.3	1982	6	CQ132873	CQ132873 Sequence
c 816	33.8	5.3	1982	6	CQ171459	CQ171459 Sequence
c 817	33.8	5.3	1982	6	CQ200573	CQ200573 Sequence
c 818	33.8	5.3	1982	6	CQ254647	CQ254647 Sequence
c 819	33.8	5.3	1982	6	CQ291733	CQ291733 Sequence
c 820	33.8	5.3	1982	6	CQ328792	CQ328792 Sequence
c 821	33.8	5.3	62580	9	AL355143	AL355143 Human DNA
822	33.8	5.3	73947	6	CQ580328	CQ580328 Sequence

	823	33.8	5.3	89871	3	AC005890 AC005890 Drosophil
c	824	33.8	5.3	94516	9	AC112126 AC112126 Homo sapi
c	825	33.8	5.3	95075	2	AL365200 AL365200 Homo sapi
c	826	33.8	5.3	97818	2	AC011259 AC011259 Homo sapi
	827	33.8	5.3	99415	3	CEY54G11A AL034488 Caenorhab
c	828	33.8	5.3	104416	2	AC020324 AC020324 Drosophil
	829	33.8	5.3	110000	9	AY129465_0 AY129465 Homo sapi
c	830	33.8	5.3	121190	2	AC151659 AC151659 Dasypus n
c	831	33.8	5.3	130230	5	BX908764 BX908764 Zebrafish
	832	33.8	5.3	132952	2	AC150396 AC150396 Branchios
c	833	33.8	5.3	138188	8	AP004754 AP004754 Oryza sat
c	834	33.8	5.3	139049	9	AC019130 AC019130 Homo sapi
	835	33.8	5.3	139520	5	AL935199 AL935199 Zebrafish
c	836	33.8	5.3	140915	2	AC022361 AC022361 Homo sapi
	837	33.8	5.3	143502	10	AL935058 AL935058 Mouse DNA
c	838	33.8	5.3	144134	9	HSA183K14 AL109913 Human DNA
	839	33.8	5.3	146158	9	AL136136 AL136136 Human DNA
c	840	33.8	5.3	146530	9	AC023158 AC023158 Homo sapi
	841	33.8	5.3	149248	9	AL445492 AL445492 Human DNA
	842	33.8	5.3	149409	9	AC004081 AC004081 Homo sapi
c	843	33.8	5.3	152546	9	AL391221 AL391221 Human DNA
c	844	33.8	5.3	154336	9	AC117409 AC117409 Homo sapi
	845	33.8	5.3	154341	9	HS1164K7 AL592209 Homo sapi
c	846	33.8	5.3	155341	10	AC137713 AC137713 Mus muscu
c	847	33.8	5.3	158987	9	AC108713 AC108713 Homo sapi
c	848	33.8	5.3	160517	2	AL589785 AL589785 Homo sapi
c	849	33.8	5.3	163647	5	AC147916 AC147916 Xenopus t
	850	33.8	5.3	165585	5	BX511206 BX511206 Zebrafish
c	851	33.8	5.3	169045	9	AC005544 AC005544 Homo sapi
c	852	33.8	5.3	172043	2	AC055750 AC055750 Homo sapi
c	853	33.8	5.3	172052	9	AL157769 AL157769 Human DNA
c	854	33.8	5.3	172977	2	AC141528 AC141528 Rattus no
	855	33.8	5.3	173008	3	AC093196 AC093196 Drosophil
c	856	33.8	5.3	174927	9	AC010881 AC010881 Homo sapi
	857	33.8	5.3	175745	9	HS246O8 Z76735 Human DNA s
c	858	33.8	5.3	176075	3	AC007291 AC007291 Drosophil
	859	33.8	5.3	179789	9	AC069543 AC069543 Homo sapi
	860	33.8	5.3	180177	10	AC129590 AC129590 Mus muscu
c	861	33.8	5.3	180596	9	AC009570 AC009570 Homo sapi
c	862	33.8	5.3	180725	2	AC119511 AC119511 Rattus no
c	863	33.8	5.3	183155	9	AC073021 AC073021 Homo sapi
c	864	33.8	5.3	183541	9	AC083868 AC083868 Homo sapi
c	865	33.8	5.3	183704	2	AC023326 AC023326 Homo sapi
	866	33.8	5.3	184330	9	AC093561 AC093561 Homo sapi
	867	33.8	5.3	185084	4	AC147708 AC147708 Canis Fam
	868	33.8	5.3	185134	10	AC134472 AC134472 Mus muscu
c	869	33.8	5.3	185819	9	AC022387 AC022387 Homo sapi
c	870	33.8	5.3	186097	2	CR735102 CR735102 Danio rer
	871	33.8	5.3	187859	10	AC104095 AC104095 Mus muscu
	872	33.8	5.3	188167	2	AC068983 AC068983 Homo sapi
c	873	33.8	5.3	188546	2	AC022396 AC022396 Homo sapi
	874	33.8	5.3	192659	10	AL732365 AL732365 Mouse DNA
	875	33.8	5.3	194453	2	AC010862 AC010862 Homo sapi
	876	33.8	5.3	196674	2	AC091802 AC091802 Mus muscu
c	877	33.8	5.3	197452	2	AL355513 AL355513 Homo sapi
	878	33.8	5.3	204235	2	AC117423 AC117423 Homo sapi
	879	33.8	5.3	204317	2	AC102172 AC102172 Mus muscu
c	880	33.8	5.3	214527	2	AC105172 AC105172 Mus muscu
	881	33.8	5.3	221820	2	AC137393 AC137393 Rattus no
c	882	33.8	5.3	227208	2	AC150218 AC150218 Callithri
	883	33.8	5.3	232417	2	AC144603 AC144603 Bos tauru
c	884	33.8	5.3	237814	10	AC091464 AC091464 Mus muscu
	885	33.8	5.3	239116	9	AP000426 AP000426 Homo sapi
c	886	33.8	5.3	240691	2	AC108297 AC108297 Rattus no
c	887	33.8	5.3	250242	2	AC111983 AC111983 Rattus no
	888	33.8	5.3	254449	3	AE014817 AE014817 Plasmodiu
	889	33.8	5.3	261511	2	AC096066 AC096066 Rattus no
	890	33.8	5.3	265099	3	AE003626 AE003626 Drosophil
	891	33.8	5.3	286027	2	AC096225 AC096225 Rattus no
	892	33.8	5.3	325898	2	AC122990 AC122990 Rattus no
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c	894	33.6	5.3	476	6	CQ474353 CQ474353 Sequence
	895	33.6	5.3	1144	8	AK059333 AK059333 Oryza sat
	896	33.6	5.3	5337	6	AX277975 AX277975 Sequence
	897	33.6	5.3	5463	9	HSM806024 BX537914 Homo sapi
c	898	33.6	5.3	12029	3	AE001401 AE001401 Plasmodiu
	899	33.6	5.3	74817	9	AP001434 AP001434 Homo sapi
	900	33.6	5.3	90578	9	AC128686 AC128686 Homo sapi
	901	33.6	5.3	100000	9	AP000020 AP000020 Homo sapi
	902	33.6	5.3	100000	9	AP000162 AP000162 Homo sapi
	903	33.6	5.3	102818	2	AP000621 AP000621 Homo sapi
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	905	33.6	5.3	110000	2	AC119074_1 Continuation (2 of
	906	33.6	5.3	116878	9	AL135780 AL135780 Human DNA
	907	33.6	5.3	121961	2	AC090556 AC090556 Homo sapi
c	908	33.6	5.3	140211	2	AC146367 AC146367 Dasypus n
c	909	33.6	5.3	146088	2	BS000630 BS000630 Pan trogl
c	910	33.6	5.3	153806	2	AC011988 AC011988 Homo sapi
	911	33.6	5.3	156393	9	AC098652 AC098652 Homo sapi
	912	33.6	5.3	158832	5	BX936429 BX936429 Zebrafish
	913	33.6	5.3	159956	9	AC093289 AC093289 Homo sapi
	914	33.6	5.3	160401	9	AC009277 AC009277 Homo sapi
c	915	33.6	5.3	163992	9	AC078889 AC078889 Homo sapi
	916	33.6	5.3	167439	2	BX936407 BX936407 Danio rer
	917	33.6	5.3	168243	9	AC008526 AC008526 Homo sapi
	918	33.6	5.3	171501	2	AC026943 AC026943 Homo sapi
	919	33.6	5.3	172579	9	AC036125 AC036125 Homo sapi
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	921	33.6	5.3	176257	2	AC119444 AC119444 Rattus no
	922	33.6	5.3	176597	2	AC080190 AC080190 Homo sapi
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c	924	33.6	5.3	180436	10	AL671919 AL671919 Mouse DNA
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	926	33.6	5.3	189354	2	AC022990 AC022990 Homo sapi
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	928	33.6	5.3	191424	9	BS000127 BS000127 Pan trogl
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	931	33.6	5.3	196085	2	AC025971 AC025971 Homo sapi
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	933	33.6	5.3	201103	2	AC115842 AC115842 Mus muscu
	934	33.6	5.3	201308	2	AC142176 AC142176 Rattus no
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	936	33.6	5.3	204257	2	AC104293 AC104293 Rattus no
	937	33.6	5.3	205332	2	AC079570 AC079570 Mus muscu
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	939	33.6	5.3	207951	2	AC012264 AC012264 Homo sapi
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c	941	33.6	5.3	211342	2	AC113877 AC113877 Rattus no
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	943	33.6	5.3	218740	10	AL662932 AL662932 Mouse DNA
	944	33.6	5.3	225170	2	AC111590 AC111590 Rattus no
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	946	33.6	5.3	231148	2	AC095425 AC095425 Rattus no
	947	33.6	5.3	234142	9	AC146183 AC146183 Pan trogl
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	949	33.6	5.3	239730	2	AC128631 AC128631 Rattus no
c	950	33.6	5.3	249793	2	AC117104 AC117104 Rattus no
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	958	33.4	5.2	448	11	BX322350 BX322350 Arabidops
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c	960	33.4	5.2	2795	9	AK123278 AK123278 Homo sapi
c	961	33.4	5.2	7219	6	AX344890 AX344890 Sequence
	962	33.4	5.2	7778	6	AR353930 AR353930 Sequence
	963	33.4	5.2	7778	6	AR535486 AR535486 Sequence
	964	33.4	5.2	11572	6	CQ586379 CQ586379 Sequence
	965	33.4	5.2	12650	2	AC019748 AC019748 Drosophil
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c1008	33.4	5.2	149349	2	BX908739
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1010	33.4	5.2	152467	2	AC140023
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c1012	33.4	5.2	158037	2	AC012126
1013	33.4	5.2	160430	2	AC146947
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1015	33.4	5.2	164907	3	AC007146
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c1036	33.4	5.2	180049	9	AC099558
c1037	33.4	5.2	180846	2	AC145151
1038	33.4	5.2	181222	2	AC125249
c1039	33.4	5.2	183616	2	AC131686
c1040	33.4	5.2	183858	10	AC102452
1041	33.4	5.2	184489	2	AC027771

CQ613607 Sequence
AC129904 Ciona sav
AC006795 Caenorhab
AP002063 Arabidops
AC025172 Homo sapi
AC023899 Mus muscu
AC020235 Drosophil
AC069472 Arabidops
AC010427 Homo sapi
AL596330 Human DNA
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Continuation (7 of
Continuation (2 of
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AC011472 Homo sapi
AC022492 Genomic s
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AC139670 Medicago
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AC004943 Homo sapi
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AC012126 Homo sapi
AC146947 Oryza sat
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AC013705 Homo sapi
AC083941 Homo sapi
AP002338 Homo sapi
AL356462 Homo sapi
AC079258 Homo sapi
AC068397 Homo sapi
AC080162 Homo sapi
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AC101949 Mus muscu
AC116421 Mus muscu
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AC060806 Homo sapi
AC124047 Rattus no
AC099558 Homo sapi
AC145151 Homo sapi
AC125249 Mus muscu
AC131686 Mus muscu
AC102452 Mus muscu
AC027771 Homo sapi

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c1048	33.4	5.2	189354	2	AC022990
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1059	33.4	5.2	201855	2	AC145152
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1063	33.4	5.2	207757	10	AC022368
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1065	33.4	5.2	211421	2	AC147918
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1067	33.4	5.2	211701	2	AC096814
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1083	33.4	5.2	231636	2	AC114444
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c1085	33.4	5.2	238665	2	AC110465
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1088	33.4	5.2	249523	2	AC079537
1089	33.4	5.2	250029	3	AE014830
c1090	33.4	5.2	267870	2	AC099359
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c1111	33.2	5.2	30894	3	CEF57A8
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AL390314 Homo sapi
AC113428 Homo sapi
CR405687 Danio rer
AC147275 Pan trogl
CR388008 Danio rer
AC119503 Rattus no
AC022990 Homo sapi
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AL390766 Human DNA
AC007647 Drosophil
AC007760 Drosophil
AP002026 Homo sapi
AC124118 Mus muscu
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AC145152 Homo sapi
AC129979 Mus muscu
AC021850 Homo sapi
AC091306 Mus muscu
AC022368 Mus muscu
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AC147918 Xenopus t
AC115146 Rattus no
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AC009660 Homo sapi
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AP004602 Oceanobac
AE017012 Bacillus
AP003133 Staphyloc
AP003361 Staphyloc
G18450 cow STS BM6
AX509614 Sequence
BV059862 S212P6053
AR394180 Sequence
U28497 Borrelia du
BT013733 Lycopersi
D21255 Human mRNA
AR034823 Sequence
E07383 cDNA encodi
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M57435 B.subtilis
AE010602 Fusobacte
AE010161 Pyrococcu
Z70781 Caenorhabdi
AC073136 Homo sapi
AC138077 Homo sapi
AL808122 Mouse DNA

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c1117	33.2	5.2	107508	5	AL732577	AL732577 Zebrafish
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c1124	33.2	5.2	130825	2	AC129715	AC129715 Medicago
c1125	33.2	5.2	131947	8	AP006382	Lotus cor
1126	33.2	5.2	137219	9	AC025187	AC025187 Homo sapi
1127	33.2	5.2	137856	9	AC097720	AC097720 Homo sapi
1128	33.2	5.2	142329	2	AC046155	Homo sapi
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1131	33.2	5.2	143794	9	AC009315	Homo sapi
c1132	33.2	5.2	145876	9	AC025773	AC025773 Homo sapi
c1133	33.2	5.2	146807	5	BX682558	BX682558 Zebrafish
1134	33.2	5.2	147474	2	AC055760	Homo sapi
1135	33.2	5.2	148198	9	HS438G17	Z93931 Human DNA s
c1136	33.2	5.2	157604	9	AC021093	AC021093 Homo sapi
c1137	33.2	5.2	157633	9	AC123776	Homo sapi
1138	33.2	5.2	159644	9	AP000820	AP000820 Homo sapi
1139	33.2	5.2	159906	2	AL590706	AL590706 Homo sapi
1140	33.2	5.2	161870	5	BX004828	Zebrafish
c1141	33.2	5.2	164142	9	AL358552	AL358552 Human DNA
1142	33.2	5.2	164304	2	AC012136	AC012136 Homo sapi
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c1144	33.2	5.2	169173	2	BX323461	BX323461 Danio rer
c1145	33.2	5.2	169546	2	AC004157	AC004157 Plasmodiu
c1146	33.2	5.2	169819	2	AC074368	Homo sapi
1147	33.2	5.2	170346	9	AC020626	AC020626 Homo sapi
c1148	33.2	5.2	171617	2	AC013616	AC013616 Homo sapi
1149	33.2	5.2	173718	9	AC073575	Homo sapi
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1151	33.2	5.2	176320	9	AP003028	AP003028 Homo sapi
c1152	33.2	5.2	176749	9	AC096748	Homo sapi
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c1154	33.2	5.2	177127	2	AC026287	AC026287 Homo sapi
1155	33.2	5.2	177947	2	AC074022	Homo sapi
c1156	33.2	5.2	179463	5	BX546474	BX546474 Zebrafish
c1157	33.2	5.2	182507	9	AC013441	AC013441 Homo sapi
1158	33.2	5.2	182614	5	AL928830	Zebrafish
c1159	33.2	5.2	183357	9	AC068759	AC068759 Homo sapi
1160	33.2	5.2	184788	9	AF003627	AF003627 Homo sapi
1161	33.2	5.2	185794	2	AC132972	Rattus no
c1162	33.2	5.2	187478	2	BX927379	BX927379 Danio rer
c1163	33.2	5.2	187486	2	AC079840	AC079840 Homo sapi
c1164	33.2	5.2	188328	2	BX663516	Danio rer
1165	33.2	5.2	190890	9	AC087385	AC087385 Homo sapi
c1166	33.2	5.2	191697	2	AC148255	AC148255 Callithri
1167	33.2	5.2	194901	2	BX927228	Danio rer
c1168	33.2	5.2	194976	2	CR631126	CR631126 Danio rer
1169	33.2	5.2	197926	2	AC073844	AC073844 Homo sapi
1170	33.2	5.2	198226	8	ATCHRIV43	AL161543 Arabidops
c1171	33.2	5.2	198612	10	AC122341	AC122341 Mus muscu
c1172	33.2	5.2	200105	9	AC026975	AC026975 Homo sapi
1173	33.2	5.2	201932	5	BX897729	Zebrafish
1174	33.2	5.2	202562	5	BX510315	BX510315 Zebrafish
c1175	33.2	5.2	203952	5	BX510913	BX510913 Zebrafish
1176	33.2	5.2	205681	2	AC119471	Rattus no
1177	33.2	5.2	205802	5	AL772132	AL772132 Zebrafish
1178	33.2	5.2	206811	10	AC099715	AC099715 Mus muscu
c1179	33.2	5.2	207242	2	CR762445	CR762445 Danio rer
1180	33.2	5.2	207704	2	AC011300	AC011300 Homo sapi
c1181	33.2	5.2	208136	2	AC151042	AC151042 Callithri
1182	33.2	5.2	209164	8	ATFCA5	Z97340 Arabidopsis
1183	33.2	5.2	210236	10	AL672193	AL672193 Mouse DNA
1184	33.2	5.2	211409	2	AC127104	AC127104 Rattus no
c1185	33.2	5.2	211429	2	BX324152	Danio rer
1186	33.2	5.2	218880	10	AC122390	AC122390 Mus muscu
1187	33.2	5.2	221014	2	AC129848	AC129848 Rattus no
1188	33.2	5.2	221210	9	AC027281	AC027281 Homo sapi
1189	33.2	5.2	221474	2	AC134320	Canis fam
1190	33.2	5.2	221622	2	CR388405	CR388405 Danio rer
1191	33.2	5.2	228196	2	CR388094	Danio rer
1192	33.2	5.2	228558	2	CR376751	Danio rer
1193	33.2	5.2	230323	2	BX936443	BX936443 Danio rer
c1194	33.2	5.2	232409	2	AC025126	AC025126 Homo sapi
1195	33.2	5.2	234983	2	AC099168	Rattus no
c1196	33.2	5.2	238439	2	AC133693	AC133693 Rattus no
c1197	33.2	5.2	240579	2	AL360154	AL360154 Homo sapi
1198	33.2	5.2	241990	2	AC123449	Rattus no
c1199	33.2	5.2	242209	2	AC094491	AC094491 Rattus no
1200	33.2	5.2	242366	2	AC106958	AC106958 Rattus no
c1201	33.2	5.2	242467	2	BX927324	Danio rer
1202	33.2	5.2	243312	2	AC099151	AC099151 Rattus no
c1203	33.2	5.2	245202	2	AC092369	AC092369 Homo sapi
c1204	33.2	5.2	247103	2	AC114453	Rattus no
c1205	33.2	5.2	248568	2	AC121714	AC121714 Rattus no
c1206	33.2	5.2	248625	2	AC137216	AC137216 Rattus no
c1207	33.2	5.2	249982	2	AC108661	AC108661 Rattus no
1208	33.2	5.2	250421	3	AE014849	AE014849 Plasmodiu
c1209	33.2	5.2	250688	2	AC094683	AC094683 Rattus no
c1210	33.2	5.2	251132	2	AC098162	AC098162 Rattus no
1211	33.2	5.2	252632	3	AE014818	AE014818 Plasmodiu
c1212	33.2	5.2	257757	3	AE014837	AE014837 Plasmodiu
1213	33.2	5.2	259403	2	AC118091	AC118091 Rattus no
1214	33.2	5.2	260983	2	AC111480	AC111480 Rattus no
1215	33.2	5.2	263130	2	AC126000	AC126000 Rattus no
c1216	33.2	5.2	263253	2	AC097819	AC097819 Rattus no
1217	33.2	5.2	263605	2	AC097296	AC097296 Rattus no
1218	33.2	5.2	266079	2	AL391060	AL391060 Homo sapi
c1219	33.2	5.2	267656	2	AC106269	AC106269 Rattus no
c1220	33.2	5.2	270166	2	AC108263	AC108263 Rattus no
1221	33.2	5.2	302881	2	BX323850	BX323850 Danio rer
c1222	33.2	5.2	313801	2	AC117340	Rattus no
c1223	33.2	5.2	342650	1	AP003582	AP003582 Nostoc sp
c1224	33	5.2	362	6	CQ483522	CQ483522 Sequence
c1225	33	5.2	390	6	CQ504341	CQ504341 Sequence
c1226	33	5.2	390	6	CQ513394	CQ513394 Sequence
1227	33	5.2	538	11	G80545	G80545 S208P6679RF
1228	33	5.2	668	11	G53384	G53384 SHGC-82487
c1229	33	5.2	832	6	AR415176	AR415176 Sequence
c1230	33	5.2	832	6	AX972010	AX972010 Sequence
c1231	33	5.2	832	6	BD110729	BD110729 EST and e
1232	33	5.2	863	3	AY328137	AY328137 Plasmodiu
c1233	33	5.2	1493	8	AK108661	AK108661 Oryza sat
1234	33	5.2	1526	9	HSM802301	AL137559 Homo sapi
1235	33	5.2	1685	9	BC050442	BC050442 Homo sapi
1236	33	5.2	2000	6	AX508101	AX508101 Sequence
c1237	33	5.2	3866	6	CQ579917	CQ579917 Sequence
c1238	33	5.2	4097	6	CQ602165	CQ602165 Sequence
1239	33	5.2	5101	6	BD193922	BD193922 Enterococ
c1240	33	5.2	5811	6	AX151407	AX151407 Sequence
c1241	33	5.2	7679	2	AC014127	AC014127 Drosophil
1242	33	5.2	10901	1	AE001305	AE001305 Chlamydia
c1243	33	5.2	11327	6	AX251185	AX251185 Sequence
c1244	33	5.2	15732	6	AX277933	AX277933 Sequence
c1245	33	5.2	15732	6	AX323620	AX323620 Sequence
1246	33	5.2	24919	3	AF098991	AF098991 Caenorhab
1247	33	5.2	33001	9	AC130408	AC130408 Homo sapi
c1248	33	5.2	34739	3	U55368	U55368 Caenorhabdi
c1249	33	5.2	43794	3	L15188	L15188 Caenorhabdi
1250	33	5.2	43880	8	SPAC17G6	Z99162 S.pombe chr
1251	33	5.2	60609	2	AC023519	AC023519 Homo sapi
1252	33	5.2	96585	8	ATF10N7	AL021636 Arabidops
1253	33	5.2	105320	3	AC116920	AC116920 Dictyoste
1254	33	5.2	110000	2	AC111750_1	Continuation (2 of
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1258	33	5.2	115848	9	AL355582	AL355582 Human DNA
1259	33	5.2	118985	2	AC087152	AC087152 Mus muscu
1260	33	5.2	119175	9	AC111001	AC111001 Homo sapi

c1261	33	5.2	120849	2	AC087148
1262	33	5.2	121026	2	AC146777
c1263	33	5.2	121606	9	AL160401
1264	33	5.2	126815	9	AL354931
1265	33	5.2	127763	9	AC093589
c1266	33	5.2	134717	10	AL626805
1267	33	5.2	135079	9	HSDJ70A9
c1268	33	5.2	140817	10	AC127231
1269	33	5.2	141295	2	AC025780
c1270	33	5.2	141627	2	AC105953
c1271	33	5.2	142357	9	AC011416
c1272	33	5.2	143486	5	BX571830
1273	33	5.2	144914	2	CR352286
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c1275	33	5.2	147603	9	HSDJ258B3
c1276	33	5.2	150336	10	AC111064
1277	33	5.2	151026	9	AC005915
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c1280	33	5.2	153539	9	AP003784
1281	33	5.2	154850	2	CR376747
c1282	33	5.2	154861	5	BX511014
1283	33	5.2	155630	2	AC015721
1284	33	5.2	155914	2	AC010825
1285	33	5.2	156242	9	AB041731
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1288	33	5.2	159254	2	BX897733
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1291	33	5.2	161217	2	BX572617
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c1294	33	5.2	165698	8	ATCHRIV76
1295	33	5.2	167103	9	AC147065
c1296	33	5.2	167167	2	AC012035
c1297	33	5.2	167352	9	AC146147
1298	33	5.2	167960	9	AC093084
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1300	33	5.2	169973	10	AC124465
c1301	33	5.2	170197	9	AC062020
c1302	33	5.2	170327	2	CR318660
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c1306	33	5.2	173783	2	AC117135
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1312	33	5.2	177102	2	AP002808
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1316	33	5.2	180166	2	AC011898
1317	33	5.2	181864	2	AC027460
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1319	33	5.2	184594	5	BX649390
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c1322	33	5.2	188676	2	AC024515
1323	33	5.2	189877	9	AC138729
c1324	33	5.2	192013	2	BX511255
c1325	33	5.2	192791	2	AC147793
c1326	33	5.2	194025	5	BX294189
1327	33	5.2	194732	9	AB042031
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1329	33	5.2	198555	2	AC150770
c1330	33	5.2	200265	2	AC099579
1331	33	5.2	201313	3	AC010688
c1332	33	5.2	202316	10	AC138134
c1333	33	5.2	202551	2	BX936451

AC087148 Mus muscu
AC146777 Medicago
AL160401 Human DNA
AL354931 Human DNA
AC093589 Homo sapi
AL626805 Mouse DNA
AL121788 Human DNA
AC127231 Mus muscu
AC025780 Homo sapi
AC105953 Mus muscu
AC011416 Homo sapi
BX571830 Zebrafish
CR352286 Danio rer
AC024945 Homo sapi
AL109919 Human DNA
AC111064 Mus muscu
AC005915 Homo sapi
BX255962 Zebrafish
AP004316 Oryza sat
AP003784 Homo sapi
CR376747 Danio rer
BX511014 Zebrafish
AC015721 Homo sapi
AC010825 Homo sapi
AB041731 Homo sapi
AL354709 Human DNA
AC009638 Homo sapi
BX897733 Danio rer
AC013645 Homo sapi
AC010722 Homo sapi
BX572617 Danio rer
BX569795 Zebrafish
AL159140 Human chr
AL161580 Arabidops
AC147065 Pan trogl
AC012035 Homo sapi
AC146147 Pan trogl
AC093084 Homo sapi
AC006120 Homo sapi
AC124465 Mus muscu
AC062020 Homo sapi
CR318660 Danio rer
AC112232 Homo sapi
AL445532 Human DNA
BX005313 Zebrafish
AC117135 Rattus no
AL929027 Mouse DNA
AL844567 Zebrafish
AC147076 Pan trogl
AC129987 Rattus no
AC012234 Homo sapi
AP002808 Homo sapi
AL731795 Mouse DNA
AC123800 Mus muscu
CR388173 Danio rer
AC011898 Homo sapi
AC027460 Homo sapi
AC138309 Mus muscu
BX649390 Zebrafish
AC046142 Homo sapi
AP006199 Homo sapi
AC024515 Homo sapi
AC138729 Pongo pyg
BX511255 Danio rer
AC147793 Mus muscu
BX294189 Zebrafish
AB042031 Homo sapi
AC124171 Mus muscu
AC150770 Xenopus t
AC099579 Mus muscu
AC010688 Drosophil
AC138134 Mus muscu
BX936451 Danio rer

c1334	33	5.2	203514	10	AC114007
1335	33	5.2	204959	10	AC107865
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c1339	33	5.2	206973	10	AC149059
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1341	33	5.2	210319	10	AC114001
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c1343	33	5.2	213071	2	AC110680
1344	33	5.2	213599	2	AC140764
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c1346	33	5.2	214297	10	AC121595
c1347	33	5.2	214656	2	AC114163
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1349	33	5.2	215962	9	AC104940
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1352	33	5.2	219582	2	AC123671
c1353	33	5.2	223146	2	AC105456
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1356	33	5.2	228644	2	AC102879
1357	33	5.2	229084	2	AC096384
c1358	33	5.2	229336	2	AC110458
1359	33	5.2	229952	2	BX957256
c1360	33	5.2	231530	10	AL671975
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1365	33	5.2	246838	2	AC094812
1366	33	5.2	246927	2	AC133791
1367	33	5.2	246935	2	AC124838
1368	33	5.2	247436	2	CR812481
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1371	33	5.2	256635	2	AC128838
c1372	33	5.2	258015	2	AC131816
1373	33	5.2	258158	2	BX957297
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1375	33	5.2	264680	2	AC107277
1376	33	5.2	268444	2	BX927360
1377	33	5.2	269849	2	AC105483
1378	33	5.2	281101	3	AE003526
1379	33	5.2	284569	2	AC101935
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c1381	33	5.2	288529	2	AC095779
1382	33	5.2	292967	14	AF369029
1383	33	5.2	293405	2	AC096156
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1392	32.8	5.1	477	6	BD132993
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1395	32.8	5.1	822	6	AR319491
c1396	32.8	5.1	933	6	AR396130
c1397	32.8	5.1	1635	8	AB045260
c1398	32.8	5.1	2780	9	BC037878
c1399	32.8	5.1	2893	6	AX833366
c1400	32.8	5.1	2893	9	AK095031
c1401	32.8	5.1	17992	3	AC091267
c1402	32.8	5.1	21126	6	BD193429
1403	32.8	5.1	38122	3	U28732
c1404	32.8	5.1	40405	9	AC012336
1405	32.8	5.1	47943	2	AC134168
c1406	32.8	5.1	50630	9	AC107054

AC114007 Mus muscu
AC107865 Mus muscu
AL669911 Mouse DNA
AC116936 Papio anu
AC132449 Mus muscu
AC149059 Mus muscu
AC108914 Mus muscu
AC114001 Mus muscu
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BX640518 Danio rer
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AC123671 Mus muscu
AC105456 Rattus no
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CR627491 Danio rer
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AC101935 Mus muscu
CR749773 Danio rer
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AC096156 Rattus no
AP002529 Homo sapi
AP004171 Mycoplasm
AC147217 Pan trogl
AE016955 Enterococ
AX151396 Sequence
AF332093 White spo
AF440570 Shrimp wh
AC151733 Mus muscu
BD132993 Anti-bact
AR232443 Sequence
AR256495 Sequence
AR319491 Sequence
AR396130 Sequence
AB045260 Tilopteri
BC037878 Homo sapi
AX833366 Sequence
AK095031 Homo sapi
AC091267 Caenorhab
BD193429 Enterococ
U28732 Caenorhabdi
AC012336 Homo sapi
AC134168 Rattus no
AC107054 Homo sapi

c1407	32.8	5.1	52086	9	AC013404	AC013404 Homo sapi
1408	32.8	5.1	68628	5	BX950173	BX950173 Zebrafish
1409	32.8	5.1	70499	9	AC104411	AC104411 Homo sapi
c1410	32.8	5.1	79691	9	AC079749	AC079749 Homo sapi
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1415	32.8	5.1	112070	9	AC068798	AC068798 Homo sapi
1416	32.8	5.1	117266	2	AC148385	AC148385 Dasypus n
c1417	32.8	5.1	127126	8	AC123899	AC123899 Medicago
1418	32.8	5.1	132393	2	AC138881	AC138881 Homo sapi
1419	32.8	5.1	138102	9	AC004866	AC004866 Homo sapi
1420	32.8	5.1	138830	9	AP004281	AP004281 Homo sapi
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1422	32.8	5.1	141568	9	AC063956	AC063956 Homo sapi
c1423	32.8	5.1	144407	9	HSJ799P18	AL122008 Human DNA
1424	32.8	5.1	148239	2	BX957225	BX957225 Danio rer
c1425	32.8	5.1	150410	2	AC129067	AC129067 Rattus no
c1426	32.8	5.1	150694	2	AC149509	AC149509 Xenopus t
1427	32.8	5.1	152269	8	AP003863	AP003863 Oryza sat
c1428	32.8	5.1	153223	2	AC018548	AC018548 Homo sapi
1429	32.8	5.1	153736	9	AC079301	AC079301 Homo sapi
c1430	32.8	5.1	155359	9	AC092583	AC092583 Homo sapi
1431	32.8	5.1	155780	9	HS336O12	AL513498 Homo sapi
c1432	32.8	5.1	156314	9	AC007671	AC007671 Homo sapi
c1433	32.8	5.1	156591	2	AC024647	AC024647 Homo sapi
c1434	32.8	5.1	156989	2	AC069176	AC069176 Homo sapi
c1435	32.8	5.1	157267	9	AC007859	AC007859 Homo sapi
1436	32.8	5.1	158388	9	AC008740	AC008740 Homo sapi
1437	32.8	5.1	158466	9	AP004292	AP004292 Homo sapi
c1438	32.8	5.1	159375	5	BX005001	BX005001 Zebrafish
c1439	32.8	5.1	161310	10	AC112971	AC112971 Mus muscu
c1440	32.8	5.1	161549	2	AC024676	AC024676 Homo sapi
1441	32.8	5.1	161732	2	AC104475	AC104475 Pan trogl
1442	32.8	5.1	162446	9	AC068776	AC068776 Homo sapi
1443	32.8	5.1	162455	10	AC125540	AC125540 Mus muscu
1444	32.8	5.1	162640	2	AC147318	AC147318 Pan trogl
c1445	32.8	5.1	165072	9	AC148684	AC148684 Macaca mu
1446	32.8	5.1	165110	2	AC068087	AC068087 Homo sapi
c1447	32.8	5.1	165652	2	AC068010	AC068010 Homo sapi
c1448	32.8	5.1	167627	9	AC079382	AC079382 Homo sapi
1449	32.8	5.1	167644	2	AC123566	AC123566 Homo sapi
1450	32.8	5.1	168137	2	BX323444	BX323444 Danio rer
c1451	32.8	5.1	168268	9	AC009124	AC009124 Homo sapi
c1452	32.8	5.1	168279	2	AC069186	AC069186 Homo sapi
1453	32.8	5.1	169147	9	AC007238	AC007238 Homo sapi
c1454	32.8	5.1	169281	9	AC079232	AC079232 Homo sapi
1455	32.8	5.1	170513	2	AC023603	AC023603 Homo sapi
c1456	32.8	5.1	170837	2	AC116884	AC116884 Mus muscu
c1457	32.8	5.1	172376	2	BX640588	BX640588 Danio rer
c1458	32.8	5.1	172945	9	AC067719	AC067719 Homo sapi
1459	32.8	5.1	173122	2	AC143021	AC143021 Macaca mu
1460	32.8	5.1	175931	9	HS73E6	AL163193 Homo sapi
1461	32.8	5.1	176983	9	AC019172	AC019172 Homo sapi
c1462	32.8	5.1	177325	5	BX649643	BX649643 Zebrafish
c1463	32.8	5.1	178081	2	AC023463	AC023463 Homo sapi
1464	32.8	5.1	178951	5	BX323819	BX323819 Zebrafish
1465	32.8	5.1	179103	2	AP001281	AP001281 Homo sapi
c1466	32.8	5.1	180129	10	AC122363	AC122363 Mus muscu
1467	32.8	5.1	180388	9	AC006206	AC006206 Homo sapi
1468	32.8	5.1	181022	9	AC011193	AC011193 Homo sapi
c1469	32.8	5.1	181106	10	AL929011	AL929011 Mouse DNA
1470	32.8	5.1	181117	9	AC019173	AC019173 Homo sapi
1471	32.8	5.1	181443	10	AC132587	AC132587 Mus muscu
c1472	32.8	5.1	182982	9	AL355522	AL355522 Human DNA
c1473	32.8	5.1	183224	10	AC139751	AC139751 Mus muscu
c1474	32.8	5.1	183681	2	AC128198	AC128198 Rattus no
c1475	32.8	5.1	184311	9	AL358176	AL358176 Human DNA
c1476	32.8	5.1	184879	10	AC124416	AC124416 Mus muscu
1477	32.8	5.1	185606	2	AC127174	AC127174 Rattus no
c1478	32.8	5.1	185646	10	AC141880	AC141880 Mus muscu
1479	32.8	5.1	186629	2	AC147308	AC147308 Pan trogl
c1480	32.8	5.1	188547	2	AC133597	AC133597 Mus muscu
c1481	32.8	5.1	190470	2	AC149786	AC149786 Otolemur
c1482	32.8	5.1	191887	2	CR407563	CR407563 Danio rer
1483	32.8	5.1	192174	2	AC128248	AC128248 Rattus no
c1484	32.8	5.1	192292	2	AC129068	AC129068 Rattus no
1485	32.8	5.1	192743	5	BX640587	BX640587 Zebrafish
c1486	32.8	5.1	193306	2	AC025512	AC025512 Homo sapi
c1487	32.8	5.1	194638	2	AC112913	AC112913 Homo sapi
1488	32.8	5.1	194943	2	AC142201	AC142201 Homo sapi
1489	32.8	5.1	196716	2	AC137884	AC137884 Mus muscu
1490	32.8	5.1	199042	2	AP001457	AP001457 Homo sapi
1491	32.8	5.1	199257	10	AL928545	AL928545 Mouse DNA
c1492	32.8	5.1	202392	9	AC079061	AC079061 Homo sapi
1493	32.8	5.1	202566	9	AC022031	AC022031 Homo sapi
1494	32.8	5.1	203003	2	AC087313	AC087313 Homo sapi
1495	32.8	5.1	204738	2	AC090346	AC090346 Homo sapi
1496	32.8	5.1	205619	2	AC108275	AC108275 Rattus no
1497	32.8	5.1	205651	2	AC106630	AC106630 Rattus no
c1498	32.8	5.1	205973	5	BX294130	BX294130 Zebrafish
c1499	32.8	5.1	213058	5	BX119974	BX119974 Zebrafish
c1500	32.8	5.1	214504	10	AC102779	AC102779 Mus muscu

ALIGNMENTS

RESULT 1
AR252633
LOCUS AR252633 1346 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 386 from patent US 6478825.
ACCESSION AR252633
VERSION AR252633.1 GI:27300541
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1346)
AUTHORS Winterbottom,J.M., Shimp,L., Boyce,T.M. and Kaes,D.
TITLE Implant, method of making same and use of the implant for the treatment of bone defects
JOURNAL Patent: US 6478825-A 386 12-NOV-2002;
FEATURES Location/Qualifiers
source 1. .1346
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 100.0%; Score 639; DB 6; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.2e-165;
Matches 639; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          7 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 66

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
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Db         67 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 126

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
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Db        127 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 186

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
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Db        187 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 246

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
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Db        247 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 306

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
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Db        307 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 366

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
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Db        367 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 426

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
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Db        427 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 486

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
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Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
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Db        547 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 606

Qy        601 CTGGACATGAAGGGGGGCATATTAATGATGCCTTCATGA 639
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Db        607 CTGGACATGAAGGGGGGCATATTAATGATGCCTTCATGA 645


RESULT 2
AR528692
LOCUS       AR528692                1346 bp    DNA     linear   PAT 08-OCT-2004
DEFINITION  Sequence 481 from patent US 6725730.
ACCESSION   AR528692
VERSION     AR528692.1  GI:53916770
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1346)
  AUTHORS   Bollinger,C.L. Jr.
  TITLE     Crane test weight assembly and method
  JOURNAL   Patent: US 6725730-A 481 27-APR-2004;
FEATURES             Location/Qualifiers
     source          1. .1346
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match           100.0%;  Score 639;  DB 6;  Length 1346;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-165;
  Matches  639;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          7 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 66

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
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Db         67 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 126

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
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Db        127 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 186

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
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Db        187 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 246

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
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Db        247 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 306

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
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Db        307 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 366

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
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Db        367 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 426

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 486

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
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Db        487 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 546

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Db        547 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 606

Qy        601 CTGGACATGAAGGGGGGCATATTAATGATGCCTTCATGA 639
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Db        607 CTGGACATGAAGGGGGGCATATTAATGATGCCTTCATGA 645


RESULT 3
AX403499
LOCUS       AX403499                1346 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 386 from Patent WO0073454.
ACCESSION   AX403499
VERSION     AX403499.1  GI:21436987
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ashkenazi,A.J., Baker,K.P., Botstein,D., Desnoyers,L., Eaton,D.,
            Ferrara,N., Gerber,H., Gerritsen,M., Goddard,A., Godowski,P.,
            Grimaldi,C.J., Gurney,A.L., Kljavin,I., Napier,M.A., Pan,J.,
            Paoni,N.F., Roy,M., Stewart,T.A., Tumas,D., Watanabe,C.K.,
            Williams,P., Wood,W.I. and Zhang,Z.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
            the same
  JOURNAL   Patent: WO 0073454-A 386 07-DEC-2000;
            Genentech Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1346
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match           100.0%;  Score 639;  DB 6;  Length 1346;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-165;
  Matches  639;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
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Db          7 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 66

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
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Db         67 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 126

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
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Db        127 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 186

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
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Db        187 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 246

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
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Db        247 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 306

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
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Db        307 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 366

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
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Db        367 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 426

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
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Db        427 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 486

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
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Db        487 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 546

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
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Db        547 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 606

Qy        601 CTGGACATGAAGGGGGGCATATTAATGATGCCTTCATGA 639
              |||||||||||||||||||||||||||||||||||||||
Db        607 CTGGACATGAAGGGGGGCATATTAATGATGCCTTCATGA 645


RESULT 4
AX464348
LOCUS       AX464348               1346 bp    DNA     linear   PAT 16-JUL-2002
DEFINITION  Sequence 481 from Patent WO0140466.
ACCESSION   AX464348
VERSION     AX464348.1  GI:21899190
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Baker,K.P., Beresini,M., Deforge,L., Desnoyers,L., Filvaroff,E.,
            Gao,W.Q., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L.,
            Sherwood,S., Smith,V., Stewart,T.A., Tumas,D., Watanabe,C.K.,
            Wood,W.L. and Zhang,Z.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
            same
  JOURNAL   Patent: WO 0140466-A 481 07-JUN-2001;
            Genentech Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1346
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 639;  DB 6;  Length 1346;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-165;
  Matches  639;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
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Db          7 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 66

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 126

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
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Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
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Db        247 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 306
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Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
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Db        307 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 366

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 426

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
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Db        427 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 486

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
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Db        487 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 546

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Db        547 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 606

Qy        601 CTGGACATGAAGGGGGGCATATTAATGATGCCTTCATGA 639
              |||||||||||||||||||||||||||||||||||||||
Db        607 CTGGACATGAAGGGGGGCATATTAATGATGCCTTCATGA 645


RESULT 5
AY359060
LOCUS       AY359060               1346 bp    mRNA    linear   PRI 03-OCT-2003
DEFINITION  Homo sapiens clone DNA61873 NX-17 (UNQ678) mRNA, complete cds.
ACCESSION   AY359060
VERSION     AY359060.1  GI:37183237
KEYWORDS    FLI_CDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1346)
  AUTHORS   Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
            Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
            Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
            Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
            Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,
            Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,
            Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K.,
            Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
            Goddard,A., Wood,W.I. and Godowski,P.
  TITLE     The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
            Effort to Identify Novel Human Secreted and Transmembrane Proteins:
            A Bioinformatics Assessment
  JOURNAL   Genome Res. 13 (10), 2265-2270 (2003)
   PUBMED   12975309
REFERENCE   2  (bases 1 to 1346)
  AUTHORS   Clark,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
            Inc., 1 DNA Way, South San Francisco, CA 94080, USA
FEATURES             Location/Qualifiers
     source          1. .1346
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     gene            1. .1346
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     CDS             7. .645
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                     /note="PRO1312"
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                     /product="NX-17"
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                     LILSGIWQRRRKNKEPSEVDDAEDKCENMITIENGIPSDPLDMKGGILMMPS"
ORIGIN

  Query Match           100.0%;  Score 639;  DB 9;  Length 1346;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-165;
  Matches  639;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
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Db          7 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 66

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
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Db         67 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 126

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
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Db        127 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 186

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 246

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 306

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
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Db        307 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 366

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
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Db        367 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 426

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
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Db        427 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 486

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
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Db        487 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 546

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 606

Qy        601 CTGGACATGAAGGGGGGCATATTAATGATGCCTTCATGA 639
              |||||||||||||||||||||||||||||||||||||||
Db        607 CTGGACATGAAGGGGGGCATATTAATGATGCCTTCATGA 645


RESULT 6
AX083382
LOCUS       AX083382                 666 bp    DNA     linear   PAT 28-FEB-2001
DEFINITION  Sequence 74 from Patent WO0112660.
ACCESSION   AX083382
VERSION     AX083382.1  GI:13185219
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kato,S. and Kimura,T.
  TITLE     Human proteins having hydrophobic domains and dnas encoding these
            proteins
  JOURNAL   Patent: WO 0112660-A 74 22-FEB-2001;
            SAGAMI CHEMICAL RESEARCH CENTER (JP) ; Protegene Inc. (JP)
FEATURES             Location/Qualifiers
     source          1. .666
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match           98.3%;  Score 628;  DB 6;  Length 666;
  Best Local Similarity  99.8%;  Pred. No. 2.4e-162;
  Matches  639;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
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Db          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
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Db        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
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Db        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
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Db        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
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Db        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
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Db        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
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Db        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGA 639
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Db        601 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGA 640


RESULT 7
AX083392
LOCUS       AX083392                1347 bp    DNA     linear   PAT 28-FEB-2001
DEFINITION  Sequence 84 from Patent WO0112660.
ACCESSION   AX083392
VERSION     AX083392.1  GI:13185232
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kato,S. and Kimura,T.
  TITLE     Human proteins having hydrophobic domains and dnas encoding these
            proteins
  JOURNAL   Patent: WO 0112660-A 84 22-FEB-2001;
            SAGAMI CHEMICAL RESEARCH CENTER (JP) ; Protegene Inc. (JP)
FEATURES             Location/Qualifiers
     source          1. .1347
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                     LTPL"
ORIGIN

  Query Match           98.3%;  Score 628;  DB 6;  Length 1347;
  Best Local Similarity  99.8%;  Pred. No. 2.4e-162;
  Matches  639;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         26 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 85

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
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Db         86 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 145

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
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Db        146 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 205

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
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Db        206 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 265

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        266 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 325

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
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Db        326 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 385

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
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Db        386 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 445

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
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Db        446 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 505

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
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Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
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Db        566 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 625

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGA 639
              |||||||||||||| |||||||||||||||||||||||||
Db        626 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGA 665


RESULT 8
BC050606
LOCUS       BC050606               1377 bp    mRNA    linear   PRI 30-JUN-2004
DEFINITION  Homo sapiens transmembrane protein 27, mRNA (cDNA clone MGC:60059
            IMAGE:5183554), complete cds.
ACCESSION   BC050606
VERSION     BC050606.1  GI:30047080
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1377)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1377)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-APR-2003) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA  94305
            Web site:       http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 110 Row: c Column: 4
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 21361864.
FEATURES                Location/Qualifiers
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                        /mol_type="mRNA"
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                        /note="Vector: pCMV-SPORT6"
     gene               1. .1377
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                        /note="synonyms: NX-17, NX17"
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                        /codon_start=1
                        /product="transmembrane protein 27"
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                     LTPL"
ORIGIN

  Query Match           98.3%;  Score 628;  DB 9;  Length 1377;
  Best Local Similarity   99.8%;  Pred. No. 2.4e-162;
  Matches  639;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          9 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 68

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
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Db         69 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 128

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
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Db        129 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 188

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
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Db        189 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 248

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
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Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
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Db        309 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 368

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
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Db        369 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 428

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
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Db        429 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 488

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
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Db        489 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 548

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
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Db        549 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 608

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGA 639
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Db        609 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGA 648


RESULT 9
BC015099
LOCUS       BC015099               1440 bp    mRNA    linear   PRI 29-JUN-2004
DEFINITION  Homo sapiens transmembrane protein 27, mRNA (cDNA clone MGC:22827
            IMAGE:3829035), complete cds.
ACCESSION   BC015099
VERSION     BC015099.1  GI:15929328
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1440)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
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            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1440)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-OCT-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: CLONTECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Institute for Systems Biology
            http://www.systemsbiology.org
            contact: amadan@systemsbiology.org
            Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
            Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 31 Row: d Column: 11
            This clone was selected for full length sequencing because it
            passed the following selection criteria: GenomeScan gene
            prediction, Similarity but not identity to protein.
FEATURES             Location/Qualifiers
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                     /lab_host="DH10B"
                     /note="Vector: pDNR-LIB"
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                     /note="synonyms: NX-17, NX17"
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                     NEEYLFKAMVAFSMRKVPNREATEISHVLLCNVTQRVSFWFVVTDPSKNHTLPAVEVQ
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                     LILSGIWQRRRKNKEPSEVDDAEDKCENMITIENGIPSDPLDMKGGHINDAFMTEDER
                     LTPL"
ORIGIN

  Query Match           98.3%;  Score 628;  DB 9;  Length 1440;
  Best Local Similarity   99.8%;  Pred. No. 2.4e-162;
  Matches  639;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;
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Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
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Db        149 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 208

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
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Db        209 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 268

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
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Db        269 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 328

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
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Db        329 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 388

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
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Db        389 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 448

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
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Db        449 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 508

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
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Db        509 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 568

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
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Db        569 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 628

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
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Db        629 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 688

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGA 639
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RESULT 10
BC014317

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LOCUS       BC014317               1605 bp    mRNA    linear   PRI 29-JUN-2004
DEFINITION  Homo sapiens transmembrane protein 27, mRNA (cDNA clone MGC:22707
            IMAGE:4048217), complete cds.
ACCESSION   BC014317
VERSION     BC014317.1  GI:15680012
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1605)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
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            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
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            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1605)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-SEP-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: CLONTECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Institute for Systems Biology
            http://www.systemsbiology.org
            contact: amadan@systemsbiology.org
            Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
            Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 31 Row: n Column: 3
            This clone was selected for full length sequencing because it
            passed the following selection criteria: Hexamer frequency ORF
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ORIGIN
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  Query Match             98.3%;  Score 628;  DB 9;  Length 1605;
  Best Local Similarity   99.8%;  Pred. No. 2.4e-162;
  Matches  639;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
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Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
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Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
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Db        441 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 500

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
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Db        501 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 560

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
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Db        561 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 620

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
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Db        621 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 680

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
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Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
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Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
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Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGA 639
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RESULT 11
BD205644
LOCUS       BD205644               1447 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  97 human secreted proteins.
ACCESSION   BD205644
VERSION     BD205644.1  GI:33015414
KEYWORDS    JP 2002533058-A/21.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1447)
  AUTHORS   Ruben,S.M., Florence,K., Ni,J., Rosen,C.A., Carter,K.C.,
            Moore,P.A., Olsen,H.S., Shi,Y., Young,P.E., Wei,F.F., Brewer,L.A.,
            Soppet,D.R., Lafleur,D.W., Endress,G.A. and Ebner,R.
  TITLE     97 human secreted proteins
  JOURNAL   Patent: JP 2002533058-A 21 08-OCT-2002;
            HUMAN GENOME SCIENCES INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002533058-A/21
            PD   08-OCT-2002
            PF   06-MAY-1999 JP 2000548451
            PR   12-MAY-1998 US    60/085093,12-MAY-1998 US    60/085094 PR
            12-MAY-1998 US    60/085105,12-MAY-1998 US    60/085180 PR
            18-MAY-1998 US    60/085927,18-MAY-1998 US    60/085906 PR
            18-MAY-1998 US    60/085924,18-MAY-1998 US    60/085922 PR
            18-MAY-1998 US    60/085923,18-MAY-1998 US    60/085921 PR
            18-MAY-1998 US    60/085925,18-MAY-1998 US    60/085928 PR
            18-MAY-1998 US    60/085920
            PI   STEVEN M RUBEN,KIMBERLY FLORENCE,JIAN NI,CRAIG A ROSEN,KENNETH

            PI   C CARTER,
            PI   PAUL A MOORE,HENRIK S OLSEN,YANGGU SHI,PAUL E YOUNG,FING FEI
            PI   WEI,
            PI   LAURIE A BREWER,DANIEL R SOPPET,DAVID W LAFLEUR,GREGORY A  PI
             ENDRESS,
            PI   REINHARD EBNER
            PC   C12N15/09,C07K14/00,C07K14/435,C07K16/18,C12N1/15,C12N1/19, PC
              C12N1/21,
            PC   C12N5/10,C12P21/02,C12N15/00,C12N5/00
            CC   97 human secreted proteins.
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            FT   source          1. .1447
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
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ORIGIN
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  Matches  638;  Conservative    1;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
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Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
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Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
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Db        257 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 316

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
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Db        317 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 376

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
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Db        377 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGMC 436

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
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Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
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Db        617 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 676

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGA 639
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Db        677 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGA 716
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RESULT 12
AF229179
LOCUS       AF229179               1345 bp    mRNA    linear   PRI 05-APR-2002
DEFINITION  Homo sapiens collectrin mRNA, complete cds.
ACCESSION   AF229179
VERSION     AF229179.1  GI:9957753
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1345)
  AUTHORS   Zhang,H., Wada,J., Hida,K., Tsuchiyama,Y., Hiragushi,K.,
            Shikata,K., Wang,H., Lin,S., Kanwar,Y.S. and Makino,H.
  TITLE     Collectrin, a collecting duct-specific transmembrane glycoprotein,
            is a novel homolog of ACE2 and is developmentally regulated in
            embryonic kidneys
  JOURNAL   J. Biol. Chem. 276 (20), 17132-17139 (2001)
  MEDLINE   21264468
   PUBMED   11278314
REFERENCE   2  (bases 1 to 1345)
  AUTHORS   Zhang,H., Wada,J. and Makino,H.
  TITLE     Human kidney specific membrane protein (NX-17)
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 1345)
  AUTHORS   Zhang,H., Wada,J. and Makino,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-JAN-2000) Department of Medicine III, Okayama
            University Medical School, 2-5-1 Shikata-cho, Okayama 700-8558,
            Japan
FEATURES             Location/Qualifiers
     source          1. .1345
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     CDS             24. .692
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                     the Mus musculus and Rattus norvegicus products encoded by
                     GenBank Accession Numbers AF178085 and AF178086,
                     respectively"
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                     /protein_id="AAG09466.1"
                     /db_xref="GI:9957754"
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                     LILSGIWQRRRKNKEPSEVDDAEDKCENMITIENGIPSDPLDMKGGHINDAFMTEDER
                     LTPL"
ORIGIN

  Query Match             98.0%;  Score 626.4;  DB 9;  Length 1345;
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  Matches  638;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
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Db         24 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 83

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
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Db         84 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 143

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
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Db        144 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 203

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
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Db        204 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 263

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
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Db        324 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 383

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
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Db        384 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 443

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
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Db        444 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 503

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
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Db        504 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 563

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
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RESULT 13
BD083420
LOCUS       BD083420                1401 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Secreted proteins and polynucleotides encoding them.
ACCESSION   BD083420
VERSION     BD083420.1  GI:22629030
KEYWORDS    JP 2001523950-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 1401)
  AUTHORS   Jacobs,K., Mccoy,J.M., Lavallie,E.R., Racie,L.A., Merberg,D.,
            Treacy,M., Spaulding,V. and Agostino,M.J.
  TITLE     Secreted proteins and polynucleotides encoding them
  JOURNAL   Patent: JP 2001523950-A 2 27-NOV-2001;
            GENETICS INSTITUTE INC
COMMENT     PN   JP 2001523950-A/2
            PD   27-NOV-2001
            PF   23-JAN-1998 JP 1998532177
            PR   24-JAN-1997 US    08/788789
            PI   KENNETH JACOBS,JOHN M MCCOY,EDWARD R LAVALLIE,LISA A RACIE, PI
              DAVID MERBERG,
            PI   MAURICE TREACY,VIKKI SPAULDING,MICHAEL J AGOSTINO PC
            C12N15/12,C12N5/10,C07K14/47,C12Q1/68,A61K38/17 CC   Strandedness:
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            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
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  Best Local Similarity   99.7%;  Pred. No. 6.7e-162;
  Matches  638;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
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Db         71 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 130

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
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Db        131 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 190

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
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Db        191 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 250

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
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Db        251 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 310

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
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Db        311 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 370

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Db        371 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTGTAAATGAC 430

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420

Db        431 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 490

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480

Db        491 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 550

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540

Db        551 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 610

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600

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Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGA 639

Db        671 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGA 710


RESULT 14
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LOCUS       AR177334                848 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 27 from patent US 6312922.
ACCESSION   AR177334
VERSION     AR177334.1  GI:17919689
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 848)
  AUTHORS   Edwards,J.-B.Dumas.Milne., Duclert,A. and Bougueleret,L.
  TITLE     Complementary DNAs
  JOURNAL   Patent: US 6312922-A 27 06-NOV-2001;
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Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120

Db         92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180

Db        152 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240

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Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300

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Db        332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420

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Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600

Db        572 GACGCTGAARATAAKTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 631

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGA 639

Db        632 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGA 671


RESULT 15
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LOCUS       BD139270                848 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Extended cDNA of secretory protein.
ACCESSION   BD139270
VERSION     BD139270.1  GI:23234215
KEYWORDS    JP 2002508182-A/22.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 848)
  AUTHORS   Bougueleret,L., Duclert,A. and Edwards,J.B.D.M.
  TITLE     Extended cDNA of secretory protein
  JOURNAL   Patent: JP 2002508182-A 22 19-MAR-2002;
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COMMENT     OS   Homo sapiens (human)
            PN   JP 2002508182-A/22
            PD   19-MAR-2002
            PF   17-DEC-1998 JP 2000539136
            PR   17-DEC-1997 US    60/069957,09-FEB-1998 US    60/074121 PR
            13-APR-1998 US    60/081563,10-AUG-1998 US    60/096116 PI   LYDIE
            BOUGUELERET,AYMERIC DUCLERT,JEAN BAPTISTE DUMAS MILNE  PI   EDWARDS
            PC   C12N15/09,C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19, PC
             C12N1/21,
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ORIGIN

  Query Match           98.0%;  Score 626;  DB 6;  Length 848;
  Best Local Similarity   99.2%;  Pred. No. 8.7e-162;
  Matches  635;  Conservative    4;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60

Db         32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120

Db         92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

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Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
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Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
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Db        332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
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Db        452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

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SUMMARIES

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	3	626	98.0	848	4	US-09-663-600A-27	Sequence 27, Appl
	4	626	98.0	848	4	US-09-621-976-5	Sequence 5, Appli
	5	626	98.0	848	4	US-09-513-999C-5	Sequence 5, Appli
	6	626	98.0	848	4	US-09-471-276-5	Sequence 5, Appli
	7	163	25.5	862	3	US-09-289-349-6	Sequence 6, Appli
	8	125	19.6	2415	3	US-08-989-299-3	Sequence 3, Appli
	9	125	19.6	2415	4	US-09-407-427-3	Sequence 3, Appli
	10	125	19.6	3388	4	US-09-949-016-5413	Sequence 5413, Ap
	11	125	19.6	3396	3	US-08-989-299-1	Sequence 1, Appli
	12	125	19.6	3396	4	US-10-158-847-141	Sequence 141, App
	13	125	19.6	3396	4	US-09-407-427-1	Sequence 1, Appli
	14	117	18.3	2920	4	US-10-158-847-137	Sequence 137, App
	15	77.4	12.1	43986	4	US-09-949-016-17155	Sequence 17155, A
c	16	69.4	10.9	2350	3	US-09-280-116-40	Sequence 40, Appl
c	17	54	8.5	11288	3	US-08-646-301A-1	Sequence 1, Appli
c	18	54	8.5	11288	3	US-08-481-968A-4	Sequence 4, Appli
c	19	54	8.5	11288	3	US-08-154-712B-4	Sequence 4, Appli
c	20	54	8.5	11288	4	US-09-947-925A-4	Sequence 4, Appli
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c	22	54	8.5	15056	4	US-09-814-351-14	Sequence 14, Appl
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c	29	36.2	5.7	134987	4	US-09-949-016-15348	Sequence 15348, A
c	30	36.2	5.7	134987	4	US-09-949-016-15349	Sequence 15349, A
c	31	36.2	5.7	134987	4	US-09-949-016-15350	Sequence 15350, A
c	32	36.2	5.7	134987	4	US-09-949-016-15507	Sequence 15507, A
c	33	36.2	5.7	134987	4	US-09-949-016-15508	Sequence 15508, A
c	34	36.2	5.7	134987	4	US-09-949-016-15509	Sequence 15509, A
	35	35.8	5.6	2625	1	US-08-188-228-57	Sequence 57, Appl
	36	35.8	5.6	2625	1	US-08-332-643-51	Sequence 51, Appl
	37	35.8	5.6	2625	1	US-08-332-638-57	Sequence 57, Appl
	38	35.8	5.6	2625	4	US-09-654-328-1	Sequence 1, Appli
	39	35.8	5.6	3712	2	US-08-738-349-3	Sequence 3, Appli
c	40	35.8	5.6	678533	4	US-09-949-016-14577	Sequence 14577, A
c	41	35.8	5.6	678533	4	US-09-949-016-14578	Sequence 14578, A
c	42	35.2	5.5	352	4	US-09-513-999C-16750	Sequence 16750, A
	43	35.2	5.5	1141	4	US-09-806-708B-22	Sequence 22, Appl
c	44	35	5.5	601	4	US-09-949-016-189182	Sequence 189182,
	45	34.6	5.4	52523	4	US-09-949-016-12433	Sequence 12433, A
	46	34.6	5.4	52530	4	US-09-949-016-13948	Sequence 13948, A
c	47	34	5.3	16207	4	US-09-949-016-16747	Sequence 16747, A
c	48	34	5.3	157032	4	US-09-949-016-16502	Sequence 16502, A
c	49	33.4	5.2	601	4	US-09-949-016-40530	Sequence 40530, A
c	50	33.4	5.2	601	4	US-09-949-016-63869	Sequence 63869, A
c	51	33.4	5.2	601	4	US-09-949-016-63944	Sequence 63944, A
	52	33.4	5.2	7778	4	US-08-956-171E-48	Sequence 48, Appl
	53	33.4	5.2	7778	4	US-08-781-986A-48	Sequence 48, Appl
	54	33.4	5.2	64049	4	US-09-949-016-15744	Sequence 15744, A
	55	33.4	5.2	69062	4	US-09-949-016-13608	Sequence 13608, A
	56	33.4	5.2	69062	4	US-09-949-016-13609	Sequence 13609, A
	57	33.4	5.2	69687	4	US-09-949-016-12890	Sequence 12890, A
	58	33.4	5.2	265038	4	US-09-949-016-15779	Sequence 15779, A
c	59	33.2	5.2	957	4	US-09-134-000C-195	Sequence 195, App
	60	33.2	5.2	3867	4	US-09-919-497-5	Sequence 5, Appli
	61	33.2	5.2	3914	2	US-08-738-349-5	Sequence 5, Appli
c	62	33	5.2	832	4	US-09-621-976-2813	Sequence 2813, Ap
	63	32.8	5.1	477	3	US-08-887-534A-81	Sequence 81, Appl
	64	32.8	5.1	477	4	US-09-527-431-81	Sequence 81, Appl
	65	32.8	5.1	477	4	US-09-446-861-81	Sequence 81, Appl
	66	32.8	5.1	822	4	US-09-328-352-2041	Sequence 2041, Ap
c	67	32.8	5.1	933	4	US-09-134-000C-2145	Sequence 2145, Ap
	68	32.6	5.1	601	4	US-09-949-016-160209	Sequence 160209,
c	69	32.6	5.1	24276	4	US-09-949-016-12714	Sequence 12714, A
	70	32.6	5.1	31739	4	US-09-949-016-16226	Sequence 16226, A
	71	32.6	5.1	96202	4	US-09-949-016-16433	Sequence 16433, A
	72	32.4	5.1	601	4	US-09-949-016-48115	Sequence 48115, A
	73	32.4	5.1	601	4	US-09-949-016-192742	Sequence 192742,
	74	32.4	5.1	37319	4	US-09-949-016-13164	Sequence 13164, A
	75	32.4	5.1	53451	4	US-09-949-016-15859	Sequence 15859, A
	76	32.4	5.1	135010	4	US-09-949-016-17234	Sequence 17234, A
c	77	32.4	5.1	155617	4	US-09-949-016-16191	Sequence 16191, A
	78	32.2	5.0	15598	4	US-08-956-171E-82	Sequence 82, Appl
	79	32.2	5.0	15598	4	US-08-781-986A-82	Sequence 82, Appl
	80	32.2	5.0	155617	4	US-09-949-016-16191	Sequence 16191, A
c	81	32	5.0	43360	3	US-09-453-702B-206	Sequence 206, App
c	82	32	5.0	45325	3	US-09-453-702B-261	Sequence 261, App
	83	32	5.0	120609	4	US-09-949-016-13915	Sequence 13915, A
c	84	32	5.0	168575	3	US-09-426-290-1	Sequence 1, Appli
c	85	32	5.0	221545	4	US-09-949-016-13875	Sequence 13875, A
c	86	31.8	5.0	505	4	US-09-621-976-15639	Sequence 15639, A
	87	31.8	5.0	601	4	US-09-949-016-67021	Sequence 67021, A
c	88	31.8	5.0	617	4	US-09-043-506A-9	Sequence 9, Appli
c	89	31.8	5.0	6730	4	US-08-956-171E-51	Sequence 51, Appl
c	90	31.8	5.0	6730	4	US-08-781-986A-51	Sequence 51, Appl
c	91	31.8	5.0	125902	4	US-09-949-016-13715	Sequence 13715, A
	92	31.8	5.0	1664976	4	US-08-916-421B-1	Sequence 1, Appli
	93	31.8	5.0	1664976	4	US-09-692-570-1	Sequence 1, Appli
	94	31.6	4.9	601	4	US-09-949-016-48265	Sequence 48265, A
	95	31.6	4.9	601	4	US-09-949-016-126012	Sequence 126012,
c	96	31.6	4.9	601	4	US-09-949-016-136771	Sequence 136771,
c	97	31.6	4.9	601	4	US-09-949-016-136772	Sequence 136772,
c	98	31.6	4.9	601	4	US-09-949-016-136773	Sequence 136773,
	99	31.6	4.9	601	4	US-09-949-016-136832	Sequence 136832,
	100	31.6	4.9	601	4	US-09-949-016-136833	Sequence 136833,

	101	31.6	4.9	601	4	US-09-949-016-180103 Sequence 180103,
	102	31.6	4.9	5416	4	US-09-949-016-12977 Sequence 12977, A
	103	31.6	4.9	16075	3	US-09-096-942-1 Sequence 1, Appli
	104	31.6	4.9	16075	3	US-09-096-867-1 Sequence 1, Appli
c	105	31.6	4.9	27236	4	US-09-949-016-12809 Sequence 12809, A
c	106	31.6	4.9	27241	4	US-09-949-016-17294 Sequence 17294, A
c	107	31.6	4.9	49189	4	US-09-949-016-15583 Sequence 15583, A
c	108	31.6	4.9	71574	4	US-09-949-016-15580 Sequence 15580, A
	109	31.6	4.9	74790	4	US-09-949-016-15321 Sequence 15321, A
	110	31.6	4.9	102520	4	US-09-949-016-17367 Sequence 17367, A
	111	31.6	4.9	102526	4	US-09-949-016-12448 Sequence 12448, A
	112	31.6	4.9	219964	4	US-09-949-016-15086 Sequence 15086, A
	113	31.6	4.9	228896	4	US-09-949-016-17127 Sequence 17127, A
c	114	31.6	4.9	346112	4	US-09-949-016-13165 Sequence 13165, A
	115	31.6	4.9	640681	4	US-09-790-988-1 Sequence 1, Appli
c	116	31.4	4.9	477	4	US-09-621-976-1624 Sequence 1624, Ap
	117	31.4	4.9	601	4	US-09-949-016-52248 Sequence 52248, A
c	118	31.4	4.9	601	4	US-09-949-016-79611 Sequence 79611, A
c	119	31.4	4.9	601	4	US-09-949-016-169973 Sequence 169973,
	120	31.4	4.9	50368	4	US-09-949-016-13256 Sequence 13256, A
	121	31.4	4.9	114139	4	US-09-949-016-16536 Sequence 16536, A
	122	31.4	4.9	157644	4	US-09-949-016-16179 Sequence 16179, A
	123	31.4	4.9	157644	4	US-09-949-016-16180 Sequence 16180, A
c	124	31.4	4.9	189560	4	US-09-949-016-17202 Sequence 17202, A
	125	31.2	4.9	537	4	US-09-134-000C-2494 Sequence 2494, Ap
c	126	31.2	4.9	601	4	US-09-949-016-136774 Sequence 136774,
	127	31.2	4.9	1001	4	US-09-671-317-297 Sequence 297, App
	128	31.2	4.9	1001	4	US-09-671-317-298 Sequence 298, App
	129	31.2	4.9	1536	4	US-09-134-000C-1957 Sequence 1957, Ap
	130	31.2	4.9	12571	3	US-09-322-478-20 Sequence 20, Appl
	131	31.2	4.9	12571	4	US-09-586-106D-20 Sequence 20, Appl
c	132	31.2	4.9	155266	4	US-09-949-016-13870 Sequence 13870, A
	133	31.2	4.9	450395	4	US-09-949-016-15473 Sequence 15473, A
c	134	31	4.9	626	4	US-08-956-171E-1046 Sequence 1046, Ap
c	135	31	4.9	626	4	US-08-781-986A-1046 Sequence 1046, Ap
c	136	31	4.9	978	3	US-08-858-207A-174 Sequence 174, App
c	137	31	4.9	1141	4	US-09-806-708B-22 Sequence 22, Appl
	138	30.8	4.8	601	4	US-09-949-016-192743 Sequence 192743,
	139	30.8	4.8	1347	3	US/08/622 INFORMATION FOR
	140	30.8	4.8	1347	3	US-09-165-922A-11 Sequence 11, Appl
	141	30.8	4.8	1497	4	US-09-220-132-94 Sequence 94, Appl
	142	30.8	4.8	8700	2	US-08-392-625-16 Sequence 16, Appl
	143	30.8	4.8	8700	2	US-08-466-961A-16 Sequence 16, Appl
	144	30.8	4.8	8700	2	US-08-645-193B-18 Sequence 18, Appl
	145	30.8	4.8	47419	4	US-09-949-016-11841 Sequence 11841, A
	146	30.8	4.8	47420	4	US-09-949-016-15484 Sequence 15484, A
	147	30.8	4.8	50381	4	US-09-949-016-17122 Sequence 17122, A
c	148	30.8	4.8	84870	4	US-09-949-016-17547 Sequence 17547, A
	149	30.8	4.8	95621	4	US-09-949-016-13237 Sequence 13237, A
	150	30.8	4.8	107458	4	US-09-949-016-15687 Sequence 15687, A
	151	30.8	4.8	161124	4	US-09-949-016-11760 Sequence 11760, A
	152	30.8	4.8	392000	4	US-10-027-983-11 Sequence 11, Appl
c	153	30.6	4.8	601	4	US-09-949-016-48376 Sequence 48376, A
	154	30.6	4.8	601	4	US-09-949-016-163904 Sequence 163904,
c	155	30.6	4.8	1020	4	US-10-121-857-69 Sequence 69, Appl
c	156	30.6	4.8	268449	4	US-09-949-016-17244 Sequence 17244, A
	157	30.6	4.8	312474	4	US-09-949-016-17434 Sequence 17434, A
c	158	30.6	4.8	360470	4	US-09-949-016-13173 Sequence 13173, A
	159	30.4	4.8	289	4	US-09-270-767-1435 Sequence 1435, Ap
	160	30.4	4.8	289	4	US-09-270-767-1943 Sequence 1943, Ap
	161	30.4	4.8	289	4	US-09-270-767-16717 Sequence 16717, A
	162	30.4	4.8	289	4	US-09-270-767-17225 Sequence 17225, A
	163	30.4	4.8	396	4	US-09-640-173-84 Sequence 84, Appl
	164	30.4	4.8	396	4	US-09-713-550-84 Sequence 84, Appl
	165	30.4	4.8	396	4	US-09-825-294-84 Sequence 84, Appl
	166	30.4	4.8	396	4	US-09-970-966-84 Sequence 84, Appl
	167	30.4	4.8	601	4	US-09-949-016-180104 Sequence 180104,
c	168	30.4	4.8	733	4	US-09-270-767-10136 Sequence 10136, A
	169	30.4	4.8	1001	3	US-09-641-638-159 Sequence 159, App
	170	30.4	4.8	1001	4	US-10-170-097-159 Sequence 159, App
c	171	30.4	4.8	3078	4	US-09-710-279-4417 Sequence 4417, Ap
	172	30.4	4.8	3292	1	US-07-814-964-12 Sequence 12, Appl
	173	30.4	4.8	3292	1	US-08-258-442-12 Sequence 12, Appl
	174	30.4	4.8	3292	1	US-08-328-809-7 Sequence 7, Appli
	175	30.4	4.8	3292	4	US-08-866-840-7 Sequence 7, Appli
	176	30.4	4.8	3292	5	PCT-US92-11107-12 Sequence 12, Appl
	177	30.4	4.8	6157	4	US-08-956-171E-184 Sequence 184, App
	178	30.4	4.8	6157	4	US-08-781-986A-184 Sequence 184, App
c	179	30.4	4.8	13193	4	US-09-949-016-17515 Sequence 17515, A
c	180	30.4	4.8	14079	4	US-09-949-016-11993 Sequence 11993, A
c	181	30.4	4.8	43562	4	US-09-949-016-16222 Sequence 16222, A
c	182	30.4	4.8	84839	4	US-09-949-016-15816 Sequence 15816, A
c	183	30.4	4.8	100928	4	US-09-949-016-16926 Sequence 16926, A
	184	30.4	4.8	107941	4	US-09-949-016-14206 Sequence 14206, A
	185	30.4	4.8	109378	4	US-09-949-016-12391 Sequence 12391, A
c	186	30.4	4.8	212139	4	US-09-949-016-16065 Sequence 16065, A
	187	30.4	4.8	235452	4	US-09-949-016-13675 Sequence 13675, A
c	188	30.4	4.8	385136	4	US-09-949-016-16073 Sequence 16073, A
	189	30.4	4.8	636591	4	US-09-949-016-11808 Sequence 11808, A
	190	30.4	4.8	636591	4	US-09-949-016-13388 Sequence 13388, A
c	191	30.2	4.7	365	4	US-09-270-767-6170 Sequence 6170, Ap
c	192	30.2	4.7	365	4	US-09-270-767-6901 Sequence 6901, Ap
c	193	30.2	4.7	365	4	US-09-270-767-21452 Sequence 21452, A
c	194	30.2	4.7	365	4	US-09-270-767-22183 Sequence 22183, A
c	195	30.2	4.7	601	4	US-09-949-016-23163 Sequence 23163, A
	196	30.2	4.7	601	4	US-09-949-016-149837 Sequence 149837,
	197	30.2	4.7	601	4	US-09-949-016-149838 Sequence 149838,
	198	30.2	4.7	601	4	US-09-949-016-149839 Sequence 149839,
c	199	30.2	4.7	601	4	US-09-949-016-187216 Sequence 187216,
c	200	30.2	4.7	2025	3	US-09-247-155-58 Sequence 58, Appl
c	201	30.2	4.7	3307	4	US-09-949-016-5348 Sequence 5348, Ap
c	202	30.2	4.7	4117	4	US-09-949-016-252 Sequence 252, App
c	203	30.2	4.7	18788	4	US-09-949-016-17090 Sequence 17090, A
	204	30.2	4.7	20441	4	US-09-949-016-14476 Sequence 14476, A
c	205	30.2	4.7	35380	4	US-09-949-016-11994 Sequence 11994, A
	206	30.2	4.7	36679	4	US-09-949-016-12732 Sequence 12732, A
	207	30.2	4.7	38207	4	US-09-949-016-17274 Sequence 17274, A
	208	30.2	4.7	44499	4	US-09-949-016-12711 Sequence 12711, A
c	209	30.2	4.7	99916	4	US-09-816-095-3 Sequence 3, Appli
c	210	30.2	4.7	105050	4	US-09-949-016-15953 Sequence 15953, A
c	211	30.2	4.7	784019	4	US-09-949-016-14033 Sequence 14033, A
c	212	30.2	4.7	828152	4	US-09-949-016-12777 Sequence 12777, A
	213	30	4.7	601	4	US-09-949-016-58024 Sequence 58024, A
c	214	30	4.7	601	4	US-09-949-016-65163 Sequence 65163, A
c	215	30	4.7	830	4	US-09-763-902B-10 Sequence 10, Appl
c	216	30	4.7	957	4	US-09-479-040-26 Sequence 26, Appl
	217	30	4.7	1001	4	US-09-671-317-296 Sequence 296, App
	218	30	4.7	1561	5	PCT-US92-00282-25 Sequence 25, Appl
	219	30	4.7	2082	4	US-09-248-796A-2564 Sequence 2564, Ap
	220	30	4.7	3162	4	US-09-328-352-2662 Sequence 2662, Ap
	221	30	4.7	4673	1	US-07-638-431-1 Sequence 1, Appli
	222	30	4.7	4673	5	PCT-US92-00018-1 Sequence 1, Appli
c	223	30	4.7	6476	3	US-09-127-670-5 Sequence 5, Appli
c	224	30	4.7	7883	4	US-09-949-016-13479 Sequence 13479, A
c	225	30	4.7	7916	4	US-09-479-040-1 Sequence 1, Appli
	226	30	4.7	8411	4	US-09-976-594-560 Sequence 560, App
	227	30	4.7	8412	4	US-09-919-039-223 Sequence 223, App
	228	30	4.7	17020	4	US-09-949-016-11818 Sequence 11818, A
	229	30	4.7	17021	4	US-09-949-016-13555 Sequence 13555, A
c	230	30	4.7	25131	4	US-09-949-016-12385 Sequence 12385, A
c	231	30	4.7	25131	4	US-09-949-016-13653 Sequence 13653, A
c	232	30	4.7	42250	4	US-09-949-016-17171 Sequence 17171, A
	233	30	4.7	42394	4	US-09-949-016-12752 Sequence 12752, A
	234	30	4.7	42395	4	US-09-949-016-15115 Sequence 15115, A
c	235	30	4.7	83428	4	US-09-949-016-13610 Sequence 13610, A
	236	30	4.7	85850	4	US-09-949-016-13424 Sequence 13424, A
	237	30	4.7	87690	4	US-09-949-016-14853 Sequence 14853, A
c	238	30	4.7	250715	4	US-09-949-016-13294 Sequence 13294, A
c	239	30	4.7	251672	4	US-09-949-016-17296 Sequence 17296, A
c	240	30	4.7	251682	4	US-09-949-016-11973 Sequence 11973, A
	241	30	4.7	253345	4	US-09-949-016-12656 Sequence 12656, A
	242	30	4.7	253364	4	US-09-949-016-13639 Sequence 13639, A
c	243	29.8	4.7	219	4	US-09-248-796A-7931 Sequence 7931, Ap
	244	29.8	4.7	261	2	US-08-482-148-11 Sequence 11, Appl
	245	29.8	4.7	261	5	PCT-US95-02944-11 Sequence 11, Appl
c	246	29.8	4.7	601	4	US-09-949-016-53684 Sequence 53684, A

	247	29.8	4.7	711	4	US-09-248-796A-12717	Sequence 12717, A
	248	29.8	4.7	786	4	US-09-270-767-12113	Sequence 12113, A
c	249	29.8	4.7	972	4	US-09-248-796A-3624	Sequence 3624, Ap
c	250	29.8	4.7	1176	4	US-09-248-796A-8908	Sequence 8908, Ap
	251	29.8	4.7	1247	2	US-08-528-057-41	Sequence 41, Appl
	252	29.8	4.7	1248	4	US-09-949-016-346	Sequence 346, App
	253	29.8	4.7	1422	1	US-08-319-704-5	Sequence 5, Appli
	254	29.8	4.7	1530	1	US-08-458-084-3	Sequence 3, Appli
	255	29.8	4.7	1530	1	US-08-205-508-3	Sequence 3, Appli
	256	29.8	4.7	1530	2	US-08-482-148-8	Sequence 8, Appli
	257	29.8	4.7	1530	5	PCT-US95-02944-8	Sequence 8, Appli
	258	29.8	4.7	1530	5	PCT-US95-02945-3	Sequence 3, Appli
	259	29.8	4.7	1545	3	US-08-139-195-1	Sequence 1, Appli
	260	29.8	4.7	1546	6	5514787-1	Patent No. 5514787
	261	29.8	4.7	1546	6	5514787-1	Patent No. 5514787
	262	29.8	4.7	2138	4	US-09-949-016-3454	Sequence 3454, Ap
	263	29.8	4.7	9734	4	US-09-949-016-16107	Sequence 16107, A
c	264	29.8	4.7	83708	4	US-09-949-016-17207	Sequence 17207, A
	265	29.8	4.7	86980	4	US-09-949-016-15344	Sequence 15344, A
c	266	29.8	4.7	90900	4	US-09-949-016-13034	Sequence 13034, A
	267	29.8	4.7	92581	4	US-09-949-016-12182	Sequence 12182, A
	268	29.8	4.7	92581	4	US-09-949-016-16542	Sequence 16542, A
	269	29.8	4.7	199471	4	US-09-949-016-14083	Sequence 14083, A
	270	29.8	4.7	250715	4	US-09-949-016-13294	Sequence 13294, A
	271	29.8	4.7	421491	4	US-09-949-016-12805	Sequence 12805, A
	272	29.8	4.7	421494	4	US-09-949-016-14060	Sequence 14060, A
	273	29.6	4.6	145	4	US-09-270-767-27822	Sequence 27822, A
c	274	29.6	4.6	421	4	US-09-270-767-4904	Sequence 4904, Ap
c	275	29.6	4.6	421	4	US-09-270-767-20186	Sequence 20186, A
	276	29.6	4.6	527	4	US-09-270-767-183	Sequence 183, App
	277	29.6	4.6	527	4	US-09-270-767-15465	Sequence 15465, A
	278	29.6	4.6	601	4	US-09-949-016-52009	Sequence 52009, A
c	279	29.6	4.6	601	4	US-09-949-016-60865	Sequence 60865, A
	280	29.6	4.6	601	4	US-09-949-016-64901	Sequence 64901, A
	281	29.6	4.6	777	4	US-09-134-000C-375	Sequence 375, App
	282	29.6	4.6	1001	4	US-09-671-317-299	Sequence 299, App
	283	29.6	4.6	1692	4	US-09-107-532A-1087	Sequence 1087, Ap
c	284	29.6	4.6	3291	3	US-09-318-448-12	Sequence 12, Appl
c	285	29.6	4.6	5769	1	US-08-652-971-1	Sequence 1, Appli
c	286	29.6	4.6	5769	2	US-08-991-258A-1	Sequence 1, Appli
c	287	29.6	4.6	5769	2	US-08-769-399-1	Sequence 1, Appli
c	288	29.6	4.6	5769	3	US-08-991-953A-1	Sequence 1, Appli
	289	29.6	4.6	7885	4	US-09-555-367A-3	Sequence 3, Appli
	290	29.6	4.6	16550	4	US-08-916-421B-3	Sequence 3, Appli
	291	29.6	4.6	16550	4	US-09-692-570-3	Sequence 3, Appli
	292	29.6	4.6	34372	4	US-09-949-016-13098	Sequence 13098, A
	293	29.6	4.6	34875	4	US-09-949-016-13099	Sequence 13099, A
c	294	29.6	4.6	40435	4	US-09-949-016-16504	Sequence 16504, A
c	295	29.6	4.6	49407	4	US-09-949-016-12532	Sequence 12532, A
c	296	29.6	4.6	49408	4	US-09-949-016-17045	Sequence 17045, A
	297	29.6	4.6	51773	4	US-09-949-016-16002	Sequence 16002, A
c	298	29.6	4.6	61198	4	US-09-949-016-17248	Sequence 17248, A
	299	29.6	4.6	94095	4	US-09-949-016-14389	Sequence 14389, A
c	300	29.6	4.6	152331	3	US-09-128-155-16	Sequence 16, Appl
c	301	29.6	4.6	154023	4	US-09-949-016-17057	Sequence 17057, A
c	302	29.6	4.6	202111	4	US-09-949-016-13877	Sequence 13877, A
c	303	29.6	4.6	264206	4	US-09-949-016-12731	Sequence 12731, A
c	304	29.6	4.6	264304	4	US-09-949-016-13249	Sequence 13249, A
	305	29.6	4.6	264665	4	US-09-949-016-13747	Sequence 13747, A
c	306	29.6	4.6	271134	4	US-09-949-016-12705	Sequence 12705, A
c	307	29.6	4.6	283538	4	US-09-949-016-13506	Sequence 13506, A
c	308	29.6	4.6	300402	4	US-09-949-016-13632	Sequence 13632, A
c	309	29.6	4.6	305491	4	US-09-949-016-17550	Sequence 17550, A
	310	29.4	4.6	543	3	US-09-134-001C-129	Sequence 129, App
	311	29.4	4.6	601	4	US-09-949-016-185618	Sequence 185618,
	312	29.4	4.6	601	4	US-09-949-016-185619	Sequence 185619,
	313	29.4	4.6	729	4	US-09-949-016-4852	Sequence 4852, Ap
	314	29.4	4.6	832	4	US-09-621-976-2813	Sequence 2813, Ap
	315	29.4	4.6	939	3	US-08-881-189B-1	Sequence 1, Appli
c	316	29.4	4.6	988	4	US-09-640-211A-188	Sequence 188, App
	317	29.4	4.6	1005	3	US-08-881-189B-22	Sequence 22, Appl
	318	29.4	4.6	2275	4	US-09-281-646B-1	Sequence 1, Appli
	319	29.4	4.6	4960	4	US-09-949-016-16594	Sequence 16594, A
	320	29.4	4.6	6082	3	US-09-439-313-535	Sequence 535, App
	321	29.4	4.6	6082	4	US-09-636-215-535	Sequence 535, App
	322	29.4	4.6	6082	4	US-09-685-166A-535	Sequence 535, App
	323	29.4	4.6	6082	4	US-09-679-426-535	Sequence 535, App
	324	29.4	4.6	6082	4	US-09-759-143-535	Sequence 535, App
	325	29.4	4.6	6082	4	US-09-651-236-535	Sequence 535, App
c	326	29.4	4.6	10186	4	US-09-949-016-15310	Sequence 15310, A
	327	29.4	4.6	10399	3	US-08-961-527-160	Sequence 160, App
	328	29.4	4.6	36791	4	US-09-949-016-17451	Sequence 17451, A
	329	29.4	4.6	87190	4	US-09-949-016-16335	Sequence 16335, A
	330	29.4	4.6	91831	4	US-09-949-016-13694	Sequence 13694, A
c	331	29.4	4.6	113966	4	US-09-949-016-12277	Sequence 12277, A
c	332	29.4	4.6	113967	4	US-09-949-016-17051	Sequence 17051, A
c	333	29.4	4.6	200663	4	US-09-949-016-12569	Sequence 12569, A
c	334	29.4	4.6	203093	4	US-09-949-016-14445	Sequence 14445, A
c	335	29.4	4.6	298336	4	US-09-949-016-16600	Sequence 16600, A
	336	29.4	4.6	385136	4	US-09-949-016-16073	Sequence 16073, A
c	337	29.4	4.6	462589	4	US-09-949-016-12900	Sequence 12900, A
c	338	29.4	4.6	476044	4	US-09-949-016-12412	Sequence 12412, A
c	339	29.4	4.6	1664976	4	US-08-916-421B-1	Sequence 1, Appli
c	340	29.4	4.6	1664976	4	US-09-692-570-1	Sequence 1, Appli
c	341	29.2	4.6	210	4	US-09-248-796A-8814	Sequence 8814, Ap
	342	29.2	4.6	510	4	US-09-270-767-28503	Sequence 28503, A
c	343	29.2	4.6	601	4	US-09-949-016-27605	Sequence 27605, A
c	344	29.2	4.6	601	4	US-09-949-016-29449	Sequence 29449, A
c	345	29.2	4.6	601	4	US-09-949-016-60866	Sequence 60866, A
	346	29.2	4.6	601	4	US-09-949-016-66348	Sequence 66348, A
c	347	29.2	4.6	601	4	US-09-949-016-134715	Sequence 134715,
c	348	29.2	4.6	601	4	US-09-949-016-150004	Sequence 150004,
c	349	29.2	4.6	601	4	US-09-949-016-166585	Sequence 166585,
c	350	29.2	4.6	601	4	US-09-949-016-166586	Sequence 166586,
c	351	29.2	4.6	601	4	US-09-949-016-205872	Sequence 205872,
c	352	29.2	4.6	678	3	US-09-308-003-41	Sequence 41, Appl
c	353	29.2	4.6	753	4	US-09-710-279-1089	Sequence 1089, Ap
c	354	29.2	4.6	837	4	US-09-134-000C-2739	Sequence 2739, Ap
c	355	29.2	4.6	861	4	US-09-248-796A-1510	Sequence 1510, Ap
	356	29.2	4.6	1080	4	US-09-270-767-12693	Sequence 12693, A
c	357	29.2	4.6	1268	4	US-09-710-279-1333	Sequence 1333, Ap
c	358	29.2	4.6	1407	4	US-09-710-279-459	Sequence 459, App
c	359	29.2	4.6	1422	3	US-09-134-001C-568	Sequence 568, App
	360	29.2	4.6	1563	4	US-09-248-796A-6700	Sequence 6700, Ap
	361	29.2	4.6	1750	2	US-08-686-599A-1	Sequence 1, Appli
	362	29.2	4.6	2090	4	US-09-461-325-33	Sequence 33, Appl
	363	29.2	4.6	2090	4	US-10-012-542-33	Sequence 33, Appl
	364	29.2	4.6	2090	4	US-10-115-123-33	Sequence 33, Appl
	365	29.2	4.6	2202	4	US-09-248-796A-4202	Sequence 4202, Ap
c	366	29.2	4.6	3133	4	US-09-710-279-3663	Sequence 3663, Ap
c	367	29.2	4.6	3190	4	US-09-710-279-3636	Sequence 3636, Ap
	368	29.2	4.6	3364	4	US-09-710-279-3633	Sequence 3633, Ap
c	369	29.2	4.6	3414	1	US-07-973-320-3	Sequence 3, Appli
c	370	29.2	4.6	3458	4	US-08-956-171E-317	Sequence 317, App
c	371	29.2	4.6	3458	4	US-08-781-986A-317	Sequence 317, App
	372	29.2	4.6	3501	4	US-09-710-279-3346	Sequence 3346, Ap
c	373	29.2	4.6	3870	4	US-09-949-016-4214	Sequence 4214, Ap
c	374	29.2	4.6	3871	4	US-09-949-016-591	Sequence 591, App
	375	29.2	4.6	3924	4	US-09-919-039-282	Sequence 282, App
c	376	29.2	4.6	3931	4	US-10-101-464A-962	Sequence 962, App
c	377	29.2	4.6	3939	4	US-10-101-464A-961	Sequence 961, App
c	378	29.2	4.6	8321	3	US-08-680-506-1	Sequence 1, Appli
c	379	29.2	4.6	11126	4	US-08-956-171E-171	Sequence 171, App
c	380	29.2	4.6	11126	4	US-08-781-986A-171	Sequence 171, App
c	381	29.2	4.6	12241	4	US-09-949-016-16746	Sequence 16746, A
c	382	29.2	4.6	12243	4	US-09-949-016-12094	Sequence 12094, A
c	383	29.2	4.6	31713	4	US-09-949-016-16960	Sequence 16960, A
c	384	29.2	4.6	57726	4	US-09-949-016-16430	Sequence 16430, A
	385	29.2	4.6	71387	4	US-09-949-016-16754	Sequence 16754, A
c	386	29.2	4.6	74962	4	US-09-685-853A-3	Sequence 3, Appli
c	387	29.2	4.6	83343	4	US-09-949-016-12242	Sequence 12242, A
c	388	29.2	4.6	83497	4	US-09-949-016-15517	Sequence 15517, A
c	389	29.2	4.6	85675	4	US-09-949-016-12333	Sequence 12333, A
c	390	29.2	4.6	85675	4	US-09-949-016-15956	Sequence 15956, A
c	391	29.2	4.6	106380	4	US-09-949-016-17553	Sequence 17553, A
c	392	29.2	4.6	128470	4	US-09-949-016-13765	Sequence 13765, A

393	29.2	4.6	187595	4	US-09-949-016-15546	Sequence 15546, A
c 394	29.2	4.6	421118	4	US-09-949-016-16297	Sequence 16297, A
395	29	4.5	499	4	US-09-621-976-2213	Sequence 2213, Ap
396	29	4.5	553	4	US-09-270-767-4692	Sequence 4692, Ap
397	29	4.5	553	4	US-09-270-767-19974	Sequence 19974, A
398	29	4.5	601	4	US-09-949-016-40615	Sequence 40615, A
399	29	4.5	601	4	US-09-949-016-105303	Sequence 105303,
c 400	29	4.5	601	4	US-09-949-016-152751	Sequence 152751,
401	29	4.5	601	4	US-09-949-016-161933	Sequence 161933,
c 402	29	4.5	601	4	US-09-949-016-193711	Sequence 193711,
403	29	4.5	601	4	US-09-949-016-196475	Sequence 196475,
404	29	4.5	1188	4	US-09-248-796A-4639	Sequence 4639, Ap
405	29	4.5	1230	4	US-09-328-352-123	Sequence 123, App
406	29	4.5	1383	4	US-09-716-129-22	Sequence 22, Appl
c 407	29	4.5	2047	3	US-08-836-261A-1	Sequence 1, Appli
408	29	4.5	2175	4	US-09-328-352-3584	Sequence 3584, Ap
409	29	4.5	2417	4	US-09-254-776B-3	Sequence 3, Appli
c 410	29	4.5	2517	3	US-09-149-476-227	Sequence 227, App
411	29	4.5	2834	4	US-09-566-921-43	Sequence 43, Appl
412	29	4.5	5917	4	US-09-949-016-3579	Sequence 3579, Ap
413	29	4.5	6019	4	US-09-949-016-869	Sequence 869, App
414	29	4.5	6019	4	US-09-949-016-2671	Sequence 2671, Ap
415	29	4.5	6140	3	US-09-439-313-536	Sequence 536, App
416	29	4.5	6140	4	US-09-636-215-536	Sequence 536, App
417	29	4.5	6140	4	US-09-685-166A-536	Sequence 536, App
418	29	4.5	6140	4	US-09-679-426-536	Sequence 536, App
419	29	4.5	6140	4	US-09-759-143-536	Sequence 536, App
420	29	4.5	6140	4	US-09-651-236-536	Sequence 536, App
c 421	29	4.5	13959	4	US-09-949-016-16673	Sequence 16673, A
c 422	29	4.5	34414	4	US-09-949-016-12330	Sequence 12330, A
c 423	29	4.5	34414	4	US-09-949-016-16157	Sequence 16157, A
c 424	29	4.5	35256	4	US-09-949-016-11991	Sequence 11991, A
425	29	4.5	41617	4	US-09-949-016-14356	Sequence 14356, A
426	29	4.5	41618	4	US-09-949-016-14681	Sequence 14681, A
c 427	29	4.5	93493	4	US-09-949-016-12063	Sequence 12063, A
c 428	29	4.5	95020	4	US-09-949-016-13272	Sequence 13272, A
c 429	29	4.5	113876	4	US-09-949-016-14828	Sequence 14828, A
c 430	29	4.5	113876	4	US-09-949-016-14829	Sequence 14829, A
c 431	29	4.5	115508	4	US-09-949-016-11800	Sequence 11800, A
c 432	29	4.5	115508	4	US-09-949-016-14826	Sequence 14826, A
c 433	29	4.5	115508	4	US-09-949-016-14827	Sequence 14827, A
434	29	4.5	135476	4	US-09-949-016-12611	Sequence 12611, A
435	29	4.5	135476	4	US-09-949-016-14413	Sequence 14413, A
436	29	4.5	136917	4	US-09-949-016-16369	Sequence 16369, A
437	29	4.5	139049	4	US-09-949-016-17030	Sequence 17030, A
c 438	29	4.5	155019	4	US-09-949-016-16029	Sequence 16029, A
439	29	4.5	168394	4	US-09-949-016-13002	Sequence 13002, A
c 440	29	4.5	173787	4	US-09-949-016-12542	Sequence 12542, A
c 441	29	4.5	173791	4	US-09-949-016-17302	Sequence 17302, A
442	29	4.5	237510	4	US-09-949-016-14273	Sequence 14273, A
c 443	29	4.5	238815	4	US-09-949-016-16274	Sequence 16274, A
c 444	29	4.5	319608	4	US-09-539-333D-1	Sequence 1, Appli
c 445	29	4.5	319608	4	US-09-679-409-1	Sequence 1, Appli
446	29	4.5	451924	4	US-09-949-016-12896	Sequence 12896, A
447	29	4.5	451925	4	US-09-949-016-17305	Sequence 17305, A
c 448	28.8	4.5	423	4	US-09-248-796A-6547	Sequence 6547, Ap
c 449	28.8	4.5	449	4	US-09-702-705-1699	Sequence 1699, Ap
c 450	28.8	4.5	449	4	US-09-736-457-1699	Sequence 1699, Ap
c 451	28.8	4.5	449	4	US-09-671-325-1699	Sequence 1699, Ap
c 452	28.8	4.5	449	4	US-09-658-824-1699	Sequence 1699, Ap
c 453	28.8	4.5	513	4	US-09-621-976-9350	Sequence 9350, Ap
454	28.8	4.5	601	4	US-09-949-016-79252	Sequence 79252, A
c 455	28.8	4.5	601	4	US-09-949-016-157402	Sequence 157402,
c 456	28.8	4.5	601	4	US-09-949-016-157509	Sequence 157509,
c 457	28.8	4.5	601	4	US-09-949-016-198545	Sequence 198545,
458	28.8	4.5	634	3	US-08-881-094-16	Sequence 16, Appl
459	28.8	4.5	674	3	US-08-881-094-13	Sequence 13, Appl
460	28.8	4.5	685	3	US-08-881-094-14	Sequence 14, Appl
c 461	28.8	4.5	720	4	US-09-248-796A-6711	Sequence 6711, Ap
462	28.8	4.5	915	4	US-09-107-532A-3508	Sequence 3508, Ap
463	28.8	4.5	1450	2	US-08-692-787-6	Sequence 6, Appli
464	28.8	4.5	2070	4	US-09-107-532A-1284	Sequence 1284, Ap
c 465	28.8	4.5	2091	3	US-09-134-001C-1459	Sequence 1459, Ap
466	28.8	4.5	2520	1	US-08-164-839-5	Sequence 5, Appli
467	28.8	4.5	2520	1	US-08-583-799-5	Sequence 5, Appli
c 468	28.8	4.5	3001	4	US-09-539-333D-181	Sequence 181, App
c 469	28.8	4.5	3001	4	US-09-539-333D-197	Sequence 197, App
470	28.8	4.5	3510	4	US-09-016-434-1324	Sequence 1324, Ap
c 471	28.8	4.5	4060	1	US-08-164-292B-1	Sequence 1, Appli
c 472	28.8	4.5	4060	1	US-08-164-292B-3	Sequence 3, Appli
c 473	28.8	4.5	4060	1	US-08-164-292B-5	Sequence 5, Appli
c 474	28.8	4.5	4060	1	US-08-164-292B-7	Sequence 7, Appli
c 475	28.8	4.5	4060	3	US-08-845-623-1	Sequence 1, Appli
c 476	28.8	4.5	4060	3	US-08-845-623-3	Sequence 3, Appli
c 477	28.8	4.5	4060	3	US-08-845-623-5	Sequence 5, Appli
c 478	28.8	4.5	4060	3	US-08-845-623-7	Sequence 7, Appli
c 479	28.8	4.5	4060	3	US-08-815-927-1	Sequence 1, Appli
c 480	28.8	4.5	4060	3	US-08-815-927-3	Sequence 3, Appli
c 481	28.8	4.5	4060	3	US-08-815-927-5	Sequence 5, Appli
c 482	28.8	4.5	4060	3	US-08-815-927-7	Sequence 7, Appli
c 483	28.8	4.5	4060	3	US-09-103-330-1	Sequence 1, Appli
c 484	28.8	4.5	4060	3	US-09-103-330-3	Sequence 3, Appli
c 485	28.8	4.5	4060	3	US-09-103-330-5	Sequence 5, Appli
c 486	28.8	4.5	4060	3	US-09-103-330-7	Sequence 7, Appli
c 487	28.8	4.5	4060	3	US-09-435-242-1	Sequence 1, Appli
c 488	28.8	4.5	4060	3	US-09-435-242-3	Sequence 3, Appli
c 489	28.8	4.5	4060	3	US-09-435-242-5	Sequence 5, Appli
c 490	28.8	4.5	4060	3	US-09-435-242-7	Sequence 7, Appli
491	28.8	4.5	4526	3	US-09-424-283-7	Sequence 7, Appli
492	28.8	4.5	5629	1	US-07-695-564-2	Sequence 2, Appli
493	28.8	4.5	5629	1	US-08-241-387-2	Sequence 2, Appli
494	28.8	4.5	5629	4	US-09-377-497-8	Sequence 8, Appli
495	28.8	4.5	5629	4	US-09-814-915A-51	Sequence 51, Appl
496	28.8	4.5	5762	4	US-09-919-172-55	Sequence 55, Appl
497	28.8	4.5	10709	4	US-09-596-002-9	Sequence 9, Appli
498	28.8	4.5	22906	4	US-09-949-016-16471	Sequence 16471, A
499	28.8	4.5	28809	4	US-09-949-016-12825	Sequence 12825, A
c 500	28.8	4.5	34446	3	US-09-103-330-35	Sequence 35, Appl
c 501	28.8	4.5	36907	4	US-09-949-016-12633	Sequence 12633, A
c 502	28.8	4.5	36913	4	US-09-949-016-15585	Sequence 15585, A
503	28.8	4.5	36938	4	US-09-949-016-13484	Sequence 13484, A
c 504	28.8	4.5	79350	4	US-09-949-016-12467	Sequence 12467, A
c 505	28.8	4.5	79351	4	US-09-949-016-16275	Sequence 16275, A
c 506	28.8	4.5	87190	4	US-09-949-016-16335	Sequence 16335, A
507	28.8	4.5	91279	4	US-09-949-016-15146	Sequence 15146, A
c 508	28.8	4.5	96866	4	US-09-949-016-13768	Sequence 13768, A
c 509	28.8	4.5	107329	4	US-09-949-016-12663	Sequence 12663, A
c 510	28.8	4.5	107329	4	US-09-949-016-12664	Sequence 12664, A
c 511	28.8	4.5	107330	4	US-09-949-016-15408	Sequence 15408, A
c 512	28.8	4.5	107330	4	US-09-949-016-15409	Sequence 15409, A
c 513	28.8	4.5	107330	4	US-09-949-016-15410	Sequence 15410, A
c 514	28.8	4.5	107330	4	US-09-949-016-15411	Sequence 15411, A
c 515	28.8	4.5	107750	4	US-09-949-016-12662	Sequence 12662, A
c 516	28.8	4.5	107751	4	US-09-949-016-15412	Sequence 15412, A
c 517	28.8	4.5	107751	4	US-09-949-016-15413	Sequence 15413, A
c 518	28.8	4.5	107751	4	US-09-949-016-15414	Sequence 15414, A
c 519	28.8	4.5	107751	4	US-09-949-016-15415	Sequence 15415, A
c 520	28.8	4.5	107925	4	US-09-949-016-11875	Sequence 11875, A
c 521	28.8	4.5	107926	4	US-09-949-016-15404	Sequence 15404, A
c 522	28.8	4.5	107926	4	US-09-949-016-15405	Sequence 15405, A
c 523	28.8	4.5	107926	4	US-09-949-016-15406	Sequence 15406, A
c 524	28.8	4.5	107926	4	US-09-949-016-15407	Sequence 15407, A
c 525	28.8	4.5	126176	4	US-09-949-016-16137	Sequence 16137, A
c 526	28.8	4.5	126176	4	US-09-949-016-16138	Sequence 16138, A
c 527	28.8	4.5	152481	4	US-09-949-016-12521	Sequence 12521, A
c 528	28.8	4.5	152798	4	US-09-949-016-12775	Sequence 12775, A
c 529	28.8	4.5	152822	4	US-09-949-016-17518	Sequence 17518, A
c 530	28.8	4.5	152822	4	US-09-949-016-17519	Sequence 17519, A
c 531	28.8	4.5	157644	4	US-09-949-016-16179	Sequence 16179, A
c 532	28.8	4.5	157644	4	US-09-949-016-16180	Sequence 16180, A
c 533	28.8	4.5	237863	4	US-09-949-016-13404	Sequence 13404, A
c 534	28.8	4.5	263693	4	US-09-949-016-12386	Sequence 12386, A
c 535	28.8	4.5	263694	4	US-09-949-016-16915	Sequence 16915, A
c 536	28.8	4.5	450395	4	US-09-949-016-15473	Sequence 15473, A
537	28.8	4.5	767677	4	US-09-949-016-12147	Sequence 12147, A
538	28.8	4.5	767677	4	US-09-949-016-17361	Sequence 17361, A

	539	28.8	4.5	784019	4	US-09-949-016-14033	Sequence 14033, A
c	540	28.8	4.5	786431	4	US-09-751-389-3	Sequence 3, Appli
	541	28.8	4.5	828152	4	US-09-949-016-12777	Sequence 12777, A
c	542	28.6	4.5	185	4	US-09-513-999C-23568	Sequence 23568, A
	543	28.6	4.5	246	4	US-09-023-655-291	Sequence 291, App
	544	28.6	4.5	285	4	US-09-313-294A-6587	Sequence 6587, Ap
c	545	28.6	4.5	350	4	US-09-706-228-3	Sequence 3, Appli
	546	28.6	4.5	399	4	US-09-621-976-8976	Sequence 8976, Ap
c	547	28.6	4.5	419	4	US-09-706-228-2	Sequence 2, Appli
	548	28.6	4.5	555	4	US-09-248-796A-3370	Sequence 3370, Ap
c	549	28.6	4.5	601	4	US-09-949-016-40529	Sequence 40529, A
c	550	28.6	4.5	601	4	US-09-949-016-62105	Sequence 62105, A
c	551	28.6	4.5	601	4	US-09-949-016-62106	Sequence 62106, A
c	552	28.6	4.5	601	4	US-09-949-016-63868	Sequence 63868, A
c	553	28.6	4.5	601	4	US-09-949-016-63943	Sequence 63943, A
c	554	28.6	4.5	601	4	US-09-949-016-108620	Sequence 108620,
c	555	28.6	4.5	601	4	US-09-949-016-155312	Sequence 155312,
c	556	28.6	4.5	601	4	US-09-949-016-161459	Sequence 161459,
c	557	28.6	4.5	601	4	US-09-949-016-173683	Sequence 173683,
c	558	28.6	4.5	601	4	US-09-949-016-173730	Sequence 173730,
	559	28.6	4.5	726	4	US-09-328-352-894	Sequence 894, App
c	560	28.6	4.5	888	3	US-09-308-003-1	Sequence 1, Appli
	561	28.6	4.5	906	4	US-09-248-796A-9375	Sequence 9375, Ap
c	562	28.6	4.5	918	4	US-09-248-796A-5697	Sequence 5697, Ap
c	563	28.6	4.5	1242	4	US-09-328-352-1870	Sequence 1870, Ap
	564	28.6	4.5	2085	3	US-09-299-843A-65	Sequence 65, Appl
	565	28.6	4.5	2085	3	US-09-088-337B-65	Sequence 65, Appl
	566	28.6	4.5	2581	1	US-08-200-900A-1	Sequence 1, Appli
	567	28.6	4.5	2581	4	US-08-794-042-1	Sequence 1, Appli
	568	28.6	4.5	2581	5	PCT-US94-00616-1	Sequence 1, Appli
c	569	28.6	4.5	2888	3	US-09-149-476-61	Sequence 61, Appl
c	570	28.6	4.5	3078	4	US-09-248-796A-6470	Sequence 6470, Ap
	571	28.6	4.5	3198	4	US-09-328-352-1410	Sequence 1410, Ap
	572	28.6	4.5	3736	3	US-09-600-776-10	Sequence 10, Appl
	573	28.6	4.5	3736	4	US-09-965-830-10	Sequence 10, Appl
	574	28.6	4.5	3793	4	US-09-489-847-126	Sequence 126, App
	575	28.6	4.5	3798	4	US-09-489-847-95	Sequence 95, Appl
	576	28.6	4.5	5061	3	US-09-355-160D-1	Sequence 1, Appli
	577	28.6	4.5	5061	4	US-10-092-219-1	Sequence 1, Appli
c	578	28.6	4.5	5695	4	US-09-949-016-13664	Sequence 13664, A
c	579	28.6	4.5	7001	3	US-08-961-527-88	Sequence 88, Appl
c	580	28.6	4.5	7953	4	US-08-956-171E-152	Sequence 152, App
c	581	28.6	4.5	7953	4	US-08-781-986A-152	Sequence 152, App
	582	28.6	4.5	22067	3	US-09-820-001-3	Sequence 3, Appli
	583	28.6	4.5	29326	4	US-09-949-016-15356	Sequence 15356, A
c	584	28.6	4.5	42000	4	US-10-081-563-25	Sequence 25, Appl
	585	28.6	4.5	63588	4	US-09-873-404-3	Sequence 3, Appli
	586	28.6	4.5	63588	4	US-10-243-735-3	Sequence 3, Appli
	587	28.6	4.5	75480	4	US-09-949-016-16090	Sequence 16090, A
	588	28.6	4.5	78491	4	US-09-949-016-15132	Sequence 15132, A
	589	28.6	4.5	80246	3	US-09-078-294-4	Sequence 4, Appli
	590	28.6	4.5	80595	3	US-09-078-294-3	Sequence 3, Appli
c	591	28.6	4.5	81819	4	US-09-949-016-16661	Sequence 16661, A
c	592	28.6	4.5	81819	4	US-09-949-016-16662	Sequence 16662, A
c	593	28.6	4.5	89625	4	US-09-949-016-17012	Sequence 17012, A
c	594	28.6	4.5	101349	4	US-09-949-016-17433	Sequence 17433, A
c	595	28.6	4.5	106924	4	US-09-949-016-13834	Sequence 13834, A
	596	28.6	4.5	107827	4	US-09-949-016-15790	Sequence 15790, A
c	597	28.6	4.5	108310	4	US-09-949-016-16366	Sequence 16366, A
	598	28.6	4.5	113060	4	US-09-949-016-14773	Sequence 14773, A
	599	28.6	4.5	113060	4	US-09-949-016-14774	Sequence 14774, A
	600	28.6	4.5	121049	4	US-09-949-016-17513	Sequence 17513, A
c	601	28.6	4.5	126029	4	US-09-949-016-14731	Sequence 14731, A
	602	28.6	4.5	147382	4	US-09-949-016-14624	Sequence 14624, A
	603	28.6	4.5	163022	4	US-09-949-016-16515	Sequence 16515, A
c	604	28.6	4.5	171700	4	US-09-949-016-12276	Sequence 12276, A
c	605	28.6	4.5	171701	4	US-09-949-016-15835	Sequence 15835, A
c	606	28.6	4.5	194714	4	US-09-949-016-11869	Sequence 11869, A
	607	28.6	4.5	198632	4	US-09-949-016-12781	Sequence 12781, A
	608	28.6	4.5	198637	4	US-09-949-016-17393	Sequence 17393, A
	609	28.6	4.5	240157	4	US-09-949-016-16264	Sequence 16264, A
c	610	28.6	4.5	245286	4	US-09-949-016-15497	Sequence 15497, A
c	611	28.6	4.5	314798	4	US-09-949-016-13539	Sequence 13539, A
c	612	28.6	4.5	331814	4	US-09-949-016-12008	Sequence 12008, A
c	613	28.6	4.5	331814	4	US-09-949-016-17056	Sequence 17056, A
c	614	28.6	4.5	392000	4	US-10-027-983-11	Sequence 11, Appl
	615	28.6	4.5	1230025	4	US-09-198-452A-1	Sequence 1, Appli
	616	28.6	4.5	1230230	4	US-09-438-185A-1	Sequence 1, Appli
	617	28.4	4.4	601	4	US-09-949-016-24014	Sequence 24014, A
	618	28.4	4.4	601	4	US-09-949-016-24015	Sequence 24015, A
c	619	28.4	4.4	601	4	US-09-949-016-26589	Sequence 26589, A
c	620	28.4	4.4	601	4	US-09-949-016-32480	Sequence 32480, A
c	621	28.4	4.4	601	4	US-09-949-016-82502	Sequence 82502, A
c	622	28.4	4.4	601	4	US-09-949-016-94528	Sequence 94528, A
c	623	28.4	4.4	601	4	US-09-949-016-94529	Sequence 94529, A
	624	28.4	4.4	601	4	US-09-949-016-125525	Sequence 125525,
	625	28.4	4.4	601	4	US-09-949-016-125526	Sequence 125526,
	626	28.4	4.4	601	4	US-09-949-016-141807	Sequence 141807,
	627	28.4	4.4	601	4	US-09-949-016-141808	Sequence 141808,
	628	28.4	4.4	601	4	US-09-949-016-141809	Sequence 141809,
c	629	28.4	4.4	601	4	US-09-949-016-179385	Sequence 179385,
c	630	28.4	4.4	601	4	US-09-949-016-187401	Sequence 187401,
c	631	28.4	4.4	601	4	US-09-949-016-189776	Sequence 189776,
c	632	28.4	4.4	601	4	US-09-949-001-269	Sequence 269, App
c	633	28.4	4.4	601	4	US-09-949-001-691	Sequence 691, App
	634	28.4	4.4	666	3	US-09-081-320-15	Sequence 15, Appl
	635	28.4	4.4	666	3	US-09-574-141A-15	Sequence 15, Appl
	636	28.4	4.4	666	3	US-09-707-780-15	Sequence 15, Appl
	637	28.4	4.4	666	4	US-09-568-189A-15	Sequence 15, Appl
c	638	28.4	4.4	717	4	US-09-248-796A-4471	Sequence 4471, Ap
	639	28.4	4.4	828	4	US-09-543-681A-3276	Sequence 3276, Ap
c	640	28.4	4.4	1182	4	US-09-248-796A-4568	Sequence 4568, Ap
	641	28.4	4.4	1935	4	US-08-956-171E-347	Sequence 347, App
	642	28.4	4.4	1935	4	US-08-781-986A-347	Sequence 347, App
	643	28.4	4.4	2680	3	US-09-081-320-12	Sequence 12, Appl
	644	28.4	4.4	2680	3	US-09-574-141A-12	Sequence 12, Appl
	645	28.4	4.4	2680	3	US-09-707-780-12	Sequence 12, Appl
	646	28.4	4.4	2680	4	US-09-568-189A-12	Sequence 12, Appl
	647	28.4	4.4	5632	3	US-09-560-594-3	Sequence 3, Appli
	648	28.4	4.4	5632	4	US-09-949-016-862	Sequence 862, App
	649	28.4	4.4	6792	3	US-09-374-454-20	Sequence 20, Appl
	650	28.4	4.4	7655	1	US-08-619-554-1	Sequence 1, Appli
	651	28.4	4.4	9072	4	US-08-956-171E-45	Sequence 45, Appl
	652	28.4	4.4	9072	4	US-08-781-986A-45	Sequence 45, Appl
	653	28.4	4.4	29636	4	US-09-949-016-12189	Sequence 12189, A
	654	28.4	4.4	29637	4	US-09-949-016-17173	Sequence 17173, A
	655	28.4	4.4	29638	4	US-09-949-016-14137	Sequence 14137, A
	656	28.4	4.4	39085	4	US-09-949-016-14479	Sequence 14479, A
	657	28.4	4.4	39088	4	US-09-949-016-14373	Sequence 14373, A
c	658	28.4	4.4	45225	4	US-09-949-016-12428	Sequence 12428, A
c	659	28.4	4.4	45226	4	US-09-949-016-13654	Sequence 13654, A
c	660	28.4	4.4	45571	4	US-09-949-016-16262	Sequence 16262, A
c	661	28.4	4.4	66219	4	US-09-949-016-12038	Sequence 12038, A
c	662	28.4	4.4	66227	4	US-09-949-016-15303	Sequence 15303, A
	663	28.4	4.4	66524	4	US-09-949-001-32	Sequence 32, Appl
	664	28.4	4.4	66525	4	US-09-949-001-38	Sequence 38, Appl
	665	28.4	4.4	72843	4	US-09-949-016-12574	Sequence 12574, A
c	666	28.4	4.4	84171	4	US-09-949-016-16356	Sequence 16356, A
	667	28.4	4.4	86116	4	US-09-949-016-14766	Sequence 14766, A
c	668	28.4	4.4	91062	4	US-09-949-016-13019	Sequence 13019, A
c	669	28.4	4.4	105055	4	US-09-949-016-14001	Sequence 14001, A
c	670	28.4	4.4	112507	4	US-09-949-016-12420	Sequence 12420, A
c	671	28.4	4.4	112507	4	US-09-949-016-12794	Sequence 12794, A
c	672	28.4	4.4	112508	4	US-09-949-016-16589	Sequence 16589, A
c	673	28.4	4.4	112508	4	US-09-949-016-16590	Sequence 16590, A
c	674	28.4	4.4	118382	4	US-09-949-016-15996	Sequence 15996, A
c	675	28.4	4.4	118382	4	US-09-949-016-15997	Sequence 15997, A
c	676	28.4	4.4	146095	4	US-09-949-016-12872	Sequence 12872, A
c	677	28.4	4.4	146104	4	US-09-949-016-13239	Sequence 13239, A
	678	28.4	4.4	157032	4	US-09-949-016-16502	Sequence 16502, A
	679	28.4	4.4	162914	4	US-09-949-016-15578	Sequence 15578, A
	680	28.4	4.4	189560	4	US-09-949-016-17202	Sequence 17202, A
c	681	28.4	4.4	194537	4	US-09-949-016-12928	Sequence 12928, A
c	682	28.4	4.4	198632	4	US-09-949-016-12781	Sequence 12781, A
c	683	28.4	4.4	198637	4	US-09-949-016-17393	Sequence 17393, A
c	684	28.4	4.4	201529	4	US-09-949-016-12740	Sequence 12740, A

	685	28.4	4.4	245286	4	US-09-949-016-15497	Sequence 15497, A
	686	28.4	4.4	319608	4	US-09-539-333D-1	Sequence 1, Appli
	687	28.4	4.4	319608	4	US-09-679-409-1	Sequence 1, Appli
c	688	28.4	4.4	363032	4	US-09-949-016-12415	Sequence 12415, A
c	689	28.4	4.4	363033	4	US-09-949-016-15754	Sequence 15754, A
	690	28.4	4.4	390890	4	US-09-949-016-14720	Sequence 14720, A
	691	28.2	4.4	227	4	US-09-513-999C-33667	Sequence 33667, A
c	692	28.2	4.4	315	4	US-09-248-796A-7925	Sequence 7925, Ap
c	693	28.2	4.4	384	4	US-09-248-796A-3021	Sequence 3021, Ap
	694	28.2	4.4	470	4	US-09-270-767-4742	Sequence 4742, Ap
	695	28.2	4.4	470	4	US-09-270-767-20024	Sequence 20024, A
	696	28.2	4.4	509	4	US-09-949-016-172217	Sequence 172217,
	697	28.2	4.4	601	4	US-09-949-016-31374	Sequence 31374, A
c	698	28.2	4.4	601	4	US-09-949-016-32478	Sequence 32478, A
c	699	28.2	4.4	601	4	US-09-949-016-32479	Sequence 32479, A
c	700	28.2	4.4	601	4	US-09-949-016-32481	Sequence 32481, A
c	701	28.2	4.4	601	4	US-09-949-016-32482	Sequence 32482, A
	702	28.2	4.4	601	4	US-09-949-016-41554	Sequence 41554, A
	703	28.2	4.4	601	4	US-09-949-016-76136	Sequence 76136, A
	704	28.2	4.4	601	4	US-09-949-016-91607	Sequence 91607, A
	705	28.2	4.4	601	4	US-09-949-016-119292	Sequence 119292,
c	706	28.2	4.4	601	4	US-09-949-016-134583	Sequence 134583,
	707	28.2	4.4	601	4	US-09-949-016-135437	Sequence 135437,
c	708	28.2	4.4	601	4	US-09-949-016-167069	Sequence 167069,
	709	28.2	4.4	601	4	US-09-949-016-172218	Sequence 172218,
	710	28.2	4.4	601	4	US-09-949-016-172219	Sequence 172219,
c	711	28.2	4.4	601	4	US-09-949-016-187399	Sequence 187399,
c	712	28.2	4.4	601	4	US-09-949-016-187400	Sequence 187400,
c	713	28.2	4.4	601	4	US-09-949-016-187402	Sequence 187402,
c	714	28.2	4.4	601	4	US-09-949-016-187403	Sequence 187403,
	715	28.2	4.4	601	4	US-09-949-016-204276	Sequence 204276,
	716	28.2	4.4	601	4	US-09-949-016-204277	Sequence 204277,
	717	28.2	4.4	690	4	US-09-489-039A-2220	Sequence 2220, Ap
	718	28.2	4.4	699	4	US-09-248-796A-353	Sequence 353, App
	719	28.2	4.4	771	4	US-08-956-171E-1071	Sequence 1071, Ap
	720	28.2	4.4	771	4	US-08-781-986A-1071	Sequence 1071, Ap
	721	28.2	4.4	1218	4	US-09-248-796A-4630	Sequence 4630, Ap
	722	28.2	4.4	1443	4	US-10-237-551-206	Sequence 206, App
	723	28.2	4.4	1666	1	US-08-076-090-1	Sequence 1, Appli
	724	28.2	4.4	1666	5	PCT-US94-06661-1	Sequence 1, Appli
	725	28.2	4.4	1668	4	US-09-543-681A-1550	Sequence 1550, Ap
c	726	28.2	4.4	2500	1	US-08-550-715-10	Sequence 10, Appl
c	727	28.2	4.4	3385	4	US-09-411-449-3	Sequence 3, Appli
c	728	28.2	4.4	3496	4	US-09-411-449-1	Sequence 1, Appli
c	729	28.2	4.4	3784	4	US-09-949-016-4855	Sequence 4855, Ap
c	730	28.2	4.4	3805	4	US-09-411-449-4	Sequence 4, Appli
c	731	28.2	4.4	3916	4	US-09-411-449-2	Sequence 2, Appli
	732	28.2	4.4	5285	2	US-08-609-049A-29	Sequence 29, Appl
	733	28.2	4.4	5285	3	US-09-170-996-29	Sequence 29, Appl
	734	28.2	4.4	5836	3	US-09-233-086-2	Sequence 2, Appli
c	735	28.2	4.4	6060	5	PCT-US96-09430-7	Sequence 7, Appli
c	736	28.2	4.4	18556	4	US-09-949-016-15177	Sequence 15177, A
c	737	28.2	4.4	19703	4	US-09-949-016-14926	Sequence 14926, A
	738	28.2	4.4	21723	4	US-09-949-016-16383	Sequence 16383, A
c	739	28.2	4.4	22581	4	US-09-949-016-15984	Sequence 15984, A
c	740	28.2	4.4	31144	4	US-09-949-016-15993	Sequence 15993, A
	741	28.2	4.4	32414	4	US-09-949-016-16443	Sequence 16443, A
c	742	28.2	4.4	33099	4	US-09-949-016-16094	Sequence 16094, A
c	743	28.2	4.4	34658	4	US-09-949-016-12629	Sequence 12629, A
c	744	28.2	4.4	36317	4	US-09-949-016-12697	Sequence 12697, A
c	745	28.2	4.4	36322	4	US-09-949-016-14047	Sequence 14047, A
c	746	28.2	4.4	43375	4	US-09-949-016-12688	Sequence 12688, A
c	747	28.2	4.4	43376	4	US-09-949-016-15515	Sequence 15515, A
c	748	28.2	4.4	46603	4	US-09-949-016-15636	Sequence 15636, A
	749	28.2	4.4	47110	4	US-09-949-016-17609	Sequence 17609, A
	750	28.2	4.4	48908	3	US-09-453-702B-137	Sequence 137, App
	751	28.2	4.4	57837	4	US-09-949-016-14371	Sequence 14371, A
	752	28.2	4.4	57839	4	US-09-949-016-17601	Sequence 17601, A
c	753	28.2	4.4	64049	4	US-09-949-016-15744	Sequence 15744, A
c	754	28.2	4.4	73818	4	US-09-949-016-16822	Sequence 16822, A
c	755	28.2	4.4	74940	4	US-09-949-016-17512	Sequence 17512, A
c	756	28.2	4.4	76563	4	US-09-949-016-17099	Sequence 17099, A
c	757	28.2	4.4	78269	4	US-09-949-016-12497	Sequence 12497, A
c	758	28.2	4.4	102008	4	US-09-949-016-16617	Sequence 16617, A
c	759	28.2	4.4	104077	4	US-09-949-016-13593	Sequence 13593, A
	760	28.2	4.4	108169	4	US-09-949-016-12898	Sequence 12898, A
	761	28.2	4.4	108169	4	US-09-949-016-15907	Sequence 15907, A
c	762	28.2	4.4	126982	4	US-09-949-016-16597	Sequence 16597, A
	763	28.2	4.4	133358	4	US-09-949-016-16964	Sequence 16964, A
	764	28.2	4.4	133360	4	US-09-949-016-12651	Sequence 12651, A
	765	28.2	4.4	133719	4	US-09-949-016-15092	Sequence 15092, A
c	766	28.2	4.4	135667	4	US-09-949-016-15051	Sequence 15051, A
	767	28.2	4.4	143550	4	US-09-949-016-14143	Sequence 14143, A
c	768	28.2	4.4	145241	4	US-09-949-016-17394	Sequence 17394, A
c	769	28.2	4.4	145241	4	US-09-949-016-17395	Sequence 17395, A
c	770	28.2	4.4	146401	4	US-09-949-016-16151	Sequence 16151, A
c	771	28.2	4.4	148783	4	US-09-949-016-15729	Sequence 15729, A
c	772	28.2	4.4	152486	4	US-09-949-016-12869	Sequence 12869, A
c	773	28.2	4.4	168174	4	US-10-071-411A-63	Sequence 63, Appl
c	774	28.2	4.4	168273	4	US-10-071-411A-2	Sequence 2, Appli
	775	28.2	4.4	421118	4	US-09-949-016-16297	Sequence 16297, A
c	776	28.2	4.4	524032	4	US-09-949-016-16928	Sequence 16928, A
c	777	28.2	4.4	524032	4	US-09-949-016-16929	Sequence 16929, A
c	778	28.2	4.4	524032	4	US-09-949-016-16930	Sequence 16930, A
c	779	28.2	4.4	524032	4	US-09-949-016-16931	Sequence 16931, A
c	780	28.2	4.4	529885	4	US-09-949-016-14340	Sequence 14340, A
c	781	28.2	4.4	529885	4	US-09-949-016-14341	Sequence 14341, A
c	782	28.2	4.4	529885	4	US-09-949-016-14342	Sequence 14342, A
c	783	28.2	4.4	529885	4	US-09-949-016-14343	Sequence 14343, A
c	784	28.2	4.4	529885	4	US-09-949-016-14344	Sequence 14344, A
c	785	28.2	4.4	529885	4	US-09-949-016-14345	Sequence 14345, A
c	786	28.2	4.4	529885	4	US-09-949-016-14346	Sequence 14346, A
c	787	28.2	4.4	529885	4	US-09-949-016-14347	Sequence 14347, A
	788	28.2	4.4	1830121	4	US-09-557-884-1	Sequence 1, Appli
	789	28.2	4.4	1830121	4	US-09-643-990A-1	Sequence 1, Appli
c	790	28	4.4	112	4	US-08-956-171E-1458	Sequence 1458, Ap
c	791	28	4.4	112	4	US-08-781-986A-1458	Sequence 1458, Ap
	792	28	4.4	363	4	US-09-248-796A-11506	Sequence 11506, A
c	793	28	4.4	367	4	US-09-513-999C-30732	Sequence 30732, A
	794	28	4.4	468	3	US-09-134-001C-823	Sequence 823, App
c	795	28	4.4	601	4	US-09-949-016-34710	Sequence 34710, A
c	796	28	4.4	601	4	US-09-949-016-56244	Sequence 56244, A
c	797	28	4.4	601	4	US-09-949-016-68654	Sequence 68654, A
c	798	28	4.4	601	4	US-09-949-016-107834	Sequence 107834,
	799	28	4.4	601	4	US-09-949-016-133751	Sequence 133751,
	800	28	4.4	601	4	US-09-949-016-150522	Sequence 150522,
c	801	28	4.4	601	4	US-09-949-016-151890	Sequence 151890,
c	802	28	4.4	601	4	US-09-949-016-158663	Sequence 158663,
c	803	28	4.4	601	4	US-09-949-016-158664	Sequence 158664,
	804	28	4.4	601	4	US-09-949-016-162920	Sequence 162920,
c	805	28	4.4	601	4	US-09-949-016-163468	Sequence 163468,
c	806	28	4.4	601	4	US-09-949-016-188025	Sequence 188025,
c	807	28	4.4	601	4	US-09-949-016-188430	Sequence 188430,
c	808	28	4.4	601	4	US-09-949-016-188431	Sequence 188431,
c	809	28	4.4	601	4	US-09-949-016-189671	Sequence 189671,
c	810	28	4.4	601	4	US-09-949-016-203312	Sequence 203312,
c	811	28	4.4	601	4	US-09-949-016-203313	Sequence 203313,
c	812	28	4.4	601	4	US-09-949-016-203314	Sequence 203314,
c	813	28	4.4	601	4	US-09-949-016-203315	Sequence 203315,
	814	28	4.4	669	4	US-09-328-352-3590	Sequence 3590, Ap
c	815	28	4.4	981	4	US-09-107-532A-11	Sequence 11, Appl
	816	28	4.4	1428	2	US-08-786-999-2	Sequence 2, Appli
	817	28	4.4	1428	3	US-08-969-987-8	Sequence 8, Appli
	818	28	4.4	1428	4	US-09-216-387-2	Sequence 2, Appli
	819	28	4.4	1491	3	US-08-999-774A-7	Sequence 7, Appli
	820	28	4.4	1494	1	US-08-585-758A-3	Sequence 3, Appli
	821	28	4.4	1494	1	US-08-977-818-3	Sequence 3, Appli
	822	28	4.4	1494	2	US-08-670-274B-3	Sequence 3, Appli
	823	28	4.4	1494	3	US-09-146-187-3	Sequence 3, Appli
	824	28	4.4	1494	4	US-09-023-655-997	Sequence 997, App
	825	28	4.4	1494	4	US-09-804-690-3	Sequence 3, Appli
	826	28	4.4	1508	4	US-09-949-016-5380	Sequence 5380, Ap
c	827	28	4.4	1965	4	US-09-614-221A-180	Sequence 180, App
c	828	28	4.4	2169	3	US-09-105-390-5	Sequence 5, Appli
	829	28	4.4	2298	4	US-09-107-532A-96	Sequence 96, Appl
	830	28	4.4	3321	4	US-09-023-655-1361	Sequence 1361, Ap

	831	28	4.4	3458	4	US-09-710-279-3510	Sequence 3510, Ap
	832	28	4.4	3581	2	US-08-738-349-1	Sequence 1, Appli
c	833	28	4.4	3948	3	US-09-302-620B-86	Sequence 86, Appl
c	834	28	4.4	3948	4	US-09-912-161-8	Sequence 8, Appli
c	835	28	4.4	3948	4	US-09-911-781-1	Sequence 1, Appli
c	836	28	4.4	3948	4	US-10-400-902-1	Sequence 1, Appli
c	837	28	4.4	4889	4	US-09-949-016-13043	Sequence 13043, A
c	838	28	4.4	6076	4	US-09-824-734-1	Sequence 1, Appli
c	839	28	4.4	8224	2	US-09-010-398-14	Sequence 14, Appl
c	840	28	4.4	8224	3	US-09-366-260-14	Sequence 14, Appl
	841	28	4.4	8989	4	US-09-949-016-16215	Sequence 16215, A
	842	28	4.4	19390	3	US-08-961-527-86	Sequence 86, Appl
c	843	28	4.4	19787	4	US-09-949-016-16345	Sequence 16345, A
	844	28	4.4	21516	4	US-09-949-016-13024	Sequence 13024, A
c	845	28	4.4	25021	4	US-09-949-016-13761	Sequence 13761, A
c	846	28	4.4	25199	4	US-09-949-016-13361	Sequence 13361, A
c	847	28	4.4	37822	4	US-09-949-016-16291	Sequence 16291, A
c	848	28	4.4	43981	4	US-09-949-016-16294	Sequence 16294, A
	849	28	4.4	46499	4	US-09-949-016-14032	Sequence 14032, A
c	850	28	4.4	49472	4	US-09-949-016-17478	Sequence 17478, A
c	851	28	4.4	50878	4	US-09-949-016-11787	Sequence 11787, A
	852	28	4.4	51849	4	US-09-949-016-15433	Sequence 15433, A
	853	28	4.4	57178	4	US-09-949-016-12838	Sequence 12838, A
	854	28	4.4	57178	4	US-09-949-016-17458	Sequence 17458, A
	855	28	4.4	68580	4	US-09-949-016-15844	Sequence 15844, A
	856	28	4.4	70828	4	US-09-949-016-12122	Sequence 12122, A
c	857	28	4.4	77586	4	US-09-949-016-13220	Sequence 13220, A
c	858	28	4.4	77586	4	US-09-949-016-13221	Sequence 13221, A
c	859	28	4.4	94156	4	US-09-949-016-12388	Sequence 12388, A
c	860	28	4.4	102406	4	US-09-949-016-14673	Sequence 14673, A
c	861	28	4.4	110266	4	US-09-949-016-14913	Sequence 14913, A
c	862	28	4.4	110266	4	US-09-949-016-14914	Sequence 14914, A
c	863	28	4.4	110266	4	US-09-949-016-14915	Sequence 14915, A
c	864	28	4.4	110266	4	US-09-949-016-14916	Sequence 14916, A
c	865	28	4.4	110266	4	US-09-949-016-14917	Sequence 14917, A
c	866	28	4.4	110266	4	US-09-949-016-14918	Sequence 14918, A
c	867	28	4.4	110266	4	US-09-949-016-14919	Sequence 14919, A
c	868	28	4.4	110266	4	US-09-949-016-14920	Sequence 14920, A
c	869	28	4.4	110266	4	US-09-949-016-14921	Sequence 14921, A
c	870	28	4.4	110266	4	US-09-949-016-14922	Sequence 14922, A
c	871	28	4.4	124884	4	US-09-661-596A-76	Sequence 76, Appl
c	872	28	4.4	124884	4	US-09-913-514-1	Sequence 1, Appli
c	873	28	4.4	125157	4	US-09-913-514-2	Sequence 2, Appli
c	874	28	4.4	158735	4	US-09-949-016-11989	Sequence 11989, A
c	875	28	4.4	158735	4	US-09-949-016-17130	Sequence 17130, A
	876	28	4.4	165651	4	US-09-949-016-13032	Sequence 13032, A
	877	28	4.4	173992	4	US-09-949-016-13379	Sequence 13379, A
c	878	28	4.4	197875	4	US-09-949-016-15425	Sequence 15425, A
	879	28	4.4	236474	4	US-09-949-016-13418	Sequence 13418, A
c	880	28	4.4	276237	4	US-09-949-016-17504	Sequence 17504, A
c	881	28	4.4	1230025	4	US-09-198-452A-1	Sequence 1, Appli
c	882	27.8	4.4	284	4	US-09-513-999C-28741	Sequence 28741, A
c	883	27.8	4.4	309	4	US-09-134-000C-272	Sequence 272, App
	884	27.8	4.4	601	4	US-09-949-016-18112	Sequence 18112, A
	885	27.8	4.4	601	4	US-09-949-016-18113	Sequence 18113, A
	886	27.8	4.4	601	4	US-09-949-016-18114	Sequence 18114, A
	887	27.8	4.4	601	4	US-09-949-016-51622	Sequence 51622, A
	888	27.8	4.4	601	4	US-09-949-016-51623	Sequence 51623, A
	889	27.8	4.4	601	4	US-09-949-016-51624	Sequence 51624, A
c	890	27.8	4.4	601	4	US-09-949-016-55104	Sequence 55104, A
	891	27.8	4.4	601	4	US-09-949-016-57937	Sequence 57937, A
c	892	27.8	4.4	601	4	US-09-949-016-68119	Sequence 68119, A
	893	27.8	4.4	601	4	US-09-949-016-91606	Sequence 91606, A
	894	27.8	4.4	601	4	US-09-949-016-91876	Sequence 91876, A
c	895	27.8	4.4	601	4	US-09-949-016-145313	Sequence 145313,
c	896	27.8	4.4	601	4	US-09-949-016-169598	Sequence 169598,
c	897	27.8	4.4	601	4	US-09-949-016-169599	Sequence 169599,
c	898	27.8	4.4	601	4	US-09-949-016-170341	Sequence 170341,
c	899	27.8	4.4	601	4	US-09-949-016-170342	Sequence 170342,
c	900	27.8	4.4	601	4	US-09-949-016-182151	Sequence 182151,
	901	27.8	4.4	601	4	US-09-949-016-192530	Sequence 192530,
	902	27.8	4.4	601	4	US-09-949-016-192531	Sequence 192531,
	903	27.8	4.4	601	4	US-09-949-016-192532	Sequence 192532,
	904	27.8	4.4	601	4	US-09-949-016-192533	Sequence 192533,
	905	27.8	4.4	601	4	US-09-949-016-194817	Sequence 194817,
	906	27.8	4.4	648	4	US-09-543-681A-152	Sequence 152, App
	907	27.8	4.4	813	4	US-09-479-040-22	Sequence 22, Appl
c	908	27.8	4.4	814	4	US-09-328-475C-257	Sequence 257, App
	909	27.8	4.4	873	4	US-09-543-681A-2289	Sequence 2289, Ap
	910	27.8	4.4	1345	2	US-08-702-153-3	Sequence 3, Appli
	911	27.8	4.4	1551	4	US-09-248-796A-5414	Sequence 5414, Ap
	912	27.8	4.4	3704	2	US-08-702-153-1	Sequence 1, Appli
c	913	27.8	4.4	5606	4	US-09-949-016-13419	Sequence 13419, A
	914	27.8	4.4	5687	3	US-09-221-017B-368	Sequence 368, App
c	915	27.8	4.4	7218	1	US-08-232-463-14	Sequence 14, Appl
	916	27.8	4.4	7563	4	US-08-956-171E-33	Sequence 33, Appl
	917	27.8	4.4	7563	4	US-08-781-986A-33	Sequence 33, Appl
	918	27.8	4.4	7916	4	US-09-479-040-1	Sequence 1, Appli
c	919	27.8	4.4	8514	4	US-09-949-016-11938	Sequence 11938, A
c	920	27.8	4.4	10580	1	US-08-196-259-1	Sequence 1, Appli
	921	27.8	4.4	11003	4	US-09-949-016-13166	Sequence 13166, A
c	922	27.8	4.4	11616	1	US-08-196-259-2	Sequence 2, Appli
	923	27.8	4.4	12360	4	US-09-949-016-14488	Sequence 14488, A
c	924	27.8	4.4	18082	4	US-09-949-016-12586	Sequence 12586, A
c	925	27.8	4.4	18083	4	US-09-949-016-15711	Sequence 15711, A
c	926	27.8	4.4	24109	4	US-09-949-016-17461	Sequence 17461, A
c	927	27.8	4.4	26624	4	US-09-949-016-13269	Sequence 13269, A
c	928	27.8	4.4	36156	4	US-09-949-016-12128	Sequence 12128, A
c	929	27.8	4.4	36156	4	US-09-949-016-13261	Sequence 13261, A
c	930	27.8	4.4	37412	4	US-09-949-016-17566	Sequence 17566, A
	931	27.8	4.4	37940	4	US-09-949-016-15550	Sequence 15550, A
c	932	27.8	4.4	46347	4	US-09-949-016-13469	Sequence 13469, A
c	933	27.8	4.4	48794	4	US-09-949-016-15637	Sequence 15637, A
	934	27.8	4.4	50073	4	US-09-949-016-16026	Sequence 16026, A
	935	27.8	4.4	55851	4	US-09-949-016-13732	Sequence 13732, A
c	936	27.8	4.4	63658	4	US-09-949-016-13238	Sequence 13238, A
c	937	27.8	4.4	64190	4	US-09-949-016-14712	Sequence 14712, A
c	938	27.8	4.4	64190	4	US-09-949-016-14713	Sequence 14713, A
c	939	27.8	4.4	64489	4	US-09-949-016-11766	Sequence 11766, A
c	940	27.8	4.4	74790	4	US-09-949-016-15321	Sequence 15321, A
c	941	27.8	4.4	75674	4	US-09-949-016-17597	Sequence 17597, A
c	942	27.8	4.4	76401	4	US-09-949-016-17153	Sequence 17153, A
c	943	27.8	4.4	76810	4	US-09-949-016-12528	Sequence 12528, A
c	944	27.8	4.4	85122	4	US-09-949-016-14693	Sequence 14693, A
	945	27.8	4.4	87567	4	US-09-949-016-13335	Sequence 13335, A
	946	27.8	4.4	91665	4	US-09-949-016-12234	Sequence 12234, A
	947	27.8	4.4	94019	4	US-09-949-016-13203	Sequence 13203, A
	948	27.8	4.4	94142	4	US-09-949-016-16553	Sequence 16553, A
c	949	27.8	4.4	106315	4	US-09-949-016-16613	Sequence 16613, A
c	950	27.8	4.4	112112	4	US-09-949-016-15639	Sequence 15639, A
c	951	27.8	4.4	119214	4	US-09-949-016-12507	Sequence 12507, A
c	952	27.8	4.4	123513	4	US-09-949-016-15794	Sequence 15794, A
	953	27.8	4.4	133278	4	US-09-949-016-12524	Sequence 12524, A
c	954	27.8	4.4	133559	4	US-09-949-016-15845	Sequence 15845, A
	955	27.8	4.4	143155	4	US-09-949-016-11925	Sequence 11925, A
	956	27.8	4.4	143164	4	US-09-949-016-14368	Sequence 14368, A
	957	27.8	4.4	143173	4	US-09-949-016-14513	Sequence 14513, A
	958	27.8	4.4	144596	4	US-09-949-016-11749	Sequence 11749, A
	959	27.8	4.4	144596	4	US-09-949-016-13035	Sequence 13035, A
c	960	27.8	4.4	160759	4	US-09-949-016-16514	Sequence 16514, A
	961	27.8	4.4	187136	4	US-09-949-016-17231	Sequence 17231, A
c	962	27.8	4.4	191433	4	US-09-949-016-16144	Sequence 16144, A
c	963	27.8	4.4	197336	4	US-09-949-016-12881	Sequence 12881, A
c	964	27.8	4.4	197337	4	US-09-949-016-14376	Sequence 14376, A
	965	27.8	4.4	222452	4	US-09-949-016-12968	Sequence 12968, A
c	966	27.8	4.4	234288	4	US-09-949-016-17272	Sequence 17272, A
c	967	27.8	4.4	254366	4	US-09-822-871-3	Sequence 3, Appli
c	968	27.8	4.4	254964	4	US-09-949-016-12583	Sequence 12583, A
c	969	27.8	4.4	254964	4	US-09-949-016-17392	Sequence 17392, A
c	970	27.8	4.4	260247	4	US-09-949-016-13358	Sequence 13358, A
c	971	27.8	4.4	260286	4	US-09-949-016-17037	Sequence 17037, A
c	972	27.8	4.4	260293	4	US-09-949-016-12106	Sequence 12106, A
c	973	27.8	4.4	264665	4	US-09-949-016-13747	Sequence 13747, A
c	974	27.8	4.4	312470	4	US-09-949-016-14043	Sequence 14043, A
c	975	27.8	4.4	336024	4	US-09-949-016-12373	Sequence 12373, A
	976	27.8	4.4	360470	4	US-09-949-016-13173	Sequence 13173, A

c 977	27.8	4.4	374159	4	US-09-949-016-15868	Sequence 15868, A
c 978	27.8	4.4	580073	4	US-08-545-528D-1	Sequence 1, Appli
c 979	27.8	4.4	636591	4	US-09-949-016-11808	Sequence 11808, A
c 980	27.8	4.4	636591	4	US-09-949-016-13388	Sequence 13388, A
981	27.8	4.4	670689	4	US-09-949-016-12505	Sequence 12505, A
c 982	27.8	4.4	670689	4	US-09-949-016-12505	Sequence 12505, A
983	27.8	4.4	670690	4	US-09-949-016-14207	Sequence 14207, A
c 984	27.8	4.4	670690	4	US-09-949-016-14207	Sequence 14207, A
c 985	27.8	4.4	1830121	4	US-09-557-884-1	Sequence 1, Appli
c 986	27.8	4.4	1830121	4	US-09-643-990A-1	Sequence 1, Appli
987	27.6	4.3	238	4	US-09-513-999C-20594	Sequence 20594, A
988	27.6	4.3	513	4	US-09-710-279-1163	Sequence 1163, Ap
989	27.6	4.3	561	3	US-09-134-001C-1258	Sequence 1258, Ap
c 990	27.6	4.3	579	4	US-09-319-588C-7	Sequence 7, Appli
991	27.6	4.3	601	4	US-09-949-016-44035	Sequence 44035, A
992	27.6	4.3	601	4	US-09-949-016-44036	Sequence 44036, A
993	27.6	4.3	601	4	US-09-949-016-131034	Sequence 131034,
c 994	27.6	4.3	601	4	US-09-949-016-135883	Sequence 135883,
c 995	27.6	4.3	601	4	US-09-949-016-135884	Sequence 135884,
c 996	27.6	4.3	601	4	US-09-949-016-136000	Sequence 136000,
c 997	27.6	4.3	601	4	US-09-949-016-136001	Sequence 136001,
c 998	27.6	4.3	601	4	US-09-949-016-136117	Sequence 136117,
c 999	27.6	4.3	601	4	US-09-949-016-136118	Sequence 136118,
c1000	27.6	4.3	601	4	US-09-949-016-148711	Sequence 148711,
c1001	27.6	4.3	601	4	US-09-949-016-149346	Sequence 149346,
1002	27.6	4.3	601	4	US-09-949-016-162447	Sequence 162447,
c1003	27.6	4.3	601	4	US-09-949-016-168313	Sequence 168313,
1004	27.6	4.3	601	4	US-09-949-016-186274	Sequence 186274,
c1005	27.6	4.3	843	3	US-09-296-284-24	Sequence 24, Appl
c1006	27.6	4.3	921	3	US-09-296-284-3	Sequence 3, Appli
c1007	27.6	4.3	996	4	US-09-248-796A-4061	Sequence 4061, Ap
c1008	27.6	4.3	1001	3	US-09-641-638-188	Sequence 188, App
c1009	27.6	4.3	1001	4	US-10-170-097-188	Sequence 188, App
c1010	27.6	4.3	1041	4	US-09-614-221A-484	Sequence 484, App
c1011	27.6	4.3	1053	4	US-09-543-681A-408	Sequence 408, App
1012	27.6	4.3	1393	4	US-09-949-016-1658	Sequence 1658, Ap
c1013	27.6	4.3	1846	3	US-09-173-581-15	Sequence 15, Appl
c1014	27.6	4.3	1846	3	US-09-420-915-15	Sequence 15, Appl
1015	27.6	4.3	1992	4	US-09-573-080A-352	Sequence 352, App
1016	27.6	4.3	2574	4	US-09-248-796A-4952	Sequence 4952, Ap
c1017	27.6	4.3	2700	3	US-09-296-284-8	Sequence 8, Appli
1018	27.6	4.3	2751	1	US-08-153-848-23	Sequence 23, Appl
1019	27.6	4.3	2751	3	US-09-299-843A-23	Sequence 23, Appl
1020	27.6	4.3	2751	3	US-09-088-337B-23	Sequence 23, Appl
1021	27.6	4.3	2751	5	PCT-US93-11153-23	Sequence 23, Appl
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c1024	27.6	4.3	3228	4	US-09-710-279-3808	Sequence 3808, Ap
c1025	27.6	4.3	4746	2	US-08-819-288-2	Sequence 2, Appli
c1026	27.6	4.3	4746	3	US-09-400-348-2	Sequence 2, Appli
c1027	27.6	4.3	4747	1	US-08-261-822A-2	Sequence 2, Appli
c1028	27.6	4.3	4747	5	PCT-US95-07744A-2	Sequence 2, Appli
1029	27.6	4.3	5715	3	US-09-107-847-1	Sequence 1, Appli
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c1033	27.6	4.3	6172	3	US-09-400-348-1	Sequence 1, Appli
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1039	27.6	4.3	20599	4	US-09-949-016-14478	Sequence 14478, A
1040	27.6	4.3	25769	4	US-09-949-016-17154	Sequence 17154, A
1041	27.6	4.3	26075	4	US-09-949-016-12004	Sequence 12004, A
1042	27.6	4.3	26076	4	US-09-949-016-13041	Sequence 13041, A
c1043	27.6	4.3	28696	4	US-09-949-016-17054	Sequence 17054, A
c1044	27.6	4.3	28780	4	US-09-949-016-12335	Sequence 12335, A
1045	27.6	4.3	31199	4	US-09-949-016-16516	Sequence 16516, A
c1046	27.6	4.3	34279	4	US-09-596-002-26	Sequence 26, Appl
1047	27.6	4.3	35100	1	US-08-306-691B-19	Sequence 19, Appl
1048	27.6	4.3	35100	5	PCT-US93-06251-19	Sequence 19, Appl
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c1051	27.6	4.3	46492	4	US-09-949-016-12954	Sequence 12954, A
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c1054	27.6	4.3	60002	4	US-09-949-016-12464	Sequence 12464, A
c1055	27.6	4.3	60003	4	US-09-949-016-13823	Sequence 13823, A
1056	27.6	4.3	64137	4	US-09-949-016-14831	Sequence 14831, A
1057	27.6	4.3	64171	4	US-09-949-016-12502	Sequence 12502, A
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1059	27.6	4.3	87629	4	US-09-949-016-15263	Sequence 15263, A
1060	27.6	4.3	87629	4	US-09-949-016-15264	Sequence 15264, A
1061	27.6	4.3	87629	4	US-09-949-016-15265	Sequence 15265, A
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1065	27.6	4.3	108341	4	US-09-949-016-16621	Sequence 16621, A
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1067	27.6	4.3	129415	4	US-09-949-016-16997	Sequence 16997, A
1068	27.6	4.3	136058	4	US-09-949-016-12565	Sequence 12565, A
1069	27.6	4.3	136480	4	US-09-949-016-17064	Sequence 17064, A
c1070	27.6	4.3	136917	4	US-09-949-016-16369	Sequence 16369, A
1071	27.6	4.3	139562	4	US-09-949-016-13451	Sequence 13451, A
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c1073	27.6	4.3	151295	4	US-09-949-016-14569	Sequence 14569, A
c1074	27.6	4.3	151295	4	US-09-949-016-14570	Sequence 14570, A
c1075	27.6	4.3	151295	4	US-09-949-016-14571	Sequence 14571, A
c1076	27.6	4.3	151295	4	US-09-949-016-14572	Sequence 14572, A
c1077	27.6	4.3	162841	4	US-09-949-016-13733	Sequence 13733, A
c1078	27.6	4.3	181251	4	US-09-949-016-15970	Sequence 15970, A
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1080	27.6	4.3	193555	4	US-09-949-016-15554	Sequence 15554, A
1081	27.6	4.3	193555	4	US-09-949-016-15555	Sequence 15555, A
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1086	27.6	4.3	363033	4	US-09-949-016-15754	Sequence 15754, A
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c1088	27.6	4.3	393753	4	US-09-949-016-14574	Sequence 14574, A
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c1090	27.6	4.3	818128	4	US-09-949-016-14547	Sequence 14547, A
c1091	27.6	4.3	818128	4	US-09-949-016-14548	Sequence 14548, A
c1092	27.6	4.3	818128	4	US-09-949-016-14549	Sequence 14549, A
c1093	27.6	4.3	818128	4	US-09-949-016-14550	Sequence 14550, A
c1094	27.6	4.3	818128	4	US-09-949-016-14551	Sequence 14551, A
c1095	27.6	4.3	818128	4	US-09-949-016-14552	Sequence 14552, A
c1096	27.6	4.3	818128	4	US-09-949-016-14553	Sequence 14553, A
c1097	27.6	4.3	818128	4	US-09-949-016-14554	Sequence 14554, A
c1098	27.6	4.3	818128	4	US-09-949-016-14555	Sequence 14555, A
c1099	27.6	4.3	818128	4	US-09-949-016-14556	Sequence 14556, A
c1100	27.6	4.3	818128	4	US-09-949-016-14557	Sequence 14557, A
c1101	27.6	4.3	818128	4	US-09-949-016-14558	Sequence 14558, A
c1102	27.6	4.3	818128	4	US-09-949-016-14559	Sequence 14559, A
c1103	27.6	4.3	818128	4	US-09-949-016-14560	Sequence 14560, A
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c1105	27.6	4.3	818128	4	US-09-949-016-14562	Sequence 14562, A
c1106	27.6	4.3	818128	4	US-09-949-016-14564	Sequence 14564, A
c1107	27.6	4.3	818128	4	US-09-949-016-14565	Sequence 14565, A
c1108	27.6	4.3	818128	4	US-09-949-016-14566	Sequence 14566, A
c1109	27.6	4.3	818128	4	US-09-949-016-14567	Sequence 14567, A
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1111	27.4	4.3	258	5	PCT-US92-04833-1	Sequence 1, Appli
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1113	27.4	4.3	351	4	US-09-543-681A-3033	Sequence 3033, Ap
c1114	27.4	4.3	399	4	US-09-621-976-8976	Sequence 8976, Ap
1115	27.4	4.3	408	3	US-09-134-001C-487	Sequence 487, App
c1116	27.4	4.3	420	4	US-09-107-532A-1825	Sequence 1825, Ap
1117	27.4	4.3	601	4	US-09-949-016-29879	Sequence 29879, A
c1118	27.4	4.3	601	4	US-09-949-016-34426	Sequence 34426, A
c1119	27.4	4.3	601	4	US-09-949-016-34515	Sequence 34515, A
c1120	27.4	4.3	601	4	US-09-949-016-52350	Sequence 52350, A
c1121	27.4	4.3	601	4	US-09-949-016-55452	Sequence 55452, A
c1122	27.4	4.3	601	4	US-09-949-016-56175	Sequence 56175, A

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c1125	27.4	4.3	601	4	US-09-949-016-57954	Sequence 57954, A
c1126	27.4	4.3	601	4	US-09-949-016-58820	Sequence 58820, A
c1127	27.4	4.3	601	4	US-09-949-016-58821	Sequence 58821, A
c1128	27.4	4.3	601	4	US-09-949-016-58822	Sequence 58822, A
1129	27.4	4.3	601	4	US-09-949-016-73723	Sequence 73723, A
c1130	27.4	4.3	601	4	US-09-949-016-77221	Sequence 77221, A
1131	27.4	4.3	601	4	US-09-949-016-78049	Sequence 78049, A
c1132	27.4	4.3	601	4	US-09-949-016-91433	Sequence 91433, A
1133	27.4	4.3	601	4	US-09-949-016-120560	Sequence 120560,
1134	27.4	4.3	601	4	US-09-949-016-120561	Sequence 120561,
1135	27.4	4.3	601	4	US-09-949-016-120562	Sequence 120562,
1136	27.4	4.3	601	4	US-09-949-016-120563	Sequence 120563,
1137	27.4	4.3	601	4	US-09-949-016-120564	Sequence 120564,
1138	27.4	4.3	601	4	US-09-949-016-120565	Sequence 120565,
c1139	27.4	4.3	601	4	US-09-949-016-124645	Sequence 124645,
1140	27.4	4.3	601	4	US-09-949-016-131987	Sequence 131987,
1141	27.4	4.3	601	4	US-09-949-016-132056	Sequence 132056,
c1142	27.4	4.3	601	4	US-09-949-016-140257	Sequence 140257,
c1143	27.4	4.3	601	4	US-09-949-016-164142	Sequence 164142,
c1144	27.4	4.3	601	4	US-09-949-016-164143	Sequence 164143,
1145	27.4	4.3	601	4	US-09-949-016-166355	Sequence 166355,
c1146	27.4	4.3	601	4	US-09-949-016-181621	Sequence 181621,
c1147	27.4	4.3	609	4	US-09-902-540-3313	Sequence 3313, Ap
1148	27.4	4.3	750	4	US-09-134-000C-1814	Sequence 1814, Ap
c1149	27.4	4.3	969	4	US-09-543-681A-3696	Sequence 3696, Ap
c1150	27.4	4.3	1000	1	US-07-960-112B-1	Sequence 1, Appli
c1151	27.4	4.3	1000	1	US-07-960-112B-3	Sequence 3, Appli
c1152	27.4	4.3	1000	1	US-08-301-316B-1	Sequence 1, Appli
c1153	27.4	4.3	1000	1	US-08-301-316B-3	Sequence 3, Appli
c1154	27.4	4.3	1000	2	US-08-473-399B-1	Sequence 1, Appli
c1155	27.4	4.3	1000	2	US-08-473-399B-3	Sequence 3, Appli
c1156	27.4	4.3	1000	3	US-08-853-831-1	Sequence 1, Appli
c1157	27.4	4.3	1000	3	US-08-853-831-3	Sequence 3, Appli
c1158	27.4	4.3	1000	4	US-09-510-885-1	Sequence 1, Appli
c1159	27.4	4.3	1000	4	US-09-510-885-3	Sequence 3, Appli
c1160	27.4	4.3	1000	5	PCT-US93-09774-1	Sequence 1, Appli
c1161	27.4	4.3	1000	5	PCT-US93-09774-3	Sequence 3, Appli
1162	27.4	4.3	1030	4	US-09-949-016-4587	Sequence 4587, Ap
c1163	27.4	4.3	1212	3	US-09-503-391-7	Sequence 7, Appli
c1164	27.4	4.3	1263	4	US-09-134-000C-3231	Sequence 3231, Ap
1165	27.4	4.3	1458	4	US-09-248-796A-3478	Sequence 3478, Ap
c1166	27.4	4.3	1618	4	US-08-956-171E-603	Sequence 603, App
c1167	27.4	4.3	1618	4	US-08-781-986A-603	Sequence 603, App
1168	27.4	4.3	1750	4	US-09-673-300-7	Sequence 7, Appli
c1169	27.4	4.3	1763	4	US-09-620-312D-637	Sequence 637, App
c1170	27.4	4.3	2298	4	US-09-248-796A-5965	Sequence 5965, Ap
c1171	27.4	4.3	2328	4	US-09-107-532A-2985	Sequence 2985, Ap
1172	27.4	4.3	2389	4	US-09-800-729-51	Sequence 51, Appl
1173	27.4	4.3	2405	4	US-09-800-729-17	Sequence 17, Appl
1174	27.4	4.3	2464	4	US-09-800-729-214	Sequence 214, App
c1175	27.4	4.3	2787	4	US-09-614-221A-203	Sequence 203, App
c1176	27.4	4.3	2870	1	US-08-468-036-28	Sequence 28, Appl
c1177	27.4	4.3	2870	2	US-08-376-843-28	Sequence 28, Appl
1178	27.4	4.3	2887	4	US-09-949-016-2186	Sequence 2186, Ap
1179	27.4	4.3	3177	4	US-09-710-279-3717	Sequence 3717, Ap
1180	27.4	4.3	3320	4	US-09-710-279-3649	Sequence 3649, Ap
1181	27.4	4.3	3502	2	US-08-724-394A-16	Sequence 16, Appl
c1182	27.4	4.3	4342	3	US-09-338-907-107	Sequence 107, App
c1183	27.4	4.3	4342	3	US-09-218-207-107	Sequence 107, App
c1184	27.4	4.3	4582	3	US-09-338-907-118	Sequence 118, App
c1185	27.4	4.3	4582	3	US-09-218-207-118	Sequence 118, App
c1186	27.4	4.3	4686	3	US-09-338-907-117	Sequence 117, App
c1187	27.4	4.3	4686	3	US-09-218-207-117	Sequence 117, App
c1188	27.4	4.3	4875	3	US-09-338-907-114	Sequence 114, App
c1189	27.4	4.3	4875	3	US-09-218-207-114	Sequence 114, App
c1190	27.4	4.3	4958	3	US-09-338-907-116	Sequence 116, App
c1191	27.4	4.3	4958	3	US-09-218-207-116	Sequence 116, App
c1192	27.4	4.3	4986	3	US-09-338-907-121	Sequence 121, App
c1193	27.4	4.3	4986	3	US-09-218-207-121	Sequence 121, App
c1194	27.4	4.3	5020	3	US-09-338-907-120	Sequence 120, App
c1195	27.4	4.3	5020	3	US-09-218-207-120	Sequence 120, App
c1196	27.4	4.3	5044	3	US-09-338-907-115	Sequence 115, App
c1197	27.4	4.3	5044	3	US-09-218-207-115	Sequence 115, App
c1198	27.4	4.3	5057	3	US-09-338-907-123	Sequence 123, App
c1199	27.4	4.3	5057	3	US-09-218-207-123	Sequence 123, App
c1200	27.4	4.3	5100	3	US-09-338-907-122	Sequence 122, App
c1201	27.4	4.3	5100	3	US-09-218-207-122	Sequence 122, App
c1202	27.4	4.3	5148	3	US-09-338-907-112	Sequence 112, App
c1203	27.4	4.3	5148	3	US-09-218-207-112	Sequence 112, App
1204	27.4	4.3	5177	4	US-09-814-915A-79	Sequence 79, Appl
c1205	27.4	4.3	5227	2	US-08-996-306-3	Sequence 3, Appli
c1206	27.4	4.3	5234	3	US-09-338-907-113	Sequence 113, App
c1207	27.4	4.3	5234	3	US-09-218-207-113	Sequence 113, App
c1208	27.4	4.3	5245	3	US-09-338-907-3	Sequence 3, Appli
c1209	27.4	4.3	5245	3	US-09-218-207-3	Sequence 3, Appli
c1210	27.4	4.3	5250	3	US-09-338-907-69	Sequence 69, Appl
c1211	27.4	4.3	5250	3	US-09-218-207-69	Sequence 69, Appl
c1212	27.4	4.3	5290	3	US-09-338-907-119	Sequence 119, App
c1213	27.4	4.3	5290	3	US-09-218-207-119	Sequence 119, App
c1214	27.4	4.3	5326	3	US-09-338-907-124	Sequence 124, App
c1215	27.4	4.3	5326	3	US-09-218-207-124	Sequence 124, App
1216	27.4	4.3	6002	4	US-09-949-016-13696	Sequence 13696, A
c1217	27.4	4.3	7090	4	US-09-714-550-18	Sequence 18, Appl
1218	27.4	4.3	15351	4	US-09-902-540-1154	Sequence 1154, Ap
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c1220	27.4	4.3	22375	4	US-09-949-016-13087	Sequence 13087, A
1221	27.4	4.3	25194	4	US-09-949-016-13887	Sequence 13887, A
c1222	27.4	4.3	31739	4	US-09-949-016-16226	Sequence 16226, A
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c1224	27.4	4.3	35935	2	US-08-735-609-1	Sequence 1, Appli
c1225	27.4	4.3	35935	2	US-08-735-609-1	Sequence 1, Appli
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c1228	27.4	4.3	35935	3	US-09-244-752-1	Sequence 1, Appli
c1229	27.4	4.3	35935	3	US-09-245-497-1	Sequence 1, Appli
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c1232	27.4	4.3	35978	4	US-09-956-335-1	Sequence 1, Appli
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1238	27.4	4.3	48149	4	US-09-949-016-15258	Sequence 15258, A
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1241	27.4	4.3	52636	4	US-09-949-016-14839	Sequence 14839, A
1242	27.4	4.3	54531	4	US-09-949-016-16267	Sequence 16267, A
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c1246	27.4	4.3	56516	3	US-09-218-207-1	Sequence 1, Appli
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c1248	27.4	4.3	56520	3	US-09-218-207-179	Sequence 179, App
1249	27.4	4.3	57103	4	US-09-949-016-13445	Sequence 13445, A
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1252	27.4	4.3	62636	4	US-09-949-016-15465	Sequence 15465, A
1253	27.4	4.3	72742	4	US-09-949-016-16161	Sequence 16161, A
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1272	27.4	4.3	137394	4	US-09-949-016-13872	Sequence 13872, A
1273	27.4	4.3	137743	4	US-09-949-016-12178	Sequence 12178, A
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c1275	27.4	4.3	143164	4	US-09-949-016-14368	Sequence 14368, A
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1277	27.4	4.3	144362	4	US-09-949-016-16066	Sequence 16066, A
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1279	27.4	4.3	161607	4	US-09-949-016-12210	Sequence 12210, A
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1296	27.2	4.3	403	4	US-09-401-064-322	Sequence 322, App
1297	27.2	4.3	403	4	US-09-401-064-358	Sequence 358, App
1298	27.2	4.3	417	4	US-09-107-433-2403	Sequence 2403, Ap
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1318	27.2	4.3	601	4	US-09-949-016-121128	Sequence 121128,
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c1322	27.2	4.3	601	4	US-09-949-016-154416	Sequence 154416,
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1324	27.2	4.3	601	4	US-09-949-016-179318	Sequence 179318,
1325	27.2	4.3	601	4	US-09-949-016-185428	Sequence 185428,
1326	27.2	4.3	601	4	US-09-949-016-188519	Sequence 188519,
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1329	27.2	4.3	604	4	US-09-270-767-23287	Sequence 23287, A
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1333	27.2	4.3	735	4	US-09-107-532A-235	Sequence 235, App
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1335	27.2	4.3	965	4	US-09-270-767-10821	Sequence 10821, A
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1337	27.2	4.3	1022	4	US-09-270-767-26538	Sequence 26538, A
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c1339	27.2	4.3	1061	4	US-09-072-967-338	Sequence 338, App
c1340	27.2	4.3	1110	4	US-09-328-352-1631	Sequence 1631, Ap
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1343	27.2	4.3	1339	4	US-09-462-917A-105	Sequence 105, App
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1345	27.2	4.3	1512	4	US-09-107-532A-3242	Sequence 3242, Ap
1346	27.2	4.3	1551	4	US-09-620-312D-923	Sequence 923, App
1347	27.2	4.3	1555	4	US-09-949-016-4803	Sequence 4803, Ap
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1356	27.2	4.3	2572	4	US-09-919-172-73	Sequence 73, Appl
1357	27.2	4.3	2876	4	US-09-489-847-22	Sequence 22, Appl
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1361	27.2	4.3	3056	4	US-09-712-691-6	Sequence 6, Appli
1362	27.2	4.3	3056	4	US-09-707-468C-6	Sequence 6, Appli
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1365	27.2	4.3	3291	5	PCT-US94-01624-1	Sequence 1, Appli
1366	27.2	4.3	3365	3	US-09-221-017B-318	Sequence 318, App
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1374	27.2	4.3	4905	1	US-08-473-119-3	Sequence 3, Appli
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1376	27.2	4.3	4905	4	US-09-170-699-3	Sequence 3, Appli
1377	27.2	4.3	4975	3	US-09-630-706-3	Sequence 3, Appli
1378	27.2	4.3	4975	4	US-09-949-016-2151	Sequence 2151, Ap
1379	27.2	4.3	5687	4	US-09-919-039-268	Sequence 268, App
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c1381	27.2	4.3	8758	4	US-09-962-276-3	Sequence 3, Appli
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1389	27.2	4.3	27284	4	US-09-949-016-15417	Sequence 15417, A
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1394	27.2	4.3	49407	4	US-09-949-016-12532	Sequence 12532, A
1395	27.2	4.3	49408	4	US-09-949-016-17045	Sequence 17045, A
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1411	27.2	4.3	113876	4	US-09-949-016-14829	Sequence 14829, A
1412	27.2	4.3	114842	4	US-09-949-016-14993	Sequence 14993, A
1413	27.2	4.3	115508	4	US-09-949-016-11800	Sequence 11800, A
1414	27.2	4.3	115508	4	US-09-949-016-14826	Sequence 14826, A

1415	27.2	4.3	115508	4	US-09-949-016-14827	Sequence 14827, A
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1418	27.2	4.3	129778	4	US-09-949-016-17075	Sequence 17075, A
1419	27.2	4.3	131254	4	US-09-949-016-13734	Sequence 13734, A
1420	27.2	4.3	150409	4	US-09-949-016-12290	Sequence 12290, A
1421	27.2	4.3	150409	4	US-09-949-016-12938	Sequence 12938, A
1422	27.2	4.3	152524	4	US-09-949-016-12683	Sequence 12683, A
1423	27.2	4.3	152524	4	US-09-949-016-13194	Sequence 13194, A
1424	27.2	4.3	194537	4	US-09-949-016-12928	Sequence 12928, A
1425	27.2	4.3	201529	4	US-09-949-016-12740	Sequence 12740, A
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1431	27.2	4.3	422592	4	US-09-949-016-14182	Sequence 14182, A
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c1435	27	4.2	458	4	US-09-270-767-10008	Sequence 10008, A
1436	27	4.2	480	4	US-09-134-000C-1160	Sequence 1160, Ap
c1437	27	4.2	522	4	US-09-248-796A-1051	Sequence 1051, Ap
1438	27	4.2	600	4	US-09-248-796A-363	Sequence 363, App
1439	27	4.2	601	4	US-09-949-016-26414	Sequence 26414, A
1440	27	4.2	601	4	US-09-949-016-26415	Sequence 26415, A
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1442	27	4.2	601	4	US-09-949-016-32168	Sequence 32168, A
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1453	27	4.2	601	4	US-09-949-016-156896	Sequence 156896,
1454	27	4.2	601	4	US-09-949-016-166356	Sequence 166356,
1455	27	4.2	601	4	US-09-949-016-177361	Sequence 177361,
c1456	27	4.2	601	4	US-09-949-016-185831	Sequence 185831,
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c1460	27	4.2	603	4	US-09-248-796A-2583	Sequence 2583, Ap
c1461	27	4.2	642	3	US-08-611-587-3	Sequence 3, Appli
1462	27	4.2	678	4	US-09-134-000C-2164	Sequence 2164, Ap
1463	27	4.2	699	4	US-09-248-796A-9722	Sequence 9722, Ap
1464	27	4.2	747	4	US-09-248-796A-1465	Sequence 1465, Ap
c1465	27	4.2	789	4	US-09-813-453B-31	Sequence 31, Appl
c1466	27	4.2	825	4	US-09-248-796A-7819	Sequence 7819, Ap
1467	27	4.2	828	4	US-09-134-000C-308	Sequence 308, App
c1468	27	4.2	877	3	US-09-221-017B-891	Sequence 891, App
c1469	27	4.2	899	4	US-09-270-767-25368	Sequence 25368, A
1470	27	4.2	993	4	US-09-134-000C-86	Sequence 86, Appl
c1471	27	4.2	1040	1	US-08-276-452A-91	Sequence 91, Appl
c1472	27	4.2	1040	2	US-08-798-744-91	Sequence 91, Appl
1473	27	4.2	1053	4	US-09-270-767-31188	Sequence 31188, A
1474	27	4.2	1077	3	US-08-839-711-6	Sequence 6, Appli
c1475	27	4.2	1182	4	US-09-270-767-10039	Sequence 10039, A
c1476	27	4.2	1470	4	US-09-328-352-1204	Sequence 1204, Ap
c1477	27	4.2	1490	3	US-08-611-587-2	Sequence 2, Appli
c1478	27	4.2	1497	4	US-09-949-016-3729	Sequence 3729, Ap
c1479	27	4.2	1501	3	US-08-611-587-12	Sequence 12, Appl
1480	27	4.2	1575	3	US-09-230-388-2	Sequence 2, Appli
1481	27	4.2	1575	4	US-09-912-176-2	Sequence 2, Appli
c1482	27	4.2	1756	4	US-09-949-016-2130	Sequence 2130, Ap
1483	27	4.2	1810	4	US-09-270-767-14920	Sequence 14920, A
c1484	27	4.2	1878	4	US-09-248-796A-6108	Sequence 6108, Ap
c1485	27	4.2	2117	4	US-08-361-304A-1	Sequence 1, Appli
c1486	27	4.2	2117	4	US-09-949-016-436	Sequence 436, App
1487	27	4.2	2172	3	US-09-484-970B-126	Sequence 126, App
1488	27	4.2	2634	4	US-09-328-352-4036	Sequence 4036, Ap
1489	27	4.2	2943	3	US-09-221-017B-153	Sequence 153, App
1490	27	4.2	3072	4	US-09-762-724-13	Sequence 13, Appl
1491	27	4.2	3279	3	US-08-446-137B-1	Sequence 1, Appli
1492	27	4.2	3543	4	US-09-710-279-3493	Sequence 3493, Ap
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1495	27	4.2	3621	4	US-09-636-077A-21	Sequence 21, Appl
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1497	27	4.2	3621	4	US-09-986-552-21	Sequence 21, Appl
1498	27	4.2	3621	4	US-09-636-596C-21	Sequence 21, Appl
1499	27	4.2	3621	4	US-10-306-686-21	Sequence 21, Appl
1500	27	4.2	3783	4	US-09-635-872A-20	Sequence 20, Appl

ALIGNMENTS

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RESULT 1
US-08-905-223-27
; Sequence 27, Application US/08905223
; Patent No. 6222029
;  GENERAL INFORMATION:
;    APPLICANT:  Edwards, Jean-Baptiste D.
;    APPLICANT:  Duelert, Aymeric
;    APPLICANT:  Lacroix, Bruno
;    TITLE OF INVENTION:  5' ESTs FOR SECRETED PROTEINS
;    NUMBER OF SEQUENCES:  503
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson & Bear
;      STREET:  501 West Broadway
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92101-3505
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Win95
;      SOFTWARE:  Word
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/905,223
;      FILING DATE:
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Israelsen, Ned A.
;      REGISTRATION NUMBER:  29,655
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 235-8550
;      TELEFAX:  (619) 235-0176
;  INFORMATION FOR SEQ ID NO:  27:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  848 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  DOUBLE
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  CDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo Sapiens
;      DEVELOPMENTAL STAGE:  Fetal
;      TISSUE TYPE:  kidney
;    FEATURE:
;      NAME/KEY:  sig_peptide
;      LOCATION:  32..73
;      IDENTIFICATION METHOD:  Von Heijne matrix
;      OTHER INFORMATION:  score 10.7
;      OTHER INFORMATION:  seq LWLLPFLVTAIHA/EL
US-08-905-223-27

  Query Match             98.0%;  Score 626;  DB 3;  Length 848;
  Best Local Similarity   99.2%;  Pred. No. 9e-188;
  Matches  635;  Conservative    4;  Mismatches    0;  Indels    1;  Gaps    1;
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Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
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Db         32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
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Db         92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
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Db        152 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
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Db        212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 271

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
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Db        272 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 331

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
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Db        332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
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Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
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Db        452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
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Db        572 GACGCTGAARATAAKTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 631

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGA 639
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Db        632 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGA 671
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RESULT 2
US-09-247-155-27
; Sequence 27, Application US/09247155A
; Patent No. 6312922
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, Jean-Baptiste
;  APPLICANT: Duclert, Aymeric
;  APPLICANT: Bougueleret, Lydie
;  TITLE OF INVENTION: Complementary DNAs
;  FILE REFERENCE: GENSET.021A
;  CURRENT APPLICATION NUMBER: US/09/247,155A
;  CURRENT FILING DATE: 1999-02-09
;  EARLIER APPLICATION NUMBER: 60/074,121
;  EARLIER FILING DATE: 1998-02-09
;  EARLIER APPLICATION NUMBER: 60/081,563
;  EARLIER FILING DATE: 1998-04-13
;  EARLIER APPLICATION NUMBER: 60/096,116
;  EARLIER FILING DATE: 1998-08-10
;  EARLIER APPLICATION NUMBER: 60/099,273
;  EARLIER FILING DATE: 1998-10-04
;  NUMBER OF SEQ ID NOS: 182
;  SOFTWARE: Patent.pm
; SEQ ID NO 27
;   LENGTH: 848
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: sig_peptide
;   LOCATION: 32..73
;   OTHER INFORMATION: Von Heijne matrix
US-09-247-155-27

  Query Match             98.0%;  Score 626;  DB 3;  Length 848;
  Best Local Similarity   99.2%;  Pred. No. 9e-188;
  Matches  635;  Conservative    4;  Mismatches    0;  Indels    1;  Gaps    1;
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Db         32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
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Db        152 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
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Db        212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 271

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
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Db        272 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 331

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
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Db        332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
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Db        392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 451

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
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Db        452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
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Db        572 GACGCTGAARATAAKTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 631

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Db        632 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGA 671
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RESULT 3
US-09-663-600A-27
; Sequence 27, Application US/09663600A
; Patent No. 6573068
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, Jean-Baptiste
;  APPLICANT:  Duclert, Aymeric
;  APPLICANT:  Bougueleret, Lydie
;  TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
;  FILE REFERENCE: 31.US3.CIP
;  CURRENT APPLICATION NUMBER: US/09/663,600A
;  CURRENT FILING DATE:  2000-09-15
;  PRIOR APPLICATION NUMBER: 09/191,997
;  PRIOR FILING DATE: 1998-11-13
;  PRIOR APPLICATION NUMBER: 60/066,677
;  PRIOR FILING DATE: 1997-11-13
;  PRIOR APPLICATION NUMBER: 60/069,957
;  PRIOR FILING DATE: 1997-12-17
;  PRIOR APPLICATION NUMBER: 60/074,121
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;  PRIOR FILING DATE: 1998-02-09
;  PRIOR APPLICATION NUMBER: 60/081,563
;  PRIOR FILING DATE: 1998-04-13
;  PRIOR APPLICATION NUMBER: 60/096,116
;  PRIOR FILING DATE: 1998-08-10
;  PRIOR APPLICATION NUMBER: 60/099,273
;  PRIOR FILING DATE: 1998-09-04
;  NUMBER OF SEQ ID NOS: 229
;  SOFTWARE: Patent.pm
; SEQ ID NO 27
;   LENGTH: 848
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: sig_peptide
;   LOCATION: 32..73
;   OTHER INFORMATION: Von Heijne matrix
US-09-663-600A-27

  Query Match             98.0%;  Score 626;  DB 4;  Length 848;
  Best Local Similarity   99.2%;  Pred. No. 9e-188;
  Matches  635;  Conservative    4;  Mismatches    0;  Indels    1;  Gaps    1;

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Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
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Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
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Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
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Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
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Db        392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 451

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
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Db        452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

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Db        632 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGA 671


RESULT 4
US-09-621-976-5
; Sequence 5, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Jobert, S.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;  FILE REFERENCE: GENSET.054PR2
;  CURRENT APPLICATION NUMBER: US/09/621,976
;  CURRENT FILING DATE:  2000-07-21
;  NUMBER OF SEQ ID NOS: 19335
;  SOFTWARE: Patent.pm
; SEQ ID NO 5
;   LENGTH: 848
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 32..697
;   NAME/KEY: sig_peptide
;   LOCATION: 32..73
;   OTHER INFORMATION: Von Heijne matrix
US-09-621-976-5

  Query Match             98.0%;  Score 626;  DB 4;  Length 848;
  Best Local Similarity   99.2%;  Pred. No. 9e-188;
  Matches  635;  Conservative    4;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
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Db         32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91

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Db        452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
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Db        632 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGA 671


RESULT 5
US-09-513-999C-5
; Sequence 5, Application US/09513999C
```

```
; Patent No. 6783961
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Duclert, A.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
;  FILE REFERENCE: 59.US2.REG
;  CURRENT APPLICATION NUMBER: US/09/513,999C
;  CURRENT FILING DATE:  2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/122,487
;  PRIOR FILING DATE: 1999-02-26
;  NUMBER OF SEQ ID NOS: 36681
;  SOFTWARE: Patent.pm
; SEQ ID NO 5
;    LENGTH: 848
;    TYPE: DNA
;    ORGANISM: Homo Sapiens
;    FEATURE:
;    NAME/KEY: CDS
;    LOCATION: 32..697
;    FEATURE:
;    NAME/KEY: sig_peptide
;    LOCATION: 32..73
;    OTHER INFORMATION: Von Heijne matrix
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: 540
;    OTHER INFORMATION: d=a or g or t
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: 543
;    OTHER INFORMATION: r=a or g
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: 581
;    OTHER INFORMATION: r=a or g
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: 586
;    OTHER INFORMATION: k=g or t
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: 725
;    OTHER INFORMATION: r=a or g
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: 788
;    OTHER INFORMATION: w=a or t
;    FEATURE:
;    NAME/KEY: UNSURE
;    LOCATION: 156
;    OTHER INFORMATION: Xaa=Ile or Lys or Arg
;    FEATURE:
;    NAME/KEY: UNSURE
;    LOCATION: 157
;    OTHER INFORMATION: Xaa=Lys or Arg
;    FEATURE:
;    NAME/KEY: UNSURE
;    LOCATION: 170
;    OTHER INFORMATION: Xaa=Asp or Asn
;    FEATURE:
;    NAME/KEY: UNSURE
;    LOCATION: 171
;    OTHER INFORMATION: Xaa=Lys or Asn
US-09-513-999C-5

  Query Match             98.0%;  Score 626;  DB 4;  Length 848;
  Best Local Similarity   99.2%;  Pred. No. 9e-188;
  Matches  635;  Conservative    4;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db         32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db         92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        152 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 271

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        272 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 331

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 451

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              ||||||||||||||||||||||||||||||:||:||||||||||||||||||||||||||

Db        512 CTGATTTTATCAGGGATCTGGCAACGTADAARAAAGAACAAAGAACCATCTGAAGTGGAT 571

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
              |||||||||:||||:||||||||||||||||||||||||||||||||||||||||||||

Db        572 GACGCTGAARATAAKTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 631

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGA 639
              |||||||||||||| ||||||||||||||||||||||||
Db        632 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGA 671


RESULT 6
US-09-471-276-5
; Sequence 5, Application US/09471276
; Patent No. 6822072
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT: Duclert A.
;  APPLICANT: Giordano, J.Y.
;  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6822072
;  FILE REFERENCE: GENSET.025CP1
;  CURRENT APPLICATION NUMBER: US/09/471,276
;  CURRENT FILING DATE: 1999-12-21
;  EARLIER APPLICATION NUMBER: 09/057,719
;  EARLIER FILING DATE: 1998-04-09
;  EARLIER APPLICATION NUMBER: 09/069,047
;  EARLIER FILING DATE: 1998-04-28
;  EARLIER APPLICATION NUMBER: PCT/IB99/00712
;  EARLIER FILING DATE: 1999-04-09
;  NUMBER OF SEQ ID NOS: 1622
;  SOFTWARE: Patent.pm
; SEQ ID NO 5
;    LENGTH: 848
;    TYPE: DNA
;    ORGANISM: Homo Sapiens
;    FEATURE:
;    NAME/KEY: CDS
;    LOCATION: 32..697
;    NAME/KEY: sig_peptide
;    LOCATION: 32..73
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;   OTHER INFORMATION: Von Heijne matrix
US-09-471-276-5

  Query Match             98.0%;  Score 626;  DB 4;  Length 848;
  Best Local Similarity   99.2%;  Pred. No. 9e-188;
  Matches  635;  Conservative    4;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 271

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 331

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 451

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              |||||||||||||||||||||||||||||:||:||||||||||||||||||||||||||
Db        512 CTGATTTTATCAGGGATCTGGCAACGTADAARAAAGAACAAAGAACCATCTGAAGTGGAT 571

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
              |||||||||:||||:||||||||||||||||||||||||||||||||||||||||||||
Db        572 GACGCTGAAARATAAKTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 631

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGA 639
              ||||||||||||| |||||||||||||||||||||||||
Db        632 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGA 671


RESULT 7
US-09-289-349-6
; Sequence 6, Application US/09289349
; Patent No. 6277574
; GENERAL INFORMATION:
;  APPLICANT: Walker, Michael, G.
;  APPLICANT: Volkmuth, Wayne
;  APPLICANT: Klinger, Tod, M.
;  APPLICANT: Azimzai, Yalda
;  APPLICANT: Yue, Henry
;  TITLE OF INVENTION: GENES ASSOCIATED WITH DISEASES OF THE KIDNEY
;  FILE REFERENCE: PB-0010 US
;  CURRENT APPLICATION NUMBER: US/09/289,349
;  CURRENT FILING DATE: 1999-04-09
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PERL Program
; SEQ ID NO 6
;   LENGTH: 862
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE: -
;   OTHER INFORMATION: 2580580CT1
US-09-289-349-6

  Query Match             25.5%;  Score 163;  DB 3;  Length 862;
  Best Local Similarity   99.4%;  Pred. No. 3.4e-41;
  Matches  174;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy        466 GTTGCAATTGCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAA 525
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTTGCAATTGCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAA 60

Qy        526 CCATCTGAAGTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGC 585
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCATCTGAAGTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGC 120

Qy        586 ATCCCCTCTGATCCCCTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGA 639
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        121 ATCCCCTCTGATCCCCTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGA 175


RESULT 8
US-08-989-299-3
; Sequence 3, Application US/08989299
; Patent No. 6194556
;  GENERAL INFORMATION:
;    APPLICANT:  Acton, Susan L.
;    APPLICANT:  Robinson, Keith E.
;    TITLE OF INVENTION:  ANGIOTENSIN CONVERTING ENZYME HOMOLOG
;    TITLE OF INVENTION:  AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FOLEY, HOAG & ELIOT LLP
;      STREET:  One Post Office Square
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109-2170
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/989,299
;      FILING DATE:  11-DEC-1997
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Arnold E., Beth
;      REGISTRATION NUMBER:  35,430
;      REFERENCE/DOCKET NUMBER:  MIA-025.01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-832-1000
;      TELEFAX:  617-832-7000
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2415 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-989-299-3

  Query Match             19.6%;  Score 125;  DB 3;  Length 2415;
  Best Local Similarity   57.3%;  Pred. No. 6.3e-29;
  Matches  293;  Conservative    0;  Mismatches  200;  Indels   18;  Gaps    3;

Qy         48 CTGTCAACCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGG 107
              |||    |||  |||||| |     | |||||||| | ||  | | | |||||||  ||
Db       1827 CTGGAGTCCATATGCAGACCAAAGCATCAAAGTGAGGATAAGCCTAAAATCAGCTCTTGG 1886

Qy        108 AGATAAAGCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTT 167
              |||||||||||||| ||| |   |||||||   ||||| ||| | |    || || |
Db       1887 AGATAAAGCATATGAATGGAACGACAATGAAATGTACCTGTTCCGATCATCTGTTGCATA 1946
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Qy        168 CTCCATGAG--AAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCC----------A 212
              | |||||  |  | ||  || ||  ||  | ||||  |||                |
Db       1947 TGCTATGAGGCAGTACTTTTTAAAAGTAAAAAATCAGATGATTCTTTTTGGGGAGGAGGA 2006

Qy        213 TGTCCTACTTTGCAATGTAACCCAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTC 272
              ||| | | |   ||| | |  |  ||  | || ||    ||  | || || |  |||
Db       2007 TGTGCGAGTGGCTAATTTGAAACCAAGAATCTCCTTTAATTTCTTTGTCACTGCACCTAA 2066

Qy        273 AAAAAA---TCACACCCTTCCTGCTGTTGAGGTGCAATCAGCCATAAGAATGAACAAGAA 329
              |||     | | | | |||||     ||| ||  ||   ||||| || |||  |  ||
Db       2067 AAATGTGTCTGATATCATTCCTAGAACTGAAGTTGAAAAGGCCATCAGGATGTCCCGGAG 2126

Qy        330 CCGGATCAACAATGCCTTCTTTCTAAATGACCAAACTCTGGAATTTTTAAAAATCCCTTC 389
              ||| |||||  |||| ||| ||| |||||| | |  || || ||| |     || |  |
Db       2127 CCGTATCAATGATGCTTTCCGTCTGAATGACAACAGCCTAGAGTTTCTGGGGATACAGCC 2186

Qy        390 CACACTTGCACCACCCATGGACCCATCTGTGCCCATCTGGATTATTATATTTGGTGTGAT 449
              |||||||  ||| || |   | ||  |||| |||| ||| | ||| | |||||  ||  |
Db       2187 AACACTTGGACCTCCTAACCAGCCCCCTGTTTCCATATGGCTGATTGTTTTTGGAGTTGT 2246

Qy        450 ATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTATCAGGGATCTGGCAACGTAG 509
              |  |  | ||  | |||| ||||    | ||||| ||  | ||||||  |  | || |
Db       2247 GATGGGAGTGATAGTGGTTGGCATTGTCATCCTGATCTTCACTGGGATCAGAGATCGGAA 2306

Qy        510 AAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              |  || || |||| |  |  || ||   ||
Db       2307 GAAGAAAAATAAAGCAAGAAGTGGAGAAAAT 2337
```

RESULT 9
US-09-407-427-3
; Sequence 3, Application US/09407427
; Patent No. 6610497
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG AND THERAPEUTIC
; TITLE OF INVENTION: AND DIAGNOSTIC USES THEREFOR
; FILE REFERENCE: MNI-132CP2
; CURRENT APPLICATION NUMBER: US/09/407,427
; CURRENT FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 09/163,648
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 08/989,299
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2415
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-407-427-3

Query Match 19.6%; Score 125; DB 4; Length 2415;
Best Local Similarity 57.3%; Pred. No. 6.3e-29;
Matches 293; Conservative 0; Mismatches 200; Indels 18; Gaps 3;

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Qy         48 CTGTCAACCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGG 107
              |||    |||  ||||||  |      | ||||||||  | ||  | | | ||||||| ||
Db       1827 CTGGAGTCCATATGCAGACCAAAGCATCAAAGTGAGGATAAGCCTAAAATCAGCTCTTGG 1886

Qy        108 AGATAAAGCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTT 167
              ||||||||||||||  ||| |   |||||||   |||||  |||  | |    || || |
Db       1887 AGATAAAGCATATGAATGGAACGACAATGAAATGTACCTGTTCCGATCATCTGTTGCATA 1946

Qy        168 CTCCATGAG--AAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCC----------A 212
              | |||||  |  | ||  || ||  ||  | ||||  |||                |
Db       1947 TGCTATGAGGCAGTACTTTTTAAAAGTAAAAAATCAGATGATTCTTTTTGGGGAGGAGGA 2006

Qy        213 TGTCCTACTTTGCAATGTAACCCAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTC 272
              ||| | | |   ||| | |  |  ||  | || ||    ||  | || || |  |||
Db       2007 TGTGCGAGTGGCTAATTTGAAACCAAGAATCTCCTTTAATTTCTTTGTCACTGCACCTAA 2066

Qy        273 AAAAAA---TCACACCCTTCCTGCTGTTGAGGTGCAATCAGCCATAAGAATGAACAAGAA 329
              |||     | | | | |||||     ||| ||  ||   ||||| || |||  |  ||
Db       2067 AAATGTGTCTGATATCATTCCTAGAACTGAAGTTGAAAAGGCCATCAGGATGTCCCGGAG 2126

Qy        330 CCGGATCAACAATGCCTTCTTTCTAAATGACCAAACTCTGGAATTTTTAAAAATCCCTTC 389
              ||| |||||  |||| ||| ||| ||||||  | |  || || ||| |     || |  |
Db       2127 CCGTATCAATGATGCTTTCCGTCTGAATGACAACAGCCTAGAGTTTCTGGGGATACAGCC 2186

Qy        390 CACACTTGCACCACCCATGGACCCATCTGTGCCCATCTGGATTATTATATTTGGTGTGAT 449
              |||||||  ||| || |   | ||  |||| |||| ||| | ||| | |||||  ||  |
Db       2187 AACACTTGGACCTCCTAACCAGCCCCCTGTTTCCATATGGCTGATTGTTTTTGGAGTTGT 2246

Qy        450 ATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTATCAGGGATCTGGCAACGTAG 509
              |  |  | ||  | |||| ||||    | ||||| ||  | ||||||  |  | || |
Db       2247 GATGGGAGTGATAGTGGTTGGCATTGTCATCCTGATCTTCACTGGGATCAGAGATCGGAA 2306

Qy        510 AAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              |  || || |||| |  |  || ||   ||
Db       2307 GAAGAAAAATAAAGCAAGAAGTGGAGAAAAT 2337
```

RESULT 10
US-09-949-016-5413
; Sequence 5413, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5413
; LENGTH: 3388
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5413

Query Match 19.6%; Score 125; DB 4; Length 3388;
Best Local Similarity 57.3%; Pred. No. 7.5e-29;
Matches 293; Conservative 0; Mismatches 200; Indels 18; Gaps 3;

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Qy         48 CTGTCAACCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGG 107
              |||    |||  ||||||  |      | ||||||||  | ||  | | | ||||||| ||
Db       1930 CTGGAGTCCATATGCAGACCAAAGCATCAAAGTGAGGATAAGCCTAAAATCAGCTCTTGG 1989

Qy        108 AGATAAAGCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTT 167
              ||||||||||||||  ||| |   |||||||   |||||  |||  | |    || || |
Db       1990 AGATAAAGCATATGAATGGAACGACAATGAAATGTACCTGTTCCGATCATCTGTTGCATA 2049

Qy        168 CTCCATGAG--AAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCC----------A 212
              | |||||  |  | ||  || ||  ||  | ||||  |||                |
Db       2050 TGCTATGAGGCAGTACTTTTTAAAAGTAAAAAATCAGATGATTCTTTTTGGGGAGGAGGA 2109

Qy        213 TGTCCTACTTTGCAATGTAACCCAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTC 272
              ||| | | |   ||| | |  |  ||  | || ||    ||  | || || |  |||
Db       2110 TGTGCGAGTGGCTAATTTGAAACCAAGAATCTCCTTTAATTTCTTTGTCACTGCACCTAA 2169

Qy        273 AAAAAA---TCACACCCTTCCTGCTGTTGAGGTGCAATCAGCCATAAGAATGAACAAGAA 329
              |||     | | | | |||||     ||| ||  ||   ||||| || |||  |  ||
Db       2170 AAATGTGTCTGATATCATTCCTAGAACTGAAGTTGAAAAGGCCATCAGGATGTCCCGGAG 2229

Qy        330 CCGGATCAACAATGCCTTCTTTCTAAATGACCAAACTCTGGAATTTTTAAAAATCCCTTC 389
              ||| |||||  |||| ||| ||| ||||||  | |  || || ||| |     || |  |
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Db       2230 CCGTATCAATGATGCTTTCCGTCTGAATGACAACAGCCTAGAGTTTCTGGGGATACAGCC 2289

Qy        390 CACACTTGCACCACCCATGGACCCATCTGTGCCCATCTGGATTATTATATTTGGTGTGAT 449
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Db       2290 AACACTTGGACCTCCTAACCAGCCCCCTGTTTCCATATGGCTGATTGTTTTTGGAGTTGT 2349

Qy        450 ATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTATCAGGGATCTGGCAACGTAG 509
              |  |  | ||  | ||||  ||||   | ||||| ||  | |||||| |  | || |
Db       2350 GATGGGAGTGATAGTGGTTGGCATTGTCATCCTGATCTTCACTGGGATCAGAGATCGGAA 2409

Qy        510 AAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              |  || || |||| |  |  || ||  ||
Db       2410 GAAGAAAAATAAAGCAAGAAGTGGAGAAAAT 2440


RESULT 11
US-08-989-299-1
; Sequence 1, Application US/08989299
; Patent No. 6194556
;  GENERAL INFORMATION:
;    APPLICANT:  Acton, Susan L.
;    APPLICANT:  Robinson, Keith E.
;    TITLE OF INVENTION:  ANGIOTENSIN CONVERTING ENZYME HOMOLOG
;    TITLE OF INVENTION:  AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FOLEY, HOAG & ELIOT LLP
;      STREET:  One Post Office Square
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109-2170
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/989,299
;      FILING DATE:  11-DEC-1997
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Arnold E., Beth
;      REGISTRATION NUMBER:  35,430
;      REFERENCE/DOCKET NUMBER:  MIA-025.01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-832-1000
;      TELEFAX:  617-832-7000
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3396 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  82..2496
US-08-989-299-1

  Query Match             19.6%;  Score 125;  DB 3;  Length 3396;
  Best Local Similarity   57.3%;  Pred. No. 7.5e-29;
  Matches  293;  Conservative    0;  Mismatches  200;  Indels   18;  Gaps    3;

Qy          48 CTGTCAACCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGG 107
               |||     |||  |||||| |       | |||||||| | ||  | | | ||||||| ||
Db        1908 CTGGAGTCCATATGCAGACCAAAGCATCAAAGTGAGGATAAGCCTAAAATCAGCTCTTGG 1967

Qy         108 AGATAAAGCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTT 167
               ||||||||||||||  ||| |   |||||||   ||||| |||  | |    || || |
Db        1968 AGATAAAGCATATGAATGGAACGACAATGAAATGTACCTGTTCCGATCATCTGTTGCATA 2027

Qy         168 CTCCATGAG--AAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCC------------A 212
               |  |||||  |  | ||   || ||  ||  | ||||   |||              |
Db        2028 TGCTATGAGGCAGTACTTTTTAAAAGTAAAAAATCAGATGATTCTTTTTGGGGAGGAGGA 2087

Qy         213 TGTCCTACTTTGCAATGTAACCCAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTC 272
               ||| | | |    ||| | |  |  ||  | || ||     ||  | || || |  |||
Db        2088 TGTGCGAGTGGCTAATTTGAAACCAAGAATCTCCTTTAATTTCTTTGTCACTGCACCTAA 2147

Qy         273 AAAAAA---TCACACCCTTCCTGCTGTTGAGGTGCAATCAGCCATAAGAATGAACAAGAA 329
               |||      | | | | |||||     ||| ||  ||   ||||| || |||  |  ||
Db        2148 AAATGTGTCTGATATCATTCCTAGAACTGAAGTTGAAAAGGCCATCAGGATGTCCCGGAG 2207

Qy         330 CCGGATCAACAATGCCTTCTTTCTAAATGACCAAACTCTGGAATTTTTAAAAATCCCTTC 389
               ||| |||||  |||| |||  ||| |||||| | |  || || ||| |    || |  |
Db        2208 CCGTATCAATGATGCTTTCCGTCTGAATGACAACAGCCTAGAGTTTCTGGGGATACAGCC 2267

Qy         390 CACACTTGCACCACCCATGGACCCATCTGTGCCCATCTGGATTATTATATTTGGTGTGAT 449
               ||||||| ||| || |   | ||  ||||  |||| ||| | ||| | ||||| ||  |
Db        2268 AACACTTGGACCTCCTAACCAGCCCCCTGTTTCCATATGGCTGATTGTTTTTGGAGTTGT 2327

Qy         450 ATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTATCAGGGATCTGGCAACGTAG 509
               |  |  | ||  | ||||  ||||   | ||||| ||  | |||||| |  | || |
Db        2328 GATGGGAGTGATAGTGGTTGGCATTGTCATCCTGATCTTCACTGGGATCAGAGATCGGAA 2387

Qy         510 AAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
               |  || || |||| |  |  || ||  ||
Db        2388 GAAGAAAAATAAAGCAAGAAGTGGAGAAAAT 2418


RESULT 12
US-10-158-847-141
; Sequence 141, Application US/10158847
; Patent No. 6592865
; GENERAL INFORMATION:
;  APPLICANT: Tom Parry et al.
;  TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
;  FILE REFERENCE: PF557
;  CURRENT APPLICATION NUMBER: US/10/158,847
;  CURRENT FILING DATE:  2002-06-03
;  PRIOR APPLICATION NUMBER: 60/295,004
;  PRIOR FILING DATE: 2001-06-04
;  NUMBER OF SEQ ID NOS: 158
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 141
;   LENGTH: 3396
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-158-847-141

  Query Match             19.6%;  Score 125;  DB 4;  Length 3396;
  Best Local Similarity   57.3%;  Pred. No. 7.5e-29;
  Matches  293;  Conservative    0;  Mismatches  200;  Indels   18;  Gaps    3;

Qy          48 CTGTCAACCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGG 107
               |||     |||  |||||| |       | |||||||| | ||  | | | ||||||| ||
Db        1908 CTGGAGTCCATATGCAGACCAAAGCATCAAAGTGAGGATAAGCCTAAAATCAGCTCTTGG 1967

Qy         108 AGATAAAGCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTT 167
               ||||||||||||||  ||| |   |||||||   ||||| |||  | |    || || |
Db        1968 AGATAAAGCATATGAATGGAACGACAATGAAATGTACCTGTTCCGATCATCTGTTGCATA 2027

Qy         168 CTCCATGAG--AAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCC------------A 212
               |  |||||  |  | ||   || ||  ||  | ||||   |||              |
Db        2028 TGCTATGAGGCAGTACTTTTTAAAAGTAAAAAATCAGATGATTCTTTTTGGGGAGGAGGA 2087

Qy         213 TGTCCTACTTTGCAATGTAACCCAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTC 272
               ||| | | |    ||| | |  |  ||  | || ||     ||  | || || |  |||
Db        2088 TGTGCGAGTGGCTAATTTGAAACCAAGAATCTCCTTTAATTTCTTTGTCACTGCACCTAA 2147

Qy         273 AAAAAA---TCACACCCTTCCTGCTGTTGAGGTGCAATCAGCCATAAGAATGAACAAGAA 329
               |||      | | | | |||||     ||| ||  ||   ||||| || |||  |  ||
Db        2148 AAATGTGTCTGATATCATTCCTAGAACTGAAGTTGAAAAGGCCATCAGGATGTCCCGGAG 2207

Qy         330 CCGGATCAACAATGCCTTCTTTCTAAATGACCAAACTCTGGAATTTTTAAAAATCCCTTC 389
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Db       2208 CCGTATCAATGATGCTTTCCGTCTGAATGACAACAGCCTAGAGTTTCTGGGGATACAGCC 2267

Qy        390 CACACTTGCACCACCCATGGACCCATCTGTGCCCATCTGGATTATTATATTTGGTGTGAT 449

Db       2268 AACACTTGGACCTCCTAACCAGCCCCCTGTTTCCATATGGCTGATTGTTTTTGGAGTTGT 2327

Qy        450 ATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTATCAGGGATCTGGCAACGTAG 509

Db       2328 GATGGGAGTGATAGTGGTTGGCATTGTCATCCTGATCTTCACTGGGATCAGAGATCGGAA 2387

Qy        510 AAGAAAGAACAAAGAACCATCTGAAGTGGAT 540

Db       2388 GAAGAAAAATAAAGCAAGAAGTGGAGAAAAT 2418


RESULT 13
US-09-407-427-1
; Sequence 1, Application US/09407427
; Patent No. 6610497
; GENERAL INFORMATION:
;  APPLICANT:  Acton, Susan L.
;  APPLICANT:  Robison, Keith E.
;  TITLE OF INVENTION:  ANGIOTENSIN CONVERTING ENZYME HOMOLOG  AND THERAPEUTIC
;  TITLE OF INVENTION:  AND DIAGNOSTIC USES THEREFOR
;  FILE REFERENCE:  MNI-132CP2
;  CURRENT APPLICATION NUMBER: US/09/407,427
;  CURRENT FILING DATE:  1999-09-29
;  PRIOR APPLICATION NUMBER:  09/163,648
;  PRIOR FILING DATE:  1998-09-30
;  PRIOR APPLICATION NUMBER:  08/989,299
;  PRIOR FILING DATE:  1997-12-11
;  NUMBER OF SEQ ID NOS:  14
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 3396
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (82)..(2496)
US-09-407-427-1

  Query Match            19.6%;  Score 125;  DB 4;  Length 3396;
  Best Local Similarity  57.3%;  Pred. No. 7.5e-29;
  Matches  293;  Conservative    0;  Mismatches  200;  Indels   18;  Gaps    3;

Qy         48 CTGTCAACCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGG 107

Db       1908 CTGGAGTCCATATGCAGACCAAAGCATCAAAGTGAGGATAAGCCTAAAATCAGCTCTTGG 1967

Qy        108 AGATAAAGCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTT 167

Db       1968 AGATAAAGCATATGAATGGAACGACAATGAAATGTACCTGTTCCGATCATCTGTTGCATA 2027

Qy        168 CTCCATGAG--AAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCC----------A 212

Db       2028 TGCTATGAGGCAGTACTTTTTAAAAGTAAAAAATCAGATGATTCTTTTTGGGGAGGAGGA 2087

Qy        213 TGTCCTACTTTGCAATGTAACCCAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTC 272

Db       2088 TGTGCGAGTGGCTAATTTGAAACCAAGAATCTCCTTTAATTTCTTTGTCACTGCACCTAA 2147

Qy        273 AAAAAA---TCACACCCTTCCTGCTGTTGAGGTGCAATCAGCCATAAGAATGAACAAGAA 329

Db       2148 AAATGTGTCTGATATCATTCCTAGAACTGAAGTTGAAAAGGCCATCAGGATGTCCCGGAG 2207

Qy        330 CCGGATCAACAATGCCTTCTTTCTAAATGACCAAACTCTGGAATTTTTAAAAATCCCTTC 389

Db       2208 CCGTATCAATGATGCTTTCCGTCTGAATGACAACAGCCTAGAGTTTCTGGGGATACAGCC 2267

Qy        390 CACACTTGCACCACCCATGGACCCATCTGTGCCCATCTGGATTATTATATTTGGTGTGAT 449

Db       2268 AACACTTGGACCTCCTAACCAGCCCCCTGTTTCCATATGGCTGATTGTTTTTGGAGTTGT 2327

Qy        450 ATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTATCAGGGATCTGGCAACGTAG 509

Db       2328 GATGGGAGTGATAGTGGTTGGCATTGTCATCCTGATCTTCACTGGGATCAGAGATCGGAA 2387

Qy        510 AAGAAAGAACAAAGAACCATCTGAAGTGGAT 540

Db       2388 GAAGAAAAATAAAGCAAGAAGTGGAGAAAAT 2418


RESULT 14
US-10-158-847-137
; Sequence 137, Application US/10158847
; Patent No. 6592865
; GENERAL INFORMATION:
;  APPLICANT: Tom Parry et al.
;  TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
;  FILE REFERENCE: PF557
;  CURRENT APPLICATION NUMBER: US/10/158,847
;  CURRENT FILING DATE:  2002-06-03
;  PRIOR APPLICATION NUMBER: 60/295,004
;  PRIOR FILING DATE: 2001-06-04
;  NUMBER OF SEQ ID NOS: 158
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 137
;   LENGTH: 2920
;   TYPE: DNA
;   ORGANISM: homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1707)..(1707)
;   OTHER INFORMATION: n equals any amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (2702)..(2702)
;   OTHER INFORMATION: n equals any amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (2749)..(2749)
;   OTHER INFORMATION: n equals any amino acid
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;   NAME/KEY: misc_feature
;   LOCATION: (2757)..(2757)
;   OTHER INFORMATION: n equals any amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (2788)..(2789)
;   OTHER INFORMATION: n equals any amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (2819)..(2819)
;   OTHER INFORMATION: n equals any amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (2835)..(2835)
;   OTHER INFORMATION: n equals any amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (2856)..(2856)
;   OTHER INFORMATION: n equals any amino acid
US-10-158-847-137

  Query Match            18.3%;  Score 117;  DB 4;  Length 2920;
  Best Local Similarity  57.6%;  Pred. No. 2.4e-26;
  Matches  276;  Conservative    0;  Mismatches  185;  Indels   18;  Gaps    3;

Qy         48 CTGTCAACCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGG 107

Db       1856 CTGGAGTCCATATGCAGACCAAAGCATCAAAGTGAGGATAAGCCTAAAATCAGCTCTTGG 1915

Qy        108 AGATAAAGCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTT 167
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Db       1916 AGATAAAGCATATGAATGGAACGACAATGAAATGTACCTGTTCCGATCATCTGTTGCATA 1975

Qy        168 CTCCATGAG--AAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCC----------A 212

Db       1976 TGCTATGAGGCAGTACTTTTTAAAAGTAAAAAATCAGATGATTCTTTTTGGGGAGGAGGA 2035

Qy        213 TGTCCTACTTTGCAATGTAACCCAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTC 272

Db       2036 TGTGCGAGTGGCTAATTTGAAACCAAGAATCTCCTTTAATTTCTTTGTCACTGCACCTAA 2095

Qy        273 AAAAAA---TCACACCCTTCCTGCTGTTGAGGTGCAATCAGCCATAAGAATGAACAAGAA 329

Db       2096 AAATGTGTCTGATATCATTCCTAGAACTGAAGTTGAAAAGGCCATCAGGATGTCCCGGAG 2155

Qy        330 CCGGATCAACAATGCCTTCTTTCTAAATGACCAAACTCTGGAATTTTTAAAAATCCCTTC 389

Db       2156 CCGTATCAATGATGCTTTCCGTCTGAATGACGACAGCCTAGAGTTTCTGGGGATACAGCC 2215

Qy        390 CACACTTGCACCACCCATGGACCCATCTGTGCCCATCTGGATTATTATATTTGGTGTGAT 449

Db       2216 AACACTTGGACCTCCTAACCAGCCCCCTGTTTCCATATGGCTGATTGTTTTTGGAGTTGT 2275

Qy        450 ATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTATCAGGGATCTGGCAACGTA 508

Db       2276 GATGGGAGTGATAGTGGTTGGCATTGTCATCCTGATCTTCACTGGGATCAGAGATCGGA 2334


RESULT 15
US-09-949-016-17155
; Sequence 17155, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17155
;   LENGTH: 43986
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-17155

  Query Match             12.1%;  Score 77.4;  DB 4;  Length 43986;
  Best Local Similarity   61.8%;  Pred. No. 3.4e-13;
  Matches  123;  Conservative    0;  Mismatches   76;  Indels    0;  Gaps    0;

Qy        310 GCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAACTCTG 369

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Qy        370 GAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCATCTGG 429

Db      38855 GAGTTTCTGGGGATACAGCCAACACTTGGACCTCCTAACCAGCCCCCTGTTTCCATATGG 38914

Qy        430 ATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTA 489

Db      38915 CTGATTGTTTTTGGAGTTGTGATGGGAGTGATAGTGGTTGGCATTGTCATCCTGATCTTC 38974

Qy        490 TCAGGGATCTGGCAACGTA 508

Db      38975 ACTGGGATCAGAGATCGGA 38993
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 24, 2005, 19:17:16 ; Search time 2039.33 Seconds
(without alignments)
11927.005 Million cell updates/sec

Title: US-09-989-724-386_COPY_7_645
Perfect score: 639
Sequence: 1 atgttgtggctgctcttttt.....tattaatgatgccttcatga 639

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

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2: gb_est2:*
3: gb_htc:*
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6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	622.4	97.4	792	4	BG400845	BG400845 602464068
4	619.4	96.9	663	6	CB139945	CB139945 K-EST0193
5	615	96.2	629	7	CV028808	CV028808 7418 Full
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7	606.2	94.9	866	4	BG429618	BG429618 602501304
8	605	94.7	855	4	BG427247	BG427247 602494304
9	600.8	94.0	804	4	BG429705	BG429705 602493709
10	599	93.7	780	4	BG429174	BG429174 602498032
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13	586	91.7	808	4	BG399473	BG399473 602441206
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16	585.4	91.6	782	4	BG433974	BG433974 602497274
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19	577	90.3	607	6	CB125058	CB125058 K-EST0173
20	577	90.3	888	4	BG400513	BG400513 602464748
21	572.4	89.6	1081	4	BM811234	BM811234 AGENCOURT
22	563	88.1	678	4	BG429011	BG429011 602501924
23	549	85.9	602	4	BG432624	BG432624 602500789
24	547.2	85.6	801	4	BG428217	BG428217 602498872
25	546.2	85.5	884	4	BG399975	BG399975 602442028
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27	535.4	83.8	743	7	CN369196	CN369196 170005999
28	519.8	81.3	669	9	AY399637	AY399637 Pan trogl
29	508.4	79.6	1051	4	BG399950	BG399950 602442002
30	499	78.1	529	6	CB134037	CB134037 K-EST0185
31	499	78.1	529	6	CB139939	CB139939 K-EST0193
32	488.8	76.5	669	9	AY399638	AY399638 Mus muscu
33	488.8	76.5	1210	3	AK002337	AK002337 Mus muscu
34	487.2	76.2	720	4	BI102475	BI102475 602889668
35	487.2	76.2	755	6	CB955052	CB955052 AGENCOURT
36	487.2	76.2	855	6	CA469220	CA469220 AGENCOURT
37	486.8	76.2	544	4	BG399046	BG399046 602440713
38	485.6	76.0	793	4	BI103785	BI103785 602887878
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45	483.2	75.6	800	6	CA480818	CA480818 AGENCOURT
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49	477.8	74.8	874	7	CF550832	CF550832 AGENCOURT
50	476.8	74.6	765	1	AV652853	AV652853 AV652853
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52	475.2	74.4	724	6	CB599934	CB599934 AGENCOURT
53	475.2	74.4	842	4	BI101926	BI101926 602887622
54	473.6	74.1	915	2	BF789250	BF789250 602105150
55	473	74.0	858	6	CA467976	CA467976 AGENCOURT
56	472.2	73.9	844	6	CA492750	CA492750 AGENCOURT
57	468.8	73.4	822	4	BG402232	BG402232 602465795
58	468.6	73.3	728	4	BG426067	BG426067 602492749
59	468.4	73.3	782	4	BG969864	BG969864 602838808
60	467.4	73.1	864	4	BG401869	BG401869 602466568
61	467.2	73.1	874	6	CA491517	CA491517 AGENCOURT
62	466.8	73.1	981	2	BF784771	BF784771 602111117
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64	462.2	72.3	750	6	CB599563	CB599563 AGENCOURT
65	461.6	72.2	874	6	CA493040	CA493040 AGENCOURT
66	461	72.1	496	4	BG430790	BG430790 602498560
67	460.8	72.1	848	6	CA493268	CA493268 AGENCOURT
68	456.6	71.5	832	4	BG402158	BG402158 602465708
69	455.2	71.2	901	2	BF786687	BF786687 602111448
70	453	70.9	628	4	BG428990	BG428990 602501903
71	450.8	70.5	592	7	CK625448	CK625448 mj09d01.y
72	450.6	70.5	730	6	CD241570	CD241570 AGENCOURT
73	449	70.3	479	6	CB133561	CB133561 K-EST0184
74	446.6	69.9	868	6	CA481303	CA481303 AGENCOURT
75	446.2	69.8	742	4	BG969794	BG969794 602838708
76	442	69.2	824	6	CA492547	CA492547 AGENCOURT
77	440	68.9	812	7	CK474508	CK474508 AGENCOURT
78	439.6	68.8	744	4	BG566957	BG566957 602589463
79	437.4	68.5	738	6	CB953900	CB953900 AGENCOURT
80	435.2	68.1	808	2	BF780136	BF780136 602103808
81	433	67.8	659	6	BY741654	BY741654 BY741654
82	431	67.4	846	2	BF780978	BF780978 602106606
83	426.2	66.7	581	2	AW106515	AW106515 um29a07.y
84	421.2	65.9	792	4	BG209271	BG209271 RST28786
85	420.4	65.8	801	4	BG218203	BG218203 RST37930
86	420.4	65.8	807	4	BI099731	BI099731 602884596
87	418	65.4	446	6	CB133508	CB133508 K-EST0184
88	415.8	65.1	830	4	BG401091	BG401091 602465157
89	411.6	64.4	779	4	BG217185	BG217185 RST36886
90	411.4	64.4	534	4	BM022547	BM022547 id61g10.y
91	409.6	64.1	866	4	BG188580	BG188580 RST7605 A
92	408.2	63.9	554	1	AI788483	AI788483 uk57g07.y
93	406.6	63.6	788	4	BG211841	BG211841 RST31414
94	406	63.5	620	7	CK624653	CK624653 mi23f12.y
95	404.8	63.3	571	1	AI315913	AI315913 uj27f01.y
96	403.6	63.2	863	2	BF211834	BF211834 601813181
97	403	63.1	704	6	CB955090	CB955090 AGENCOURT

	98	402.8	63.0	547	1	AI789468	AI789468 uk99e12.y
	99	402	62.9	754	4	BG181765	BG181765 RST618 At
	100	400	62.6	892	6	CA468414	CA468414 AGENCOURT
	101	398	62.3	546	1	AI789448	AI789448 uk99d02.y
	102	396.4	62.0	539	2	AW012244	AW012244 ul88g07.y
	103	395.8	61.9	781	4	BG193796	BG193796 RST12932
	104	394.6	61.8	508	2	BF550608	BF550608 UI-R-C1-k
	105	392.8	61.5	586	4	BI345729	BI345729 374635 MA
	106	392.4	61.4	582	5	BP370260	BP370260 BP370260
	107	389.8	61.0	505	1	AI746613	AI746613 ul01d01.y
	108	387.6	60.7	511	7	CK624505	CK624505 mi22a01.y
	109	387.4	60.6	499	1	AJ681737	AJ681737 AJ681737
	110	386.4	60.5	828	4	BG195252	BG195252 RST14433
	111	386	60.4	574	2	AW045074	AW045074 um17d10.y
	112	385.4	60.3	519	1	AI747322	AI747322 ul05a06.y
	113	385	60.3	891	6	CA469320	CA469320 AGENCOURT
	114	384	60.1	525	1	AI882207	AI882207 ul31g03.y
	115	382.6	59.9	794	6	CB955392	CB955392 AGENCOURT
	116	382	59.8	549	7	CN369195	CN369195 170006000
	117	381.6	59.7	513	1	AA445683	AA445683 vf62h07.r
	118	381.6	59.7	928	7	CF582583	CF582583 AGENCOURT
	119	379.2	59.3	547	4	BI965141	BI965141 id34a06.y
	120	379.2	59.3	569	4	BI966990	BI966990 id27a07.y
	121	375	58.7	405	6	CB137251	CB137251 K-EST0189
	122	374.2	58.6	541	1	AA131483	AA131483 zo08e05.r
	123	373.8	58.5	485	2	AW106894	AW106894 um34h05.y
	124	367.4	57.5	734	4	BG183334	BG183334 RST2228 A
	125	367.4	57.5	881	6	CA468090	CA468090 AGENCOURT
	126	360.4	56.4	536	1	AI663506	AI663506 uk33f11.y
	127	358.8	56.2	533	1	AI663460	AI663460 uk33b03.y
	128	355	55.6	499	1	AI882240	AI882240 ul56b05.y
	129	352.8	55.2	452	1	AA289223	AA289223 vc93f01.r
	130	352.8	55.2	463	1	AA275670	AA275670 vc33c12.r
	131	347.8	54.4	489	2	AW259149	AW259149 um89b04.y
	132	347.8	54.4	804	4	BG431368	BG431368 602499982
	133	343	53.7	688	4	BG776793	BG776793 602663969
	134	342.8	53.6	566	2	AW475605	AW475605 un68h06.y
	135	340.4	53.3	482	1	AA273463	AA273463 vc37b10.r
	136	338.6	53.0	925	2	BF784692	BF784692 602111325
c	137	329	51.5	514	1	AI765078	AI765078 wh56h04.x
	138	319.6	50.0	504	1	AJ682987	AJ682987 AJ682987
	139	318.4	49.8	474	1	AI931440	AI931440 ul68d11.y
	140	317	49.6	405	1	AA109637	AA109637 mm01f02.r
	141	312.6	48.9	457	5	BY006328	BY006328 BY006328
	142	310.6	48.6	532	9	CG532959	CG532959 OST117705
	143	309.6	48.5	427	2	BB847292	BB847292 BB847292
	144	309	48.4	437	2	BB844940	BB844940 BB844940
	145	308.2	48.2	644	7	CK627074	CK627074 mj31a04.y
	146	303.6	47.5	410	1	AA066328	AA066328 mm14d08.r
	147	302	47.3	413	2	BB847970	BB847970 BB847970
	148	301.8	47.2	416	2	BB848103	BB848103 BB848103
	149	298.2	46.7	361	4	BG181204	BG181204 RST129 At
	150	297.8	46.6	716	4	BG400370	BG400370 602464583
	151	297	46.5	408	2	BB848163	BB848163 BB848163
	152	295.2	46.2	547	6	CB222923	CB222923 1JEJ17E10
	153	291.8	45.7	386	1	AA109535	AA109535 mm01g04.r
	154	288	45.1	826	4	BG194741	BG194741 RST13907
	155	287.8	45.0	416	2	BB846622	BB846622 BB846622
	156	282.6	44.2	479	5	BP769681	BP769681 BP769681
	157	281.6	44.1	392	2	AW260024	AW260024 um82c07.y
	158	281.4	44.0	437	2	BB844950	BB844950 BB844950
	159	281	44.0	412	5	BY006356	BY006356 BY006356
	160	280.8	43.9	427	2	BB848288	BB848288 BB848288
	161	279.4	43.7	506	9	CG668483	CG668483 OST464441
	162	278.2	43.5	429	5	BY006674	BY006674 BY006674
	163	276.8	43.3	838	6	CA494798	CA494798 AGENCOURT
	164	276	43.2	509	9	CG611484	CG611484 OST296516
	165	275.6	43.1	492	1	AA065156	AA065156 zm50a10.r
	166	272.6	42.7	426	2	BB847279	BB847279 BB847279
	167	270.4	42.3	375	2	BB843933	BB843933 BB843933
	168	269.6	42.2	421	2	BB848169	BB848169 BB848169
	169	268.8	42.1	428	2	AW259271	AW259271 um89h04.y
	170	268.4	42.0	640	4	BM439885	BM439885 pgr1n.pk0
	171	268	41.9	372	2	BB843467	BB843467 BB843467
	172	260.2	40.7	369	2	BB843868	BB843868 BB843868
	173	260	40.7	370	2	BB843459	BB843459 BB843459
	174	259.4	40.6	407	2	BB845600	BB845600 BB845600
	175	257	40.2	458	2	BB846267	BB846267 BB846267
	176	256.8	40.2	290	6	CB137087	CB137087 K-EST0189
	177	256.4	40.1	698	6	CD217554	CD217554 pgr1n.pk0
	178	253.8	39.7	430	5	BY006046	BY006046 BY006046
	179	249	39.0	375	2	BB843929	BB843929 BB843929
c	180	248.2	38.8	459	2	AW244613	AW244613 BR_END09H
	181	248	38.8	455	2	BB845438	BB845438 BB845438
	182	247.4	38.7	345	5	BY005657	BY005657 BY005657
	183	246.4	38.6	341	2	BB846895	BB846895 BB846895
	184	243.6	38.1	418	2	BB848084	BB848084 BB848084
	185	239.2	37.4	340	2	BB843625	BB843625 BB843625
	186	239	37.4	366	2	BB847608	BB847608 BB847608
	187	238.6	37.3	378	5	BY086677	BY086677 BY086677
	188	237.8	37.2	693	2	BF031348	BF031348 601559115
	189	237.4	37.2	304	1	AA068066	AA068066 ml77h10.r
	190	236	36.9	372	2	BB843455	BB843455 BB843455
	191	233.6	36.6	338	2	BB847006	BB847006 BB847006
	192	232.6	36.4	355	1	AA076448	AA076448 zm91d10.r
	193	231.2	36.2	1064	2	BF212565	BF212565 601813769
	194	229.2	35.9	322	4	BG193281	BG193281 RST12409
	195	228	35.7	366	2	BB843831	BB843831 BB843831
	196	227	35.5	430	5	BY006662	BY006662 BY006662
	197	226.8	35.5	1113	6	CA493126	CA493126 AGENCOURT
	198	225.2	35.2	358	5	BY005603	BY005603 BY005603
	199	223	34.9	303	1	AI119252	AI119252 ue24c07.y
	200	222.8	34.9	329	4	BG189097	BG189097 RST8135 A
	201	216.4	33.9	317	2	BB848179	BB848179 BB848179
	202	216	33.8	857	7	CN059437	CN059437 Salamande
	203	215.6	33.7	494	2	BF654521	BF654521 278735 MA
	204	215	33.6	407	5	BY006237	BY006237 BY006237
	205	214.2	33.5	375	2	BB843943	BB843943 BB843943
	206	213.8	33.5	326	2	AW259274	AW259274 um89h10.y
	207	213	33.3	527	6	CB954911	CB954911 AGENCOURT
	208	212.4	33.2	345	2	BB843573	BB843573 BB843573
	209	208.8	32.7	312	7	CN790738	CN790738 4125362 B
	210	207	32.4	335	2	BB847020	BB847020 BB847020
	211	206.8	32.4	355	4	BG184374	BG184374 RST3298 A
	212	203.8	31.9	621	4	BI394480	BI394480 pgp1n.pk0
	213	201	31.5	373	2	BB843794	BB843794 BB843794
	214	196	30.7	835	4	BG564304	BG564304 602590019
	215	193.8	30.3	237	1	AA239693	AA239693 mv23h03.r
c	216	187.4	29.3	360	4	BG182824	BG182824 RST1685 A
c	217	184.4	28.9	652	5	BP769682	BP769682 BP769682
	218	182.8	28.6	249	1	AI317693	AI317693 uj16e02.y
	219	182.2	28.5	728	7	CF521338	CF521338 AGENCOURT
	220	181.6	28.4	267	2	BB599302	BB599302 BB599302
	221	181.2	28.4	733	7	CF522498	CF522498 AGENCOURT
	222	180.6	28.3	730	7	CF522204	CF522204 AGENCOURT
	223	180.6	28.3	743	7	CF519814	CF519814 AGENCOURT
	224	180.6	28.3	749	7	CF521728	CF521728 AGENCOURT
	225	180.6	28.3	776	7	CF547505	CF547505 AGENCOURT
	226	180.6	28.3	854	6	CB559638	CB559638 AGENCOURT
	227	180.6	28.3	874	6	CB559915	CB559915 AGENCOURT
	228	180.6	28.3	876	5	BU904475	BU904475 AGENCOURT
	229	179.6	28.1	845	5	BU904947	BU904947 AGENCOURT
	230	176.6	27.6	927	5	BU904108	BU904108 AGENCOURT
	231	173.2	27.1	217	1	AA197784	AA197784 mv03g11.r
	232	169.4	26.5	310	5	BY005681	BY005681 BY005681
c	233	169	26.4	615	2	AW107491	AW107491 um17d10.x
	234	168.4	26.4	919	5	BU904746	BU904746 AGENCOURT
	235	164.6	25.8	260	2	BB598752	BB598752 BB598752
	236	161.2	25.2	762	2	BB432035	BB432035 BB432035
	237	157.8	24.7	209	2	AW916399	AW916399 EST347690
	238	156.8	24.5	307	2	BB843809	BB843809 BB843809
	239	156.8	24.5	374	5	BY042134	BY042134 BY042134
	240	150	23.5	335	7	CK961894	CK961894 4076310 B
	241	149.8	23.4	285	2	BB843715	BB843715 BB843715
	242	145.8	22.8	617	6	CA342735	CA342735 672680 NC
	243	145.8	22.8	765	5	BX887952	BX887952 BX887952

	244	145.8	22.8	767	5	BX868900	BX868900 BX868900
	245	144.8	22.7	769	5	BX913677	BX913677 BX913677
c	246	144.8	22.7	903	7	CF582582	CF582582 AGENCOURT
	247	144.2	22.6	750	5	BX879965	BX879965 BX879965
	248	143.8	22.5	182	1	AA104963	AA104963 mm65a05.r
	249	140.6	22.0	791	5	BX304379	BX304379 BX304379
	250	137.6	21.5	391	5	BY050206	BY050206 BY050206
	251	137	21.4	668	4	BG400436	BG400436 602464461
	252	128	20.0	852	7	CK237456	CK237456 AGENCOURT
	253	127.4	19.9	810	7	CK239284	CK239284 AGENCOURT
	254	127.4	19.9	909	6	CA975643	CA975643 AGENCOURT
	255	126.8	19.8	784	7	CF348736	CF348736 AGENCOURT
	256	126.8	19.8	787	7	CN512318	CN512318 AGENCOURT
	257	126.8	19.8	860	7	CK016244	CK016244 AGENCOURT
	258	126.2	19.7	1035	1	AL551235	AL551235 AL551235
	259	125.8	19.7	804	6	CD758550	CD758550 AGENCOURT
	260	125.8	19.7	818	6	CD759140	CD759140 AGENCOURT
	261	125.8	19.7	836	7	CK236662	CK236662 AGENCOURT
	262	125.2	19.6	350	1	AA065710	AA065710 mm44c03.r
	263	125	19.6	1690	3	CR599955	CR599955 full-leng
	264	125	19.6	3337	3	BC032938	BC032938 Homo sapi
	265	125	19.6	3339	3	BC048144	BC048144 Homo sapi
	266	124.6	19.5	762	5	BX304380	BX304380 BX304380
	267	124.4	19.5	302	9	CG668510	CG668510 OST464486
	268	124.2	19.4	763	5	BX926439	BX926439 BX926439
	269	124.2	19.4	767	7	CK239480	CK239480 AGENCOURT
	270	124.2	19.4	773	7	CK239430	CK239430 AGENCOURT
	271	124.2	19.4	888	6	CA787423	CA787423 AGENCOURT
	272	124.2	19.4	965	6	CA473387	CA473387 AGENCOURT
	273	122.8	19.2	747	6	CA491783	CA491783 AGENCOURT
	274	122.6	19.2	816	7	CK236057	CK236057 AGENCOURT
	275	122.6	19.2	836	7	CK238801	CK238801 AGENCOURT
	276	118	18.5	854	6	CA474850	CA474850 AGENCOURT
	277	117	18.3	862	6	CA471692	CA471692 AGENCOURT
	278	116.6	18.2	891	6	CA472074	CA472074 AGENCOURT
	279	115.4	18.1	829	6	CA496216	CA496216 AGENCOURT
	280	115.2	18.0	702	4	BG971735	BG971735 602838272
	281	115.2	18.0	703	5	BU376588	BU376588 603809540
	282	114.2	17.9	733	5	BX862922	BX862922 BX862922
	283	114.2	17.9	1013	7	CO581670	CO581670 ILLUMIGEN
	284	110	17.2	659	6	CA364229	CA364229 639103 NC
	285	109.8	17.2	1603	3	AK008530	AK008530 Mus muscu
	286	107.2	16.8	620	5	BU472823	BU472823 603761782
c	287	106.6	16.7	492	2	AW260204	AW260204 um74f04.x
	288	106.4	16.7	590	4	BI884757	BI884757 fo68g09.y
c	289	105.6	16.5	590	5	BP772872	BP772872 BP772872
	290	104.8	16.4	685	6	CA965680	CA965680 CcLX05a15
	291	101.4	15.9	447	5	BY153686	BY153686 BY153686
c	292	100.4	15.7	499	1	AI931939	AI931939 ul68b06.x
	293	99.8	15.6	381	5	BY153900	BY153900 BY153900
	294	99.4	15.6	265	2	BB561901	BB561901 BB561901
	295	99.2	15.5	773	6	CB559001	CB559001 AGENCOURT
	296	96.8	15.1	584	5	BP371391	BP371391 BP371391
	297	96.6	15.1	787	5	BX911789	BX911789 BX911789
	298	96	15.0	765	5	BX878953	BX878953 BX878953
	299	96	15.0	777	5	BX867294	BX867294 BX867294
	300	95.8	15.0	246	2	BB561792	BB561792 BB561792
	301	95.6	15.0	694	7	CK957623	CK957623 4097741 B
	302	94.8	14.8	480	6	CA965795	CA965795 CcLX05a19
c	303	94.6	14.8	487	1	AI746288	AI746288 ul05a06.x
	304	93.2	14.6	423	6	CD284299	CD284299 G39172.71
	305	92.4	14.5	773	6	CB308042	CB308042 AGENCOURT
	306	90.6	14.2	1154	4	BM460886	BM460886 AGENCOURT
	307	89.8	14.1	689	5	BX878867	BX878867 BX878867
	308	89	13.9	772	5	BX877877	BX877877 BX877877
	309	89	13.9	794	5	BX880013	BX880013 BX880013
	310	88.2	13.8	552	5	BX086254	BX086254 BX086254
	311	87.6	13.7	674	7	CK948392	CK948392 4073275 B
	312	87.6	13.7	695	7	CK950473	CK950473 4075812 B
	313	86.8	13.6	837	6	CA473716	CA473716 AGENCOURT
	314	86.4	13.5	732	5	BX867401	BX867401 BX867401
	315	86.4	13.5	863	7	CF663100	CF663100 CcLX07a30
c	316	86	13.5	654	1	AI314694	AI314694 uj27f01.x
c	317	84.4	13.2	676	5	BP770276	BP770276 BP770276
	318	82.8	13.0	778	4	BI831019	BI831019 603080858
	319	82.4	12.9	688	6	BY708410	BY708410 BY708410
	320	82.2	12.9	483	2	BF938662	BF938662 fm79g08.y
c	321	81.4	12.7	285	4	BG184375	BG184375 RST3299 A
	322	81.2	12.7	418	2	BB687602	BB687602 BB687602
	323	81.2	12.7	832	6	CB197355	CB197355 AGENCOURT
	324	80.4	12.6	322	2	BB146668	BB146668 BB146668
c	325	79.4	12.4	574	1	AI116021	AI116021 ue25h10.x
c	326	78.2	12.2	498	4	BM022245	BM022245 id61g10.x
	327	77	12.1	283	2	BB054531	BB054531 BB054531
c	328	77	12.1	1156	6	CD508270	CD508270 CDA89-H06
	329	76.6	12.0	307	4	BG185958	BG185958 RST4913 A
	330	76.6	12.0	679	5	BX319688	BX319688 BX319688
	331	76.4	12.0	637	7	CN984278	CN984278 53231_126
	332	75.8	11.9	184	4	BG196762	BG196762 RST15989
	333	75.6	11.8	450	1	AJ655099	AJ655099 AJ655099
c	334	75.4	11.8	392	2	BF334479	BF334479 MR1-CT035
	335	74.4	11.6	337	2	BB497528	BB497528 BB497528
	336	74.4	11.6	944	6	CB180137	CB180137 AGENCOURT
c	337	74.2	11.6	779	7	CK778629	CK778629 965794 MA
	338	72.8	11.4	680	5	BX319687	BX319687 BX319687
	339	72	11.3	241	2	BB010750	BB010750 BB010750
	340	71.6	11.2	290	2	BB009853	BB009853 BB009853
	341	71.6	11.2	296	2	BB005788	BB005788 BB005788
	342	71.6	11.2	306	2	BB497018	BB497018 BB497018
c	343	71.6	11.2	669	6	CA043283	CA043283 ssalphc00
c	344	71.4	11.2	699	6	CD810900	CD810900 RTInt_1-C
	345	70.8	11.1	277	2	BB006347	BB006347 BB006347
	346	70.8	11.1	308	2	BB361016	BB361016 BB361016
	347	70.4	11.0	789	7	CN975696	CN975696 25583_125
	348	70.4	11.0	867	7	CN975873	CN975873 25775_125
	349	70	11.0	273	2	BB010292	BB010292 BB010292
	350	69.2	10.8	545	2	BE684228	BE684228 184549 MA
	351	68.8	10.8	532	1	AA273481	AA273481 vc37c10.r
	352	68.4	10.7	303	1	AV235006	AV235006 AV235006
	353	68.4	10.7	718	5	BU262937	BU262937 603508618
	354	67.6	10.6	421	1	AA273564	AA273564 vc38f10.r
	355	67.6	10.6	710	5	BX912444	BX912444 BX912444
	356	67	10.5	567	5	BX086253	BX086253 BX086253
	357	66.8	10.5	233	2	BB051098	BB051098 BB051098
	358	66.8	10.5	274	2	BB529929	BB529929 BB529929
	359	66.6	10.4	289	4	BG200773	BG200773 RST20223
	360	65.8	10.3	738	5	BX884918	BX884918 BX884918
c	361	65.6	10.3	426	1	AI035384	AI035384 uc90d12.x
	362	65	10.2	452	4	BG428060	BG428060 602501471
c	363	65	10.2	631	1	AI105157	AI105157 EST214446
c	364	61.6	9.6	985	2	BF781108	BF781108 602106752
c	365	60.6	9.5	618	6	CB502807	CB502807 ssalmge50
	366	59.8	9.4	600	6	CB504196	CB504196 ssalplnb5
c	367	59.8	9.4	776	9	CE561073	CE561073 tigr-gss-
c	368	59.6	9.3	615	6	CA041633	CA041633 ssalmge00
	369	59.2	9.3	322	7	CK676494	CK676494 ZF101-P00
	370	56.2	8.8	527	1	AI476983	AI476983 fb58b12.y
c	371	55.2	8.6	782	5	BU689227	BU689227 UI-CF-EC1
	372	54.8	8.6	778	7	CR451583	CR451583 CR451583
	373	54.4	8.5	708	7	CK676883	CK676883 ZF101-P00
c	374	54	8.5	421	4	BJ748996	BJ748996 BJ748996
	375	53.2	8.3	715	6	CD494891	CD494891 CDA13-D01
	376	53	8.3	230	6	CA969172	CA969172 CcLX06a21
c	377	52.4	8.2	278	1	AA480295	AA480295 ne32d11.s
	378	52.2	8.2	648	5	BU124645	BU124645 603147949
	379	51.8	8.1	472	1	AJ693058	AJ693058 AJ693058
c	380	51.4	8.0	798	7	CK777040	CK777040 964032 MA
c	381	51.2	8.0	382	7	CR465430	CR465430 CR465430
	382	50.8	7.9	451	2	BE722366	BE722366 190570 MA
	383	50.4	7.9	696	1	AJ660081	AJ660081 AJ660081
	384	50.2	7.9	464	2	BB744916	BB744916 BB744916
c	385	49.8	7.8	905	9	CNS028U9	AL186426 Tetraodon
	386	49.4	7.7	501	4	BM445902	BM445902 1IL1C3.ab
	387	49	7.7	730	5	BU453964	BU453964 603767942
	388	47.2	7.4	435	2	BB683122	BB683122 BB683122
c	389	46.8	7.3	732	4	BG679057	BG679057 602627005

	390	46	7.2	645	8	AQ938648	AQ938648 NL1-CP14C
c	391	44.2	6.9	555	8	AQ774104	AQ774104 HS_2269_B
c	392	43.8	6.9	597	1	AI790451	AI790451 ul01d01.x
	393	42.8	6.7	443	2	BB746485	BB746485 BB746485
	394	41.6	6.5	341	6	CB694151	CB694151 AMGNNUC:C
c	395	41.2	6.4	1101	9	CNS0100X	AL098379 Drosophil
	396	40.2	6.3	564	4	BJ072047	BJ072047 BJ072047
	397	40.2	6.3	883	9	CC522543	CC522543 CH240_370
c	398	39.6	6.2	816	4	BG414759	BG414759 HVSMEK000
c	399	39.4	6.2	599	1	AI408820	AI408820 EST237111
	400	39	6.1	601	7	CO513169	CO513169 s13dSG23F
	401	38.6	6.0	755	1	AL965162	AL965162 AL965162
c	402	38.6	6.0	898	7	CR570022	CR570022 CR570022
c	403	38.4	6.0	590	1	AI790369	AI790369 uk99d02.x
	404	38.4	6.0	659	4	BJ042217	BJ042217 BJ042217
	405	38.4	6.0	3420	9	CL975853	CL975853 OsIFCC028
c	406	38.2	6.0	483	8	AZ838144	AZ838144 2M0133P11
	407	38.2	6.0	554	2	BF000287	BF000287 7h25d04.x
	408	38.2	6.0	693	6	CD671500	CD671500 fg05b10.y
	409	38.2	6.0	897	5	BX350573	BX350573 BX350573
	410	38	5.9	606	7	CO792766	CO792766 NT015D_H1
c	411	38	5.9	897	8	AZ187101	AZ187101 SP_1008_B
c	412	38	5.9	959	9	CNS003FH	AL064643 Drosophil
c	413	37.8	5.9	247	1	AA805317	AA805317 oc15a12.s
c	414	37.8	5.9	1101	9	CNS00AYO	AL056506 Drosophil
	415	37.6	5.9	433	5	BP611658	BP611658 BP611658
	416	37.6	5.9	770	8	BH715665	BH715665 BOMMN46TR
c	417	37.6	5.9	779	9	BX166858	BX166858 Danio rer
	418	37.6	5.9	4007	3	BC042495	BC042495 Homo sapi
	419	37.4	5.9	368	7	CR554138	CR554138 DKFZp469I
	420	37.4	5.9	556	7	CO515645	CO515645 s13dSG60B
	421	37.4	5.9	602	7	CK560637	CK560637 rswpb0_00
c	422	37.2	5.8	227	1	AV299928	AV299928 AV299928
	423	37.2	5.8	422	1	AA999188	AA999188 UI-R-C0-h
	424	37.2	5.8	444	2	BE100097	BE100097 UI-R-BJ1-
	425	37.2	5.8	672	9	CG449148	CG449148 OGVGY89TV
c	426	37.2	5.8	674	9	CG445838	CG445838 OGVGY90TH
c	427	37.2	5.8	856	8	BZ649802	BZ649802 OGANW60TC
	428	37.2	5.8	904	9	CNS018JR	AL109425 Drosophil
c	429	37	5.8	548	8	BH087546	BH087546 RPCI-24-2
c	430	37	5.8	634	9	CNS021MB	AL177068 Tetraodon
	431	37	5.8	683	9	CE159770	CE159770 tigr-gss-
c	432	37	5.8	868	8	AZ542161	AZ542161 ENTFP30TF
c	433	36.8	5.8	427	8	AQ588324	AQ588324 CITBI-E1-
	434	36.8	5.8	584	1	AI792241	AI792241 ov04f11.y
	435	36.8	5.8	772	7	CO159871	CO159871 FLD1_16_C
c	436	36.8	5.8	835	2	BF031601	BF031601 601557768
c	437	36.8	5.8	856	7	CO368226	CO368226 RTK1_39_H
c	438	36.8	5.8	859	7	CO368315	CO368315 RTK1_39_H
c	439	36.8	5.8	971	9	CNS006UK	AL065943 Drosophil
c	440	36.6	5.7	573	8	AQ335796	AQ335796 HS_5016_B
c	441	36.6	5.7	1142	8	CC210944	CC210944 CH261-65M
c	442	36.4	5.7	389	7	CO951292	CO951292 UMC-pd12f
	443	36.4	5.7	407	1	AA701368	AA701368 zi63g04.s
	444	36.4	5.7	441	5	BY369950	BY369950 BY369950
	445	36.4	5.7	456	1	AI801563	AI801563 to91a10.x
c	446	36.4	5.7	562	9	CNS016OR	AL107013 Drosophil
	447	36.4	5.7	639	1	AL703198	AL703198 DKFZp686D
	448	36.4	5.7	729	9	AG029823	AG029823 Pan trogl
c	449	36.4	5.7	1003	4	BG166160	BG166160 602340783
c	450	36.2	5.7	387	8	BH261633	BH261633 CH230-185
c	451	36.2	5.7	391	7	CO754641	CO754641 Mdfrt3051
	452	36.2	5.7	497	8	AZ225739	AZ225739 RPCI-23-6
c	453	36.2	5.7	600	1	AA891752	AA891752 EST195555
c	454	36.2	5.7	735	9	CE095212	CE095212 tigr-gss-
c	455	36.2	5.7	763	9	AG508553	AG508553 Mus muscu
c	456	36.2	5.7	768	7	CO892554	CO892554 BovGen_20
c	457	36.2	5.7	843	9	CC930588	CC930588 ZMMBBc054
c	458	36.2	5.7	928	9	CNS00DKY	AL071865 Drosophil
	459	36.2	5.7	940	9	CNS02SKB	AL211988 Tetraodon
	460	36.2	5.7	966	8	BZ821427	BZ821427 PUGCF69TD
c	461	36.2	5.7	1101	9	CNS00C1G	AL058608 Drosophil
	462	36.2	5.7	1525	8	CC307565	CC307565 TAM32-30G
c	463	36	5.6	423	5	BY496253	BY496253 BY496253
c	464	36	5.6	750	6	CA312017	CA312017 UI-CF-FN0
c	465	36	5.6	755	8	BH567239	BH567239 BOGED67TF
	466	36	5.6	758	7	CO395765	CO395765 AGENCOURT
c	467	36	5.6	758	8	BH720418	BH720418 BOMIE30TR
c	468	36	5.6	889	9	CR798301	CR798301 GR0AAA17A
c	469	35.8	5.6	420	5	BQ836491	BQ836491 rf46e12.y
c	470	35.8	5.6	460	5	BU093947	BU093947 rf75b01.y
c	471	35.8	5.6	499	6	CA995792	CA995792 rg06b01.y
	472	35.8	5.6	500	2	AW259551	AW259551 up30b07.x
c	473	35.8	5.6	591	5	BQ836159	BQ836159 rf42f05.y
c	474	35.8	5.6	713	8	CC247387	CC247387 CH261-15B
c	475	35.8	5.6	721	7	CF388937	CF388937 RTDR2_16_
	476	35.8	5.6	741	7	CN312136	CN312136 170005326
	477	35.8	5.6	766	4	BI766088	BI766088 603053069
	478	35.8	5.6	835	7	CO366547	CO366547 RTK1_28_B
	479	35.8	5.6	841	7	CO366468	CO366468 RTK1_28_B
	480	35.8	5.6	850	7	CO163214	CO163214 FLD1_40_E
	481	35.8	5.6	932	5	BQ722429	BQ722429 AGENCOURT
c	482	35.8	5.6	1240	8	CC228921	CC228921 CH261-157
	483	35.6	5.6	263	1	AA378979	AA378979 EST91850
	484	35.6	5.6	456	9	CE372141	CE372141 tigr-gss-
	485	35.6	5.6	503	2	BB704634	BB704634 BB704634
c	486	35.6	5.6	565	8	BZ944484	BZ944484 CH240_83B
	487	35.6	5.6	736	2	AW964192	AW964192 EST376265
c	488	35.6	5.6	849	7	CK019144	CK019144 AGENCOURT
c	489	35.6	5.6	903	2	BF699219	BF699219 602126868
c	490	35.6	5.6	1106	9	CNS04L9U	AL295851 Tetraodon
	491	35.4	5.5	553	8	AQ882301	AQ882301 HS_5366_A
c	492	35.4	5.5	561	8	AZ072313	AZ072313 RPCI-23-3
c	493	35.4	5.5	575	9	CR823052	CR823052 GR0AAA53A
c	494	35.4	5.5	729	8	BZ054520	BZ054520 jnr34a01.
	495	35.4	5.5	880	9	CG268394	CG268394 OG3AE44TH
	496	35.4	5.5	906	9	CG212280	CG212280 OG3CG07TH
c	497	35.4	5.5	971	8	AZ668799	AZ668799 ENTHX37TR
c	498	35.4	5.5	1427	8	CC237540	CC237540 CH261-191
	499	35.2	5.5	315	7	CO882458	CO882458 BovGen_10
	500	35.2	5.5	557	8	AZ297461	AZ297461 RPCI-23-1
c	501	35.2	5.5	611	2	AW018063	AW018063 614066C08
	502	35.2	5.5	633	8	CC349360	CC349360 OGRAU76TV
	503	35.2	5.5	660	8	BH816590	BH816590 AM__Ba002
	504	35.2	5.5	674	6	CB844251	CB844251 M15E-5207
c	505	35.2	5.5	689	9	CC708559	CC708559 OGDAE22TM
c	506	35.2	5.5	761	4	BG173675	BG173675 602336814
	507	35.2	5.5	802	8	BZ086594	BZ086594 lkh12e06.
	508	35.2	5.5	845	9	CG159433	CG159433 PUJDK47TB
	509	35.2	5.5	850	7	CN440718	CN440718 BE04023A1
	510	35.2	5.5	933	9	CNS014I1	AL104179 Drosophil
	511	35.2	5.5	1055	8	CC254220	CC254220 CH261-4N2
c	512	35.2	5.5	1223	8	BZ552912	BZ552912 pacs1-60_
	513	35.2	5.5	2391	9	AY413037	AY413037 Homo sapi
c	514	35	5.5	428	4	BM276470	BM276470 PfESToaa8
c	515	35	5.5	461	2	AW154879	AW154879 EST290171
	516	35	5.5	464	9	BX982998	BX982998 Reverse s
c	517	35	5.5	606	8	AZ338670	AZ338670 1M0069O16
c	518	35	5.5	616	6	CD127956	CD127956 MF1-0016P
	519	35	5.5	640	9	CR493911	CR493911 Medicago
	520	35	5.5	656	5	BW333847	BW333847 BW333847
c	521	35	5.5	661	9	AG136352	AG136352 Pan trogl
	522	35	5.5	686	5	BW332316	BW332316 BW332316
	523	35	5.5	688	5	BP008792	BP008792 BP008792
	524	35	5.5	693	5	BP014380	BP014380 BP014380
	525	35	5.5	705	5	BW360038	BW360038 BW360038
	526	35	5.5	709	9	CE784423	CE784423 tigr-gss-
	527	35	5.5	747	8	CC428361	CC428361 PUHSR26TD
	528	35	5.5	764	5	BU331649	BU331649 603499341
	529	35	5.5	790	8	CC360604	CC360604 PUHIX03TD
	530	35	5.5	840	7	CN507473	CN507473 AGENCOURT
	531	35	5.5	878	9	CNS0187R	AL108993 Drosophil
	532	35	5.5	975	9	CNS0102Y	AL098452 Drosophil
c	533	35	5.5	1001	9	CNS0140O	AL103554 Drosophil
c	534	35	5.5	1238	9	CL048477	CL048477 CH216-68A
	535	34.8	5.4	180	6	CD227264	CD227264 CCC1_50_H

	536	34.8	5.4	414	1	AI022458	AI022458 ow96h10.x
	537	34.8	5.4	422	2	AW770915	AW770915 hl93b09.x
	538	34.8	5.4	449	8	AQ056271	AQ056271 CIT-HSP-2
c	539	34.8	5.4	502	4	BG886608	BG886608 EST512459
c	540	34.8	5.4	504	5	BW384184	BW384184
	541	34.8	5.4	505	8	AZ900918	AZ900918 RPCI-24-1
c	542	34.8	5.4	539	2	BE472513	BE472513 EST417366
	543	34.8	5.4	590	8	AQ579847	AQ579847 T135353b
c	544	34.8	5.4	653	7	CF179990	CF179990 815038 MA
c	545	34.8	5.4	1078	1	AL574873	AL574873 AL574873
c	546	34.8	5.4	1201	9	CNS0169D	AL106459 Drosophil
	547	34.6	5.4	341	7	CK340616	CK340616 C0934F09-
c	548	34.6	5.4	463	9	CE636619	CE636619 tigr-gss-
	549	34.6	5.4	490	8	AQ565741	AQ565741 HS_5380_A
c	550	34.6	5.4	504	2	BE415221	BE415221 MWL025.F0
	551	34.6	5.4	532	6	CD397785	CD397785 Gm_ck1872
c	552	34.6	5.4	558	4	BM140408	BM140408 WHE0483_c
	553	34.6	5.4	586	5	BQ127188	BQ127188 ii60h06.x
	554	34.6	5.4	590	7	CK345625	CK345625 L0278G01-
	555	34.6	5.4	619	9	CE276694	CE276694 tigr-gss-
	556	34.6	5.4	629	7	CK344224	CK344224 K0855D02-
c	557	34.6	5.4	630	1	AV061247	AV061247 AV061247
	558	34.6	5.4	639	7	CK345029	CK345029 L0032A02-
	559	34.6	5.4	686	7	CO042440	CO042440 UI-M-FY0-
	560	34.6	5.4	787	6	CB601856	CB601856 AGENCOURT
c	561	34.6	5.4	876	5	BX340974	BX340974 BX340974
c	562	34.6	5.4	890	8	BH150894	BH150894 ENTQF05TF
c	563	34.6	5.4	964	8	CC175242	CC175242 ZMMBBc029
c	564	34.6	5.4	998	8	CC071561	CC071561 CSU-K33r.
c	565	34.6	5.4	1101	9	CNS00LT2	AL078714 Drosophil
	566	34.6	5.4	1113	9	CNS05K7Q	AL341135 Tetraodon
c	567	34.6	5.4	3290	3	BC060657	BC060657 Mus muscu
c	568	34.4	5.4	456	8	AQ538338	AQ538338 RPCI-11-3
	569	34.4	5.4	508	8	AQ698017	AQ698017 HS_5539_B
c	570	34.4	5.4	605	8	AZ449248	AZ449248 1M0247H20
	571	34.4	5.4	634	6	CB956853	CB956853 AGENCOURT
c	572	34.4	5.4	649	4	BM065314	BM065314 KS07002C0
	573	34.4	5.4	677	5	BW232214	BW232214 BW232214
	574	34.4	5.4	706	7	CN045430	CN045430 v11_p56_c
c	575	34.4	5.4	738	4	BJ541117	BJ541117 BJ541117
c	576	34.4	5.4	746	6	CB819951	CB819951 EST 943 G
c	577	34.4	5.4	762	4	BI932559	BI932559 EST552448
	578	34.4	5.4	807	8	BZ442121	BZ442121 BONGL63TF
c	579	34.4	5.4	856	8	CC152013	CC152013 NDL.42J18
c	580	34.4	5.4	871	8	CC131066	CC131066 NDL.34D20
	581	34.4	5.4	977	9	CL021629	CL021629 CH216-8K1
	582	34.4	5.4	1101	7	CN646598	CN646598 ILLUMIGEN
c	583	34.4	5.4	1101	9	CNS00FOO	AL070854 Drosophil
	584	34.4	5.4	1114	8	CC277770	CC277770 CH261-95C
	585	34.2	5.4	218	1	AI545491	AI545491 fb66b03.x
c	586	34.2	5.4	333	1	AV046616	AV046616 AV046616
	587	34.2	5.4	343	7	CO896667	CO896667 BovGen_24
c	588	34.2	5.4	427	5	BP598533	BP598533 BP598533
c	589	34.2	5.4	428	5	BQ762985	BQ762985 EBro02_SQ
c	590	34.2	5.4	510	4	BM137551	BM137551 WHE0483-0
	591	34.2	5.4	577	7	CN442275	CN442275 BE04028B2
c	592	34.2	5.4	586	9	CG160426	CG160426 PUKEC37TB
	593	34.2	5.4	602	2	AW776073	AW776073 EST335138
	594	34.2	5.4	619	2	BF520410	BF520410 EST457880
c	595	34.2	5.4	627	9	CG851558	CG851558 ZMMBBb034
	596	34.2	5.4	636	2	AW685916	AW685916 NF036D12N
c	597	34.2	5.4	643	6	CA333025	CA333025 hab33f01.
	598	34.2	5.4	657	4	BG245117	BG245117 602357508
	599	34.2	5.4	671	9	CE011684	CE011684 tigr-gss-
c	600	34.2	5.4	690	4	BM440928	BM440928 EBro08_SQ
c	601	34.2	5.4	698	8	CC113063	CC113063 NDL.34C7.
	602	34.2	5.4	706	6	CF067996	CF067996 EST668717
	603	34.2	5.4	716	5	BW308197	BW308197 BW308197
c	604	34.2	5.4	723	4	BJ746315	BJ746315 BJ746315
	605	34.2	5.4	729	9	CG841606	CG841606 Ynhw2220
c	606	34.2	5.4	754	5	BW154312	BW154312 BW154312
c	607	34.2	5.4	789	2	BF036247	BF036247 601459345
c	608	34.2	5.4	800	6	CA917064	CA917064 EST641211
c	609	34.2	5.4	820	8	BH076145	BH076145 RPCI-24-3
c	610	34.2	5.4	835	6	CB170001	CB170001 CZI603001
	611	34.2	5.4	850	7	CN174723	CN174723 AGENCOURT
	612	34.2	5.4	907	9	CL996038	CL996038 ZMMBHf000
	613	34.2	5.4	936	9	CL992191	CL992191 ZMMBHf000
	614	34.2	5.4	937	9	CG102077	CG102077 PUKEA37TD
	615	34.2	5.4	955	9	CL133305	CL133305 ISB1-103F
c	616	34.2	5.4	979	9	CL046558	CL046558 CH216-64I
c	617	34.2	5.4	990	9	CG102076	CG102076 PUKEA37TB
c	618	34.2	5.4	1070	9	CG863867	CG863867 ZMMBBc027
c	619	34.2	5.4	1124	9	CC891785	CC891785 ZMMBBc052
	620	34.2	5.4	1217	9	AG436482	AG436482 Mus muscu
	621	34	5.3	375	6	CB691609	CB691609 AMGNNUC:C
c	622	34	5.3	388	6	CB805306	CB805306 AMGNNUC:S
c	623	34	5.3	478	2	AW941442	AW941442 HL04319.3
	624	34	5.3	481	6	CD188741	CD188741 MS1-0063U
	625	34	5.3	482	6	CD531632	CD531632 11H24 Ara
	626	34	5.3	500	8	BH774126	BH774126 uzmb003f0
c	627	34	5.3	513	7	CN751173	CN751173 ApHL3SD-I
	628	34	5.3	536	6	CD178401	CD178401 MS1-0014P
	629	34	5.3	574	8	AQ762153	AQ762153 HS_3099_B
c	630	34	5.3	600	9	CG849353	CG849353 ZMMBBb033
	631	34	5.3	640	9	AG196671	AG196671 Pan trogl
c	632	34	5.3	669	7	CF228850	CF228850 PtaXM0018
	633	34	5.3	684	9	CL810283	CL810283 OR_CBa002
	634	34	5.3	690	8	BZ002426	BZ002426 oe187d10.
	635	34	5.3	748	5	BU365745	BU365745 603790234
	636	34	5.3	759	7	CK439188	CK439188 GQ0034b.T
c	637	34	5.3	761	7	CK774522	CK774522 963290 MA
c	638	34	5.3	820	8	BH179705	BH179705 015_M_12-
c	639	34	5.3	820	9	CNS07LQ7	AL616657 T3 end of
c	640	34	5.3	841	8	AZ668946	AZ668946 ENTMI67TR
c	641	34	5.3	898	8	AZ543791	AZ543791 ENTDR03TR
c	642	34	5.3	904	8	BZ143305	BZ143305 CH230-412
	643	34	5.3	914	9	CL075401	CL075401 CH216-136
c	644	34	5.3	924	9	CNS014CR	AL103989 Drosophil
	645	34	5.3	1064	4	BM470198	BM470198 AGENCOURT
	646	34	5.3	1204	9	CNS016E2	AL106628 Drosophil
c	647	34	5.3	1371	9	AG304808	AG304808 Mus muscu
	648	34	5.3	1706	3	AK013555	AK013555 Mus muscu
	649	34	5.3	4069	3	HSM803684	AL832376 Homo sapi
	650	34	5.3	4932	3	HSM803655	AL832347 Homo sapi
c	651	33.8	5.3	332	5	BQ981484	BQ981484 QGE13O12.
c	652	33.8	5.3	372	1	AV148268	AV148268 AV148268
	653	33.8	5.3	416	8	AQ123571	AQ123571 HS_3103_B
c	654	33.8	5.3	421	9	CE364358	CE364358 tigr-gss-
	655	33.8	5.3	500	4	BM781215	BM781215 MLN1_5_G0
	656	33.8	5.3	520	6	CD484094	CD484094 atr01-7ms
	657	33.8	5.3	541	2	BE753323	BE753323 206287 MA
c	658	33.8	5.3	546	6	CA639805	CA639805 wre1n.pk0
	659	33.8	5.3	547	7	CF233309	CF233309 PtaJXO002
	660	33.8	5.3	550	8	BZ535367	BZ535367 OGAHN18TC
	661	33.8	5.3	555	7	CF236220	CF236220 PtaJXT10B
	662	33.8	5.3	581	8	AQ187530	AQ187530 HS_3132_A
c	663	33.8	5.3	586	7	CN821340	CN821340 HRO4424_B
	664	33.8	5.3	589	4	BJ073550	BJ073550 BJ073550
	665	33.8	5.3	615	6	CA322973	CA322973 UI-M-FV0-
c	666	33.8	5.3	624	8	AZ944500	AZ944500 2M0205C13
c	667	33.8	5.3	675	6	CB533491	CB533491 758124 MA
	668	33.8	5.3	676	8	AZ867176	AZ867176 2M0177J22
	669	33.8	5.3	686	9	CE811066	CE811066 tigr-gss-
c	670	33.8	5.3	719	5	BU379185	BU379185 603810889
c	671	33.8	5.3	728	6	CD838357	CD838357 RFO2.110O
c	672	33.8	5.3	732	8	B52482	B52482 CIT-HSP-200
c	673	33.8	5.3	732	9	CNS02PJB	AL208064 Tetraodon
	674	33.8	5.3	754	9	CC587169	CC587169 CH240_384
c	675	33.8	5.3	779	8	BZ063480	BZ063480 11f37f08.
c	676	33.8	5.3	788	9	CC713983	CC713983 OGVFY71TH
	677	33.8	5.3	791	6	CB316855	CB316855 AGENCOURT
c	678	33.8	5.3	793	9	CC981670	CC981670 ZUADM83TV
	679	33.8	5.3	798	9	CL674642	CL674642 PRI0112c_
	680	33.8	5.3	811	5	BX714403	BX714403 BX714403
	681	33.8	5.3	828	9	CL660154	CL660154 PRI0136b_

	682	33.8	5.3	837	2	BF573690	BF573690 602077285
c	683	33.8	5.3	841	9	CL661311	CL661311 PRI0139c_
c	684	33.8	5.3	867	7	CK414480	CK414480 AUF_IpGi1
c	685	33.8	5.3	890	8	AZ681799	AZ681799 ENTLT51TF
	686	33.8	5.3	906	8	BZ813926	BZ813926 PUFFZ34TD
	687	33.8	5.3	940	6	CA496292	CA496292 AGENCOURT
	688	33.8	5.3	1021	5	BM907791	BM907791 AGENCOURT
c	689	33.8	5.3	1189	6	CA469072	CA469072 AGENCOURT
	690	33.6	5.3	164	5	BQ254451	BQ254451 NISC_jp05
	691	33.6	5.3	249	4	BG202625	BG202625 RST21988
c	692	33.6	5.3	277	1	AL926772	AL926772 AL926772
c	693	33.6	5.3	289	2	BB405483	BB405483 BB405483
c	694	33.6	5.3	325	1	AI072651	AI072651 UI-R-C2-n
c	695	33.6	5.3	435	5	BW591908	BW591908 BW591908
	696	33.6	5.3	439	8	AQ638593	AQ638593 927P1-3F1
	697	33.6	5.3	538	9	CC733795	CC733795 OGUBA35TH
c	698	33.6	5.3	563	7	CN723384	CN723384 E0859E06-
	699	33.6	5.3	566	9	CG680914	CG680914 94E22_21T
	700	33.6	5.3	570	2	AW076387	AW076387 614066E07
	701	33.6	5.3	602	2	AW076371	AW076371 614066C08
c	702	33.6	5.3	609	2	AW018079	AW018079 614066E07
	703	33.6	5.3	632	8	BZ917529	BZ917529 CH240_103
	704	33.6	5.3	655	7	CK369135	CK369135 zmrws055_
c	705	33.6	5.3	661	7	CF626917	CF626917 zmrws05_0
	706	33.6	5.3	680	9	AG153091	AG153091 Pan trog1
c	707	33.6	5.3	694	7	CF637559	CF637559 zmrww00_0
	708	33.6	5.3	694	8	BZ011928	BZ011928 oeg74h07.
	709	33.6	5.3	722	9	CR326738	CR326738 Medicago
	710	33.6	5.3	724	7	CK371621	CK371621 zmrww005_
c	711	33.6	5.3	725	9	CW534793	CW534793 OP__Ba003
	712	33.6	5.3	728	9	CC961291	CC961291 BOIFU82TF
c	713	33.6	5.3	747	4	BG671678	BG671678 DRNBWD10
	714	33.6	5.3	747	8	BH794562	BH794562 ME_MBa000
	715	33.6	5.3	755	7	CF206372	CF206372 RR890915I
	716	33.6	5.3	756	9	CG311283	CG311283 OGXDO91TH
	717	33.6	5.3	762	9	CG924320	CG924320 MBEAH93TF
	718	33.6	5.3	766	7	CO521288	CO521288 3530_1_14
	719	33.6	5.3	767	9	AG561860	AG561860 Mus muscu
c	720	33.6	5.3	806	5	BU427148	BU427148 603961856
c	721	33.6	5.3	813	4	BI949878	BI949878 HVSMEl001
	722	33.6	5.3	819	9	CR013125	CR013125 Forward s
c	723	33.6	5.3	835	9	CR805940	CR805940 GR0AAA27C
c	724	33.6	5.3	915	9	CL123010	CL123010 ISB1-83B8
c	725	33.6	5.3	918	2	BF338893	BF338893 602036151
c	726	33.6	5.3	932	9	CL123435	CL123435 ISB1-83L2
	727	33.6	5.3	933	8	BZ793199	BZ793199 PUFER63TD
c	728	33.6	5.3	941	9	CL123974	CL123974 ISB1-84K9
	729	33.6	5.3	952	9	CNS00D9R	AL060405 Drosophil
	730	33.6	5.3	958	8	B12563	B12563 F2L10-T7 IG
	731	33.6	5.3	1049	8	CC299605	CC299605 CH261-67K
c	732	33.6	5.3	1053	9	CNS01UBT	AL167618 Tetraodon
	733	33.6	5.3	1101	9	CNS008QR	AL052316 Drosophil
	734	33.6	5.3	1101	9	CNS00GHQ	AL072203 Drosophil
	735	33.6	5.3	1101	9	CNS00Z8B	AL097349 Drosophil
	736	33.6	5.3	1102	8	CC239507	CC239507 CH261-118
	737	33.6	5.3	2559	3	AK086139	AK086139 Mus muscu
c	738	33.4	5.2	155	9	CG574068	CG574068 OST206522
c	739	33.4	5.2	255	1	AI407269	AI407269 EST235557
c	740	33.4	5.2	314	1	AV310978	AV310978 AV310978
	741	33.4	5.2	323	2	BE183540	BE183540 CM2-HT067
c	742	33.4	5.2	342	5	BW166942	BW166942 BW166942
c	743	33.4	5.2	358	9	BX181693	BX181693 Danio rer
c	744	33.4	5.2	368	8	AZ916976	AZ916976 4911.fd63
	745	33.4	5.2	377	5	BW296376	BW296376 BW296376
c	746	33.4	5.2	394	8	AZ748354	AZ748354 RPCI-24-1
	747	33.4	5.2	441	2	AW829157	AW829157 ra36d06.y
c	748	33.4	5.2	444	2	BF711921	BF711921 MI-P-O3-a
c	749	33.4	5.2	445	2	AW371158	AW371158 CM0-BT028
	750	33.4	5.2	448	2	AW001845	AW001845 wt81a02.x
	751	33.4	5.2	457	1	AA705375	AA705375 zj89g12.s
	752	33.4	5.2	463	2	BF079828	BF079828 230527 MA
c	753	33.4	5.2	473	1	AA179941	AA179941 zp14d07.r
	754	33.4	5.2	485	4	BM276292	BM276292 PfESToaa7
	755	33.4	5.2	500	1	AU087293	AU087293 AU087293
	756	33.4	5.2	519	2	AW783011	AW783011 ra22c11.y
	757	33.4	5.2	519	2	AW870870	AW870870 ra51g06.y
	758	33.4	5.2	521	4	BM275773	BM275773 PfESToaa8
	759	33.4	5.2	531	9	CL358700	CL358700 RPCI44_41
	760	33.4	5.2	550	4	BM275920	BM275920 PfESToaa8
	761	33.4	5.2	556	2	BF705631	BF705631 230514 MA
	762	33.4	5.2	556	4	BM275493	BM275493 PfESToaa5
	763	33.4	5.2	557	4	BM275752	BM275752 PfESToaa8
c	764	33.4	5.2	557	8	AQ503986	AQ503986 RPCI-11-3
	765	33.4	5.2	561	4	BM273572	BM273572 PfESToaa5
	766	33.4	5.2	561	4	BM274403	BM274403 PfESToaa4
	767	33.4	5.2	562	4	BM275344	BM275344 PfESToaa6
	768	33.4	5.2	570	9	CG086583	CG086583 PUICM29TD
c	769	33.4	5.2	588	2	BE508543	BE508543 dc17f06.x
	770	33.4	5.2	594	8	BH265140	BH265140 CH230-199
	771	33.4	5.2	598	1	AV385323	AV385323 AV385323
c	772	33.4	5.2	606	5	BX644159	BX644159 DKFZp781E
c	773	33.4	5.2	606	8	BH168645	BH168645 VV_SBa000
	774	33.4	5.2	614	6	CA406324	CA406324 1002473 H
c	775	33.4	5.2	616	6	CD835177	CD835177 BN45.044J
	776	33.4	5.2	633	9	CE058121	CE058121 tigr-gss-
	777	33.4	5.2	649	9	CE266155	CE266155 tigr-gss-
	778	33.4	5.2	657	9	BX989204	BX989204 Reverse s
c	779	33.4	5.2	660	4	BJ398016	BJ398016 BJ398016
c	780	33.4	5.2	663	4	BJ402922	BJ402922 BJ402922
	781	33.4	5.2	663	5	BX506735	BX506735 DKFZp779A
	782	33.4	5.2	672	5	BU334828	BU334828 603871295
	783	33.4	5.2	682	9	CL910065	CL910065 OA_ABa001
c	784	33.4	5.2	688	5	BW013688	BW013688 BW013688
c	785	33.4	5.2	701	4	BJ372526	BJ372526 BJ372526
	786	33.4	5.2	706	8	BH934661	BH934661 odf87f06.
c	787	33.4	5.2	728	5	BU118538	BU118538 603143186
	788	33.4	5.2	732	5	BP682269	BP682269 BP682269
c	789	33.4	5.2	732	9	CG995790	CG995790 ZMMBBb038
c	790	33.4	5.2	733	5	BW462094	BW462094 BW462094
c	791	33.4	5.2	735	4	BJ398404	BJ398404 BJ398404
	792	33.4	5.2	739	4	BJ662428	BJ662428 BJ662428
c	793	33.4	5.2	746	5	BW169027	BW169027 BW169027
c	794	33.4	5.2	747	5	BW174954	BW174954 BW174954
	795	33.4	5.2	751	9	AG502990	AG502990 Mus muscu
	796	33.4	5.2	757	4	BG021518	BG021518 de86e06.y
	797	33.4	5.2	757	8	BZ758771	BZ758771 620_2U2_E
c	798	33.4	5.2	769	5	BW173943	BW173943 BW173943
c	799	33.4	5.2	778	5	BW187253	BW187253 BW187253
	800	33.4	5.2	781	5	BP674035	BP674035 BP674035
c	801	33.4	5.2	794	7	CK197095	CK197095 FGAS00556
	802	33.4	5.2	874	8	CC432926	CC432926 PUHFG40TD
	803	33.4	5.2	877	5	BU212512	BU212512 603952974
	804	33.4	5.2	905	9	CG030102	CG030102 PUFYH63TD
c	805	33.4	5.2	917	9	CNS0159N	AL105173 Drosophil
	806	33.4	5.2	929	9	CL740099	CL740099 OR_BBa007
	807	33.4	5.2	945	7	CN509076	CN509076 AGENCOURT
c	808	33.4	5.2	1006	9	CNS00L23	AL067871 Drosophil
c	809	33.4	5.2	1023	9	CG057433	CG057433 PUFYH76TB
	810	33.4	5.2	1101	9	CNS00FN4	AL070798 Drosophil
	811	33.4	5.2	1101	9	CNS00L9Y	AL068053 Drosophil
	812	33.4	5.2	1101	9	CNS017FC	AL107970 Drosophil
c	813	33.4	5.2	1183	9	CNS0078G	AL066645 Drosophil
	814	33.2	5.2	234	6	CD197430	CD197430 MS1-0095G
	815	33.2	5.2	272	6	CD183199	CD183199 MS1-0037T
	816	33.2	5.2	315	9	CG846428	CG846428 OG4AC86TV
	817	33.2	5.2	338	5	BQ451451	BQ451451 PfESToaa9
	818	33.2	5.2	346	9	AG254421	AG254421 Lotus cor
	819	33.2	5.2	382	8	AQ037484	AQ037484 CIT-HSP-2
	820	33.2	5.2	395	9	CE660031	CE660031 tigr-gss-
c	821	33.2	5.2	397	4	BI706263	BI706263 fq03e03.y
c	822	33.2	5.2	415	8	AZ172939	AZ172939 SP_0123_A
	823	33.2	5.2	424	5	BQ633388	BQ633388 PfESToab4
c	824	33.2	5.2	451	2	BF702125	BF702125 MI-P-A1-a
	825	33.2	5.2	470	2	BE519200	BE519200 946094E06
c	826	33.2	5.2	493	6	CB342972	CB342972 CA32EN000
	827	33.2	5.2	495	7	CV243928	CV243928 WS0253.B2

c 828	33.2	5.2	511	1	AJ680634	AJ680634	AJ680634
c 829	33.2	5.2	531	8	AQ386042	AQ386042	RPCI11-13
830	33.2	5.2	536	6	CB971321	CB971321	CAB10005_
831	33.2	5.2	561	4	BG965269	BG965269	602831069
c 832	33.2	5.2	562	5	BQ260567	BQ260567	fz62e01.y
c 833	33.2	5.2	573	9	CE814143	CE814143	tigr-gss-
834	33.2	5.2	588	5	BW368014	BW368014	BW368014
835	33.2	5.2	594	8	CC422672	CC422672	PUHIY17TB
836	33.2	5.2	600	5	BU920579	BU920579	6062-05 M
c 837	33.2	5.2	600	9	CG845377	CG845377	OG4AC73TH
838	33.2	5.2	601	5	BW366888	BW366888	BW366888
839	33.2	5.2	602	8	BZ890719	BZ890719	CH240_233
c 840	33.2	5.2	607	2	AW929347	AW929347	EST338135
c 841	33.2	5.2	615	2	AW738583	AW738583	EST340010
842	33.2	5.2	623	6	CD068172	CD068172	MA2-0001T
c 843	33.2	5.2	640	8	BZ323308	BZ323308	ia76f10.g
844	33.2	5.2	643	8	BZ778436	BZ778436	ic63g12.g
845	33.2	5.2	657	9	CE783781	CE783781	tigr-gss-
846	33.2	5.2	657	9	CL598913	CL598913	OB__Ba006
c 847	33.2	5.2	663	9	CE406264	CE406264	tigr-gss-
c 848	33.2	5.2	669	4	BG492032	BG492032	602535608
c 849	33.2	5.2	669	9	AG130476	AG130476	Pan trogl
c 850	33.2	5.2	677	2	BF098239	BF098239	EST428848
c 851	33.2	5.2	683	1	AV733431	AV733431	AV733431
c 852	33.2	5.2	684	6	CA932073	CA932073	MTU4TA.P2
853	33.2	5.2	687	7	CN537865	CN537865	UI-M-HS0-
c 854	33.2	5.2	692	6	CA931764	CA931764	MTU4TA.P2
855	33.2	5.2	693	8	BZ004985	BZ004985	oei76h07.
c 856	33.2	5.2	699	8	AQ535160	AQ535160	RPCI-11-3
857	33.2	5.2	711	8	BH496268	BH496268	BOGFS41TR
c 858	33.2	5.2	739	4	BI924851	BI924851	EST544740
859	33.2	5.2	742	7	CN537075	CN537075	UI-M-HS0-
860	33.2	5.2	755	7	CV464237	CV464237	taj37g08.
861	33.2	5.2	773	7	CN534541	CN534541	UI-M-HS0-
862	33.2	5.2	785	9	CC891191	CC891191	ZMMBBc051
c 863	33.2	5.2	801	9	CNS072UA	AL426680	clone BA0
864	33.2	5.2	808	5	BU115662	BU115662	603138762
865	33.2	5.2	812	9	CG056031	CG056031	PUFYQ77TD
c 866	33.2	5.2	824	9	CG200892	CG200892	PUFYI15TB
c 867	33.2	5.2	826	8	CC332098	CC332098	OGMBC11TV
868	33.2	5.2	828	8	CC332093	CC332093	OGMBC11TH
869	33.2	5.2	849	8	CC353693	CC353693	PUHCX50TD
c 870	33.2	5.2	856	8	BZ997271	BZ997271	PUGIP94TD
c 871	33.2	5.2	860	9	CG078874	CG078874	PUFYW86TD
872	33.2	5.2	862	9	CG078871	CG078871	PUFYW86TB
c 873	33.2	5.2	870	9	CG952701	CG952701	MBEII49TF
c 874	33.2	5.2	875	9	AG151070	AG151070	Pan trogl
875	33.2	5.2	887	8	CC010878	CC010878	PUDHC05TD
876	33.2	5.2	900	8	CC017067	CC017067	PUDEM91TD
c 877	33.2	5.2	911	8	CC353689	CC353689	PUHCX50TB
878	33.2	5.2	915	8	CC273192	CC273192	CH261-112
879	33.2	5.2	927	9	CNS075N1	AL430307	clone BA0
880	33.2	5.2	944	9	CG924641	CG924641	MBEFT79TR
c 881	33.2	5.2	949	9	CG247681	CG247681	OG0GH93TV
882	33.2	5.2	955	8	AZ681935	AZ681935	ENTKY83TR
883	33.2	5.2	971	9	CG200894	CG200894	PUFYI15TD
884	33.2	5.2	972	9	CG033019	CG033019	PUFSS94TB
c 885	33.2	5.2	1004	9	CNS073LK	AL427662	clone BA0
c 886	33.2	5.2	1121	8	CC215865	CC215865	CH261-117
887	33.2	5.2	1868	9	AY413038	AY413038	Pan trogl
c 888	33.2	5.2	2075	3	CR683378	CR683378	Tetraodon
889	33	5.2	206	6	CD227240	CD227240	CCC1_50_H
c 890	33	5.2	293	5	BQ655643	BQ655643	NXRV097_C
c 891	33	5.2	299	4	BG209349	BG209349	RST28864
892	33	5.2	299	8	AQ892955	AQ892955	HS_3156_B
893	33	5.2	340	8	AQ633870	AQ633870	RPCI-11-4
894	33	5.2	360	1	AV190568	AV190568	AV190568
895	33	5.2	360	6	C43295	C43295	C43295 Yuji
896	33	5.2	360	6	C60783	C60783	C60783 Yuji
897	33	5.2	363	8	AQ421948	AQ421948	RPCI-11-1
c 898	33	5.2	365	5	BY184642	BY184642	BY184642
c 899	33	5.2	370	5	BM890562	BM890562	Chr21-12-
c 900	33	5.2	370	6	CD196055	CD196055	MS1-0092T
901	33	5.2	371	5	BX499441	BX499441	DKFZp779I
c 902	33	5.2	424	4	BG155902	BG155902	saa78g12.
903	33	5.2	451	9	CNS029TR	AL187704	Tetraodon
c 904	33	5.2	460	6	CB737850	CB737850	AMGNNUC:M
c 905	33	5.2	466	9	TA55A04P	AL455767	T. brucei
c 906	33	5.2	475	9	AG219052	AG219052	Drosophil
c 907	33	5.2	477	8	AQ702331	AQ702331	HS_5431_A
908	33	5.2	478	7	CF189950	CF189950	k5m23j2.r
909	33	5.2	500	5	BP185741	BP185741	BP185741
c 910	33	5.2	505	8	AQ061558	AQ061558	CIT-HSP-2
911	33	5.2	521	9	TA320B05Q	AL491824	T. brucei
912	33	5.2	537	1	AJ683450	AJ683450	AJ683450
c 913	33	5.2	539	6	C92029	C92029	C92029 Dict
c 914	33	5.2	549	9	CL868454	CL868454	EY10882-5
c 915	33	5.2	552	9	CG570667	CG570667	OST199790
c 916	33	5.2	562	9	CE618292	CE618292	tigr-gss-
c 917	33	5.2	566	6	CD194506	CD194506	MS1-0086U
918	33	5.2	581	8	AQ633460	AQ633460	RPCI-11-4
919	33	5.2	586	4	BJ763465	BJ763465	BJ763465
920	33	5.2	593	1	AU307628	AU307628	AU307628
921	33	5.2	593	6	CB389688	CB389688	OSTF121D1
922	33	5.2	614	8	AQ519491	AQ519491	HS_5167_B
923	33	5.2	649	8	BZ890382	BZ890382	CH240_208
c 924	33	5.2	666	1	AJ806163	AJ806163	AJ806163
c 925	33	5.2	668	5	BU398986	BU398986	603534889
926	33	5.2	668	8	AQ081878	AQ081878	RPCI11-56
c 927	33	5.2	668	8	BZ947282	BZ947282	CH240_112
c 928	33	5.2	678	8	BZ775938	BZ775938	ih96h12.g
929	33	5.2	679	9	CE766905	CE766905	tigr-gss-
c 930	33	5.2	693	8	BH997586	BH997586	oee38d10.
931	33	5.2	695	8	AQ419120	AQ419120	RPCI-11-1
932	33	5.2	698	7	CF788352	CF788352	860294 MA
c 933	33	5.2	705	9	CE168173	CE168173	tigr-gss-
934	33	5.2	712	7	CO869244	CO869244	Ep_CT_03H
935	33	5.2	715	9	AG111414	AG111414	Pan trogl
c 936	33	5.2	725	8	BZ775664	BZ775664	ih95a10.g
937	33	5.2	744	9	AG469579	AG469579	Mus muscu
938	33	5.2	748	9	CL154359	CL154359	104_339_1
939	33	5.2	839	7	CO979185	CO979185	GM89004A1
940	33	5.2	853	9	CNS06TTH	AL414987	T7 end of
c 941	33	5.2	855	2	BF208879	BF208879	601872385
c 942	33	5.2	857	4	BI183073	BI183073	UNL-P-FN-
943	33	5.2	858	7	CV280583	CV280583	WS0136.B2
944	33	5.2	880	7	CV280805	CV280805	WS0137.B2
c 945	33	5.2	889	9	CR197090	CR197090	Reverse s
946	33	5.2	895	9	CG975113	CG975113	MBEDW71TF
c 947	33	5.2	899	8	BH131485	BH131485	ENTOQ01TR
948	33	5.2	913	9	CNS06FX7	AL396977	T7 end of
949	33	5.2	937	8	BH163216	BH163216	ENTRD36TR
950	33	5.2	954	7	CV280832	CV280832	WS0137.B2
c 951	33	5.2	955	9	CNS06JAN	AL401349	T7 end of
c 952	33	5.2	1014	9	CNS0185Q	AL108920	Drosophil
953	33	5.2	1019	9	CNS02AX6	AL189123	Tetraodon
954	33	5.2	1043	8	CC220688	CC220688	CH261-78C
c 955	33	5.2	1101	9	CNS000D1	AL065414	Drosophil
956	33	5.2	1101	9	CNS0039E	AL063919	Drosophil
957	33	5.2	1106	8	CC221194	CC221194	CH261-78D
958	33	5.2	1116	4	BM465404	BM465404	AGENCOURT
959	33	5.2	1136	8	CC305772	CC305772	CH261-52L
c 960	33	5.2	3305	3	BC009162	BC009162	Mus muscu
c 961	32.8	5.1	322	1	AI299805	AI299805	qn09d02.x
c 962	32.8	5.1	376	5	BP514532	BP514532	BP514532
963	32.8	5.1	387	8	AQ145342	AQ145342	HS_3104_A
c 964	32.8	5.1	400	8	AQ010400	AQ010400	HS_2172_B
c 965	32.8	5.1	401	2	AW363212	AW363212	CM4-CT031
c 966	32.8	5.1	418	5	BY445144	BY445144	BY445144
c 967	32.8	5.1	454	2	BF706198	BF706198	280565 MA
c 968	32.8	5.1	455	8	AQ729180	AQ729180	HS_5467_B
969	32.8	5.1	457	9	CL875681	CL875681	abf07d09.
c 970	32.8	5.1	479	1	AJ676318	AJ676318	AJ676318
c 971	32.8	5.1	506	5	BP036637	BP036637	BP036637
972	32.8	5.1	511	4	BM356575	BM356575	12IV-A6 T
c 973	32.8	5.1	514	8	AQ206291	AQ206291	HS_3237_B

c 974	32.8	5.1	521	6	CD532851	CD532851	29A14 Ara
c 975	32.8	5.1	527	8	BH035642	BH035642	RPCI-24-2
c 976	32.8	5.1	535	8	AQ880267	AQ880267	HS_5043_B
977	32.8	5.1	538	2	AW068565	AW068565	cn21b10.y
c 978	32.8	5.1	542	4	BJ233620	BJ233620	BJ233620
c 979	32.8	5.1	550	2	AW907218	AW907218	EST343341
c 980	32.8	5.1	559	7	CO231205	CO231205	WS0019.B2
981	32.8	5.1	573	4	BG228598	BG228598	ux46c04.x
c 982	32.8	5.1	580	5	BQ116338	BQ116338	EST601901
983	32.8	5.1	586	8	BH358335	BH358335	CH230-34B
984	32.8	5.1	594	9	CR490046	CR490046	Medicago
985	32.8	5.1	615	5	BW027158	BW027158	BW027158
c 986	32.8	5.1	635	2	AW975453	AW975453	EST387562
987	32.8	5.1	637	4	BJ239476	BJ239476	BJ239476
988	32.8	5.1	657	6	CA126961	CA126961	SCVPLR104
989	32.8	5.1	658	8	BH289492	BH289492	CH230-62I
990	32.8	5.1	664	6	CB455776	CB455776	712949 MA
c 991	32.8	5.1	684	8	BZ035853	BZ035853	oef04h08.
c 992	32.8	5.1	719	8	CC143054	CC143054	NDL.25J19
c 993	32.8	5.1	745	5	BQ028743	BQ028743	UI-H-DF0-
c 994	32.8	5.1	747	8	BH423682	BH423682	BOHIC37TF
c 995	32.8	5.1	780	9	CC787867	CC787867	ZMMBBb015
c 996	32.8	5.1	782	5	BU271769	BU271769	603508433
997	32.8	5.1	812	9	CR085456	CR085456	Forward s
998	32.8	5.1	820	5	BX729764	BX729764	BX729764
999	32.8	5.1	823	4	BI453099	BI453099	603170084
1000	32.8	5.1	827	8	BZ439312	BZ439312	BONIY93TR
1001	32.8	5.1	830	9	CL830791	CL830791	OR_CBa005
c1002	32.8	5.1	833	8	BZ797266	BZ797266	PUFDQ73TB
c1003	32.8	5.1	835	8	BZ612534	BZ612534	WHACO53TR
1004	32.8	5.1	836	8	CC356420	CC356420	PUEKC47TD
1005	32.8	5.1	837	9	CNS016E6	AL106632	Drosophil
1006	32.8	5.1	841	8	BZ099095	BZ099095	CH230-217
c1007	32.8	5.1	841	9	CG070120	CG070120	PUFPO06TB
1008	32.8	5.1	846	9	CC610207	CC610207	OGVBD74TV
c1009	32.8	5.1	856	8	BZ262120	BZ262120	CH230-521
1010	32.8	5.1	858	9	CG219879	CG219879	OG3AV73TV
1011	32.8	5.1	865	4	BG620812	BG620812	602617734
c1012	32.8	5.1	913	8	CC379954	CC379954	PUHBO21TB
c1013	32.8	5.1	914	9	CL483138	CL483138	SAIL_377_
c1014	32.8	5.1	927	9	CG247441	CG247441	OG3AV86TH
c1015	32.8	5.1	932	4	BF970504	BF970504	602272680
1016	32.8	5.1	933	5	BX441654	BX441654	BX441654
c1017	32.8	5.1	948	8	CC001721	CC001721	PUEBD68TD
1018	32.8	5.1	951	9	CL510467	CL510467	SAIL_830_
1019	32.8	5.1	972	9	CL069021	CL069021	CH216-115
1020	32.8	5.1	978	5	BX334501	BX334501	BX334501
c1021	32.8	5.1	1019	9	CG185383	CG185383	PUKCP62TB
1022	32.8	5.1	1021	1	AL537269	AL537269	AL537269
1023	32.8	5.1	1081	4	BG244546	BG244546	602356615
1024	32.8	5.1	1101	9	CNS0039G	AL063921	Drosophil
c1025	32.8	5.1	1199	3	CR685040	CR685040	Tetraodon
c1026	32.8	5.1	1201	3	CR685733	CR685733	Tetraodon
1027	32.8	5.1	1231	9	AG288105	AG288105	Mus muscu
c1028	32.8	5.1	1305	5	BM910063	BM910063	AGENCOURT
c1029	32.6	5.1	259	7	CF542814	CF542814	S014680-0
c1030	32.6	5.1	315	2	BB226169	BB226169	BB226169
c1031	32.6	5.1	325	1	AV160528	AV160528	AV160528
1032	32.6	5.1	348	2	BE524020	BE524020	M45A5STM
c1033	32.6	5.1	383	7	CO947323	CO947323	UMC-p6mm3
c1034	32.6	5.1	414	2	BF289612	BF289612	EST454203
c1035	32.6	5.1	419	5	BY425333	BY425333	BY425333
c1036	32.6	5.1	425	7	CF542815	CF542815	S014680w-
1037	32.6	5.1	426	5	BQ107045	BQ107045	NXLV086_A
c1038	32.6	5.1	430	5	BY241290	BY241290	BY241290
c1039	32.6	5.1	456	8	BH180478	BH180478	016_L_10-
c1040	32.6	5.1	456	9	CNS07MBO	AL617430	T7 end of
1041	32.6	5.1	469	4	BJ698961	BJ698961	BJ698961
c1042	32.6	5.1	479	6	BY777480	BY777480	BY777480
c1043	32.6	5.1	480	8	BZ228305	BZ228305	CH230-305
c1044	32.6	5.1	484	5	BY056401	BY056401	BY056401
1045	32.6	5.1	494	8	BZ229864	BZ229864	CH230-488
c1046	32.6	5.1	497	5	BW580790	BW580790	BW580790
1047	32.6	5.1	500	5	BP189973	BP189973	BP189973
1048	32.6	5.1	505	5	BX100252	BX100252	BX100252
1049	32.6	5.1	521	5	BP131035	BP131035	BP131035
c1050	32.6	5.1	523	1	AI407480	AI407480	EST235769
c1051	32.6	5.1	533	6	CB078967	CB078967	hj74h07.g
1052	32.6	5.1	534	8	AQ947718	AQ947718	Sheared D
c1053	32.6	5.1	537	2	BF591940	BF591940	7o22b10.x
c1054	32.6	5.1	537	5	BU020721	BU020721	QHE28D09.
1055	32.6	5.1	544	2	BE330344	BE330344	so77e03.y
c1056	32.6	5.1	564	2	BE593278	BE593278	WS1_99_G0
1057	32.6	5.1	567	7	CN680439	CN680439	E0137E07-
c1058	32.6	5.1	569	8	AQ645910	AQ645910	RPCI93-Dp
1059	32.6	5.1	576	2	BF302155	BF302155	602033109
1060	32.6	5.1	580	7	CF472975	CF472975	RTDS1_1_C
c1061	32.6	5.1	583	7	CO981832	CO981832	GM89012B1
c1062	32.6	5.1	588	2	BB692657	BB692657	BB692657
c1063	32.6	5.1	593	8	AQ382602	AQ382602	RPCI11-13
c1064	32.6	5.1	598	6	CA855023	CA855023	PfESToac4
1065	32.6	5.1	612	6	CA450745	CA450745	UI-M-FV0-
c1066	32.6	5.1	615	8	AZ960177	AZ960177	2M0228E11
c1067	32.6	5.1	618	9	CE560710	CE560710	tigr-gss-
1068	32.6	5.1	620	7	CN681107	CN681107	E0146C07-
c1069	32.6	5.1	624	7	CV524383	CV524383	Mdlv2_401
1070	32.6	5.1	625	5	BU448080	BU448080	603767219
c1071	32.6	5.1	634	9	CR319984	CR319984	Medicago
c1072	32.6	5.1	639	1	AJ425426	AJ425426	AJ425426
c1073	32.6	5.1	641	9	CL598565	CL598565	OB__Ba006
1074	32.6	5.1	643	5	BW282653	BW282653	BW282653
c1075	32.6	5.1	652	9	CW507609	CW507609	OP__Ba000
c1076	32.6	5.1	659	5	BW153139	BW153139	BW153139
1077	32.6	5.1	661	7	CN107631	CN107631	EC2CAA30C
c1078	32.6	5.1	672	7	CN917913	CN917913	030131ABP
1079	32.6	5.1	677	5	BW248782	BW248782	BW248782
1080	32.6	5.1	703	2	BB243465	BB243465	BB243465
c1081	32.6	5.1	704	5	BU377883	BU377883	603813555
c1082	32.6	5.1	704	9	CL562137	CL562137	OB__Ba002
c1083	32.6	5.1	712	9	CL545485	CL545485	OB__Ba007
c1084	32.6	5.1	715	9	CL600389	CL600389	OB__Ba006
c1085	32.6	5.1	717	9	CL578193	CL578193	OB__Ba003
1086	32.6	5.1	719	4	BI736145	BI736145	603359311
c1087	32.6	5.1	727	9	CL832337	CL832337	OR_CBa005
1088	32.6	5.1	730	5	BU056450	BU056450	UI-M-FO0-
c1089	32.6	5.1	733	8	AQ163697	AQ163697	nbxb0002C
1090	32.6	5.1	765	9	BX232538	BX232538	Danio rer
1091	32.6	5.1	779	7	CN500338	CN500338	AGENCOURT
1092	32.6	5.1	790	5	BU554607	BU554607	AGENCOURT
1093	32.6	5.1	798	8	BZ281619	BZ281619	CH230-480
c1094	32.6	5.1	800	6	CA509830	CA509830	UI-R-FS0-
1095	32.6	5.1	803	9	CL907339	CL907339	OA_ABa000
c1096	32.6	5.1	806	8	BZ148019	BZ148019	CH230-358
c1097	32.6	5.1	807	8	BZ599751	BZ599751	WHACU28TR
c1098	32.6	5.1	823	9	CR336022	CR336022	Medicago
c1099	32.6	5.1	835	5	BW118094	BW118094	BW118094
1100	32.6	5.1	848	8	BZ825233	BZ825233	PUGAU45TD
c1101	32.6	5.1	855	8	BZ395697	BZ395697	EINAZ58TR
c1102	32.6	5.1	856	8	AZ530793	AZ530793	ENTCD02TF
1103	32.6	5.1	860	9	CNS00CJG	AL059155	Drosophil
1104	32.6	5.1	865	8	BH160322	BH160322	ENTTK32TF
c1105	32.6	5.1	867	8	AZ680304	AZ680304	ENTMS17TR
c1106	32.6	5.1	870	9	CC579126	CC579126	CH240_458
c1107	32.6	5.1	872	8	AZ683925	AZ683925	ENTIZ19TR
c1108	32.6	5.1	877	8	AZ542514	AZ542514	ENTEY19TR
1109	32.6	5.1	880	9	BX144255	BX144255	Danio rer
c1110	32.6	5.1	888	4	BG401528	BG401528	602466066
1111	32.6	5.1	890	8	BH839439	BH839439	LMCR15001
1112	32.6	5.1	897	8	BH159932	BH159932	ENTSO48TR
c1113	32.6	5.1	899	5	BU588232	BU588232	AGENCOURT
1114	32.6	5.1	922	8	AZ527771	AZ527771	ENTBK83TF
c1115	32.6	5.1	927	9	CL727603	CL727603	OR_BBa005
c1116	32.6	5.1	952	8	AZ671364	AZ671364	ENTHT40TR
1117	32.6	5.1	958	7	CF226072	CF226072	AGENCOURT
c1118	32.6	5.1	971	9	CL095976	CL095976	ISB1-27F2
1119	32.6	5.1	974	9	CL995440	CL995440	ZMMBHf000

c1120	32.6	5.1	993	9	CL090053	CL090053	ISB1-14I2	c1193	32.4	5.1	560	2	AW216826	AW216826	EST295540		
c1121	32.6	5.1	1005	8	CC213755	CC213755	CH261-76B	c1194	32.4	5.1	563	1	AL818057	AL818057	AL818057		
1122	32.6	5.1	1006	5	BM910422	BM910422	AGENCOURT	1195	32.4	5.1	565	6	CA854631	CA854631	PfESToac3		
1123	32.6	5.1	1019	9	CNS03XR5	AL265370	Tetraodon	1196	32.4	5.1	566	4	BM275446	BM275446	PfESToaa5		
c1124	32.6	5.1	1023	5	BQ964210	BQ964210	AGENCOURT	1197	32.4	5.1	567	9	AY409958	AY409958	Mus muscu		
1125	32.6	5.1	1030	9	CW000073	CW000073	ZMMBHf001	1198	32.4	5.1	572	6	CA855263	CA855263	PfESToac3		
1126	32.6	5.1	1043	9	CNS03MBE	AL250547	Tetraodon	1199	32.4	5.1	573	4	BM274679	BM274679	PfESToaa7		
c1127	32.6	5.1	1045	9	CL110512	CL110512	ISB1-53L8	1200	32.4	5.1	575	6	CA855884	CA855884	PfESToac5		
1128	32.6	5.1	1069	5	BQ072985	BQ072985	AGENCOURT	1201	32.4	5.1	579	7	CK344183	CK344183	K0850A12-		
c1129	32.6	5.1	1101	9	CNS00D0Z	AL059786	Drosophil	1202	32.4	5.1	582	4	BM275739	BM275739	PfESToaa5		
c1130	32.6	5.1	1151	1	AL563512	AL563512	AL563512	c1203	32.4	5.1	583	6	CA990879	CA990879	EST644387		
c1131	32.6	5.1	1177	8	CC211219	CC211219	CH261-74B	c1204	32.4	5.1	586	9	CE831533	CE831533	tigr-gss-		
1132	32.6	5.1	1202	3	CR687899	CR687899	Tetraodon	1205	32.4	5.1	591	6	CA854936	CA854936	PfESToac4		
1133	32.6	5.1	1235	4	BI663676	BI663676	603288387	1206	32.4	5.1	591	8	BH303511	BH303511	CH230-37D		
1134	32.6	5.1	2093	3	AK042491	AK042491	Mus muscu	1207	32.4	5.1	596	7	CF726517	CF726517	UI-M-HB0-		
1135	32.6	5.1	2726	3	AK080953	AK080953	Mus muscu	c1208	32.4	5.1	601	2	BB654705	BB654705	BB654705		
c1136	32.4	5.1	236	8	AQ907157	AQ907157	GSSTc0895	c1209	32.4	5.1	601	4	BI310308	BI310308	EST531205		
c1137	32.4	5.1	245	7	CV018664	CV018664	tbt_00316	c1210	32.4	5.1	609	4	BI310472	BI310472	EST531222		
1138	32.4	5.1	247	6	CD277775	CD277775	T139C0018	1211	32.4	5.1	609	5	BQ074777	BQ074777	fz25h07.x		
c1139	32.4	5.1	253	1	AV376393	AV376393	AV376393	c1212	32.4	5.1	610	6	CA858804	CA858804	EST636059		
c1140	32.4	5.1	270	1	AV211119	AV211119	AV211119	c1213	32.4	5.1	610	6	CA858889	CA858889	EST636144		
c1141	32.4	5.1	278	4	BI311526	BI311526	EST531327	c1214	32.4	5.1	611	5	BP534789	BP534789	BP534789		
1142	32.4	5.1	290	2	BB066089	BB066089	BB066089	1215	32.4	5.1	613	6	CA854889	CA854889	PfESToac1		
c1143	32.4	5.1	305	6	CA918548	CA918548	EST642695	c1216	32.4	5.1	613	7	CN703328	CN703328	E0474E01-		
c1144	32.4	5.1	329	5	BY131042	BY131042	BY131042	1217	32.4	5.1	615	6	CA856135	CA856135	PfESToac5		
c1145	32.4	5.1	337	7	CK899510	CK899510	SGP155424	c1218	32.4	5.1	616	4	BI311562	BI311562	EST531331		
1146	32.4	5.1	341	6	CA814926	CA814926	CA12EI201	c1219	32.4	5.1	616	8	AZ471098	AZ471098	1M0285F06		
c1147	32.4	5.1	342	5	BY074521	BY074521	BY074521	1220	32.4	5.1	620	7	CV233611	CV233611	WS01211.B		
1148	32.4	5.1	344	8	CC325733	CC325733	RRH099 Ba	1221	32.4	5.1	620	9	CE731126	CE731126	tigr-gss-		
c1149	32.4	5.1	346	5	BY034593	BY034593	BY034593	c1222	32.4	5.1	624	2	BB652581	BB652581	BB652581		
c1150	32.4	5.1	348	6	CA816839	CA816839	CA12EI201	c1223	32.4	5.1	624	4	BJ165102	BJ165102	BJ165102		
c1151	32.4	5.1	350	6	CA990161	CA990161	EST643669	c1224	32.4	5.1	626	7	CN703121	CN703121	E0471H01-		
1152	32.4	5.1	380	2	AW021655	AW021655	df26e06.y	c1225	32.4	5.1	626	7	CN703319	CN703319	E0474D03-		
c1153	32.4	5.1	387	6	CA991062	CA991062	EST644570	1226	32.4	5.1	626	8	AZ835438	AZ835438	2M0129J09		
c1154	32.4	5.1	391	4	BI492595	BI492595	df26e06.w	c1227	32.4	5.1	627	5	BQ122974	BQ122974	EST608538		
1155	32.4	5.1	408	8	AZ312446	AZ312446	1M0028I18	c1228	32.4	5.1	629	7	CN703402	CN703402	E0475C11-		
c1156	32.4	5.1	409	5	BY061085	BY061085	BY061085	c1229	32.4	5.1	630	7	CV258940	CV258940	WS0201.B2		
1157	32.4	5.1	413	5	BY239082	BY239082	BY239082	c1230	32.4	5.1	632	7	CK505049	CK505049	rswcc0_00		
1158	32.4	5.1	415	5	BY270956	BY270956	BY270956	1231	32.4	5.1	637	2	BB619213	BB619213	BB619213		
c1159	32.4	5.1	436	7	CN576797	CN576797	rc51d07.x	c1232	32.4	5.1	638	4	BI309837	BI309837	EST531158		
1160	32.4	5.1	445	2	BB840308	BB840308	BB840308	c1233	32.4	5.1	641	6	BY729862	BY729862	BY729862		
c1161	32.4	5.1	447	2	BB862013	BB862013	BB862013	c1234	32.4	5.1	642	2	BB652217	BB652217	BB652217		
c1162	32.4	5.1	447	9	CG548485	CG548485	OST150093	1235	32.4	5.1	648	2	BB615617	BB615617	BB615617		
c1163	32.4	5.1	452	1	AA682865	AA682865	zj15g12.s	c1236	32.4	5.1	652	2	BB615655	BB615655	BB615655		
c1164	32.4	5.1	452	2	BB859617	BB859617	BB859617	1237	32.4	5.1	653	6	BY737882	BY737882	BY737882		
1165	32.4	5.1	455	2	BF714363	BF714363	mab29e12.	c1238	32.4	5.1	653	7	CO116735	CO116735	GR__Eb019		
1166	32.4	5.1	457	5	BY263284	BY263284	BY263284	c1239	32.4	5.1	659	6	CA990320	CA990320	EST643828		
c1167	32.4	5.1	459	2	BE860812	BE860812	UI-M-AM1-	c1240	32.4	5.1	664	2	BB665208	BB665208	BB665208		
c1168	32.4	5.1	464	5	BY060445	BY060445	BY060445	c1241	32.4	5.1	670	2	BB663222	BB663222	BB663222		
c1169	32.4	5.1	468	8	AQ231655	AQ231655	HS_2055_A	c1242	32.4	5.1	671	5	BQ124361	BQ124361	EST609937		
c1170	32.4	5.1	470	1	AJ498609	AJ498609	AJ498609	c1243	32.4	5.1	672	2	BB629997	BB629997	BB629997		
c1171	32.4	5.1	472	6	CA990781	CA990781	EST644289	1244	32.4	5.1	674	6	BY742275	BY742275	BY742275		
c1172	32.4	5.1	474	7	CK392874	CK392874	K0851B03-	1245	32.4	5.1	674	9	CG761795	CG761795	ZMMBBb033		
c1173	32.4	5.1	475	6	CA857919	CA857919	EST635174	c1246	32.4	5.1	675	6	CA858444	CA858444	EST635699		
1174	32.4	5.1	494	7	CO884501	CO884501	BovGen_12	1247	32.4	5.1	677	8	AQ779818	AQ779818	HS_5572_B		
c1175	32.4	5.1	494	8	BH451622	BH451622	BOHEI31TF	c1248	32.4	5.1	678	9	CE260651	CE260651	tigr-gss-		
1176	32.4	5.1	496	9	CE069468	CE069468	tigr-gss-	1249	32.4	5.1	681	9	CL837877	CL837877	OR_CBa006		
c1177	32.4	5.1	502	7	CV243947	CV243947	WS0253.B2	c1250	32.4	5.1	685	2	BB645670	BB645670	BB645670		
c1178	32.4	5.1	511	2	BF479202	BF479202	L48-2860T	1251	32.4	5.1	685	7	CK743422	CK743422	atr02-13m		
c1179	32.4	5.1	516	2	AW035954	AW035954	EST282813	1252	32.4	5.1	686	1	AI822229	AI822229	L0-605T3		
1180	32.4	5.1	519	1	AL036430	AL036430	DKFZp564B	c1253	32.4	5.1	686	5	BQ124743	BQ124743	EST610319		
c1181	32.4	5.1	529	9	CL712741	CL712741	OR_BBa003	1254	32.4	5.1	687	9	BX957556	BX957556	Reverse s		
c1182	32.4	5.1	531	7	CF164867	CF164867	B0748H06-	c1255	32.4	5.1	688	6	CB504296	CB504296	ssalplnb5		
1183	32.4	5.1	547	4	BM275089	BM275089	PfESToaa7	1256	32.4	5.1	689	7	CF731945	CF731945	UI-M-GZ0-		
1184	32.4	5.1	548	4	BM274513	BM274513	PfESToaa4	1257	32.4	5.1	690	8	AZ978046	AZ978046	2M0254J09		
c1185	32.4	5.1	548	8	AQ590358	AQ590358	HS_5401_A	1258	32.4	5.1	693	9	CR208369	CR208369	Reverse s		
1186	32.4	5.1	549	7	CK344024	CK344024	K0823C06-	c1259	32.4	5.1	703	4	BI311426	BI311426	EST531317		
1187	32.4	5.1	553	5	BU878051	BU878051	V042F01 P	1260	32.4	5.1	704	9	CE156579	CE156579	tigr-gss-		
1188	32.4	5.1	555	6	CD201553	CD201553	MS1-0128T	c1261	32.4	5.1	709	9	CR499604	CR499604	Medicago		
c1189	32.4	5.1	555	7	CV252063	CV252063	WS0119.B2	c1262	32.4	5.1	719	8	CC409281	CC409281	PUEIO96TD		
1190	32.4	5.1	556	4	BM273698	BM273698	PfESToaa5	1263	32.4	5.1	720	6	CB012723	CB012723	Hc_ad_43B		
1191	32.4	5.1	556	8	AQ772808	AQ772808	HS_3045_B	c1264	32.4	5.1	720	9	CR006466	CR006466	Reverse s		
1192	32.4	5.1	557	4	BM274584	BM274584	PfESToaa4	c1265	32.4	5.1	721	2	BB615948	BB615948	BB615948		

c1266	32.4	5.1	723	2	BF723239	BF723239	mab29e12.
1267	32.4	5.1	723	7	CV233329	CV233329	WS0121.B2
c1268	32.4	5.1	724	9	AG049897	AG049897	Pan trogl
1269	32.4	5.1	728	4	BJ353046	BJ353046	BJ353046
1270	32.4	5.1	734	4	BJ404315	BJ404315	BJ404315
c1271	32.4	5.1	735	6	CA989872	CA989872	EST643380
1272	32.4	5.1	737	9	CL619466	CL619466	OR_BBa001
c1273	32.4	5.1	753	8	AQ156001	AQ156001	nbxb0002E
c1274	32.4	5.1	759	6	CA858415	CA858415	EST635670
1275	32.4	5.1	762	9	CNS01QC4	AL155924	Anopheles
c1276	32.4	5.1	772	8	BZ221260	BZ221260	CH230-259
c1277	32.4	5.1	774	4	BJ742856	BJ742856	BJ742856
1278	32.4	5.1	790	5	BP144824	BP144824	BP144824
1279	32.4	5.1	802	9	AG526975	AG526975	Mus muscu
1280	32.4	5.1	806	8	BZ655528	BZ655528	OGCAS96TM
1281	32.4	5.1	814	9	CR220781	CR220781	Reverse s
c1282	32.4	5.1	818	2	BF697814	BF697814	602129991
c1283	32.4	5.1	819	6	CA326842	CA326842	UI-M-FY0-
1284	32.4	5.1	822	2	BF178739	BF178739	601806831
1285	32.4	5.1	826	7	CV233938	CV233938	WS01212.B
1286	32.4	5.1	827	8	BH499886	BH499886	BOGQL58TR
c1287	32.4	5.1	829	9	CG791954	CG791954	ZMMBBb028
1288	32.4	5.1	874	2	BE915922	BE915922	601669193
1289	32.4	5.1	883	2	BF165079	BF165079	601778231
1290	32.4	5.1	893	9	CC502751	CC502751	CH240_341
c1291	32.4	5.1	902	9	CG247133	CG247133	OG1AJ16TV
c1292	32.4	5.1	911	5	BQ897390	BQ897390	AGENCOURT
1293	32.4	5.1	911	9	CG252689	CG252689	OGWHB22TV
1294	32.4	5.1	915	8	BZ674428	BZ674428	PUBGD27TD
c1295	32.4	5.1	922	9	CG056641	CG056641	PUJFL33TD
1296	32.4	5.1	924	9	CG247121	CG247121	OG1AJ16TH
1297	32.4	5.1	926	8	BZ561866	BZ561866	pacs2-164
c1298	32.4	5.1	950	5	BU140981	BU140981	603137602
c1299	32.4	5.1	965	8	BH153294	BH153294	ENTQV42TF
1300	32.4	5.1	1080	5	BU351195	BU351195	603527481
1301	32.4	5.1	1181	3	AK020902	AK020902	Mus muscu
1302	32.4	5.1	2856	3	AK030744	AK030744	Mus muscu
c1303	32.4	5.1	2917	3	AK086539	AK086539	Mus muscu
c1304	32.4	5.1	3507	3	AK029769	AK029769	Mus muscu
c1305	32.4	5.1	3510	3	AK031461	AK031461	Mus muscu
c1306	32.4	5.1	4060	3	AK049603	AK049603	Mus muscu
c1307	32.4	5.1	4179	3	AK053583	AK053583	Mus muscu
1308	32.2	5.0	224	5	BU531113	BU531113	AGENCOURT
1309	32.2	5.0	243	1	AA674982	AA674982	vq57g02.r
1310	32.2	5.0	243	9	CG667431	CG667431	OST460752
c1311	32.2	5.0	245	1	AI839683	AI839683	UI-M-AN0-
1312	32.2	5.0	276	1	AV014433	AV014433	AV014433
1313	32.2	5.0	280	1	AV277264	AV277264	AV277264
c1314	32.2	5.0	299	1	AI413146	AI413146	me02b05.x
c1315	32.2	5.0	299	8	BH344570	BH344570	CH230-131
1316	32.2	5.0	322	1	AV318796	AV318796	AV318796
c1317	32.2	5.0	322	2	BE983316	BE983316	UI-M-CG0p
c1318	32.2	5.0	328	6	CA311780	CA311780	UI-CF-FN0
1319	32.2	5.0	336	1	AA598029	AA598029	29278 Lam
c1320	32.2	5.0	340	2	BE945085	BE945085	UI-M-BZ0-
1321	32.2	5.0	351	1	AL865915	AL865915	AL865915
1322	32.2	5.0	356	4	BI360029	BI360029	384841 MA
c1323	32.2	5.0	365	8	AQ826248	AQ826248	HS_5555_A
1324	32.2	5.0	375	1	AA758763	AA758763	ah80d08.s
c1325	32.2	5.0	382	5	BY423772	BY423772	BY423772
1326	32.2	5.0	393	5	BU058675	BU058675	UI-M-FP0-
1327	32.2	5.0	395	8	B49231	B49231	RPCI11-5I15
1328	32.2	5.0	396	7	T21344	T21344	3352 Lambda
1329	32.2	5.0	399	9	CG530384	CG530384	OST111993
1330	32.2	5.0	403	7	Z84032	Z84032	SSZ84032 Po
c1331	32.2	5.0	407	9	CE569909	CE569909	tigr-gss-
c1332	32.2	5.0	413	1	AI842131	AI842131	UI-M-AN1-
c1333	32.2	5.0	417	8	BZ853035	BZ853035	CH240_196
c1334	32.2	5.0	418	2	AW434736	AW434736	UI-R-BJ0p
c1335	32.2	5.0	426	5	BU700664	BU700664	UI-M-DJ1-
c1336	32.2	5.0	428	2	BE994871	BE994871	UI-M-CG0p
1337	32.2	5.0	431	2	BF785899	BF785899	602112531
c1338	32.2	5.0	431	8	BZ835007	BZ835007	CH240_287
c1339	32.2	5.0	433	5	BY443128	BY443128	BY443128
c1340	32.2	5.0	434	2	AW047531	AW047531	UI-M-BH1-
1341	32.2	5.0	435	8	AQ487687	AQ487687	RPCI-11-2
1342	32.2	5.0	436	4	BM172758	BM172758	900113 Av
c1343	32.2	5.0	442	2	BF463216	BF463216	UI-M-CG0p
c1344	32.2	5.0	443	9	AJ592005	AJ592005	Arabidops
c1345	32.2	5.0	443	9	AJ592445	AJ592445	Arabidops
c1346	32.2	5.0	445	8	AQ964268	AQ964268	LERGU89TR
c1347	32.2	5.0	454	1	AI841482	AI841482	UI-M-AH0-
1348	32.2	5.0	458	7	R90496	R90496	16851 Lambd
c1349	32.2	5.0	467	5	BY488886	BY488886	BY488886
c1350	32.2	5.0	474	8	AQ186359	AQ186359	HS_3085_A
1351	32.2	5.0	478	7	R90431	R90431	16786 Lambd
c1352	32.2	5.0	485	9	CL881660	CL881660	abf50g07.
1353	32.2	5.0	489	6	CA321298	CA321298	UI-M-FV0-
1354	32.2	5.0	492	6	CA560379	CA560379	K0271F06-
1355	32.2	5.0	492	6	CA560594	CA560594	K0274F05-
c1356	32.2	5.0	496	8	B35428	B35428	HS-1029-A1-
1357	32.2	5.0	503	2	BE013353	BE013353	124670 MA
c1358	32.2	5.0	505	2	BE911875	BE911875	601662617
1359	32.2	5.0	525	8	AZ388071	AZ388071	1M0147H13
1360	32.2	5.0	531	2	BE380697	BE380697	601270695
c1361	32.2	5.0	531	8	BH285857	BH285857	CH230-39L
1362	32.2	5.0	534	8	AZ245242	AZ245242	RPCI-23-3
c1363	32.2	5.0	539	6	CD775719	CD775719	UI-M-AQ0-
1364	32.2	5.0	547	8	AQ726781	AQ726781	HS_5407_B
1365	32.2	5.0	550	7	W54606	W54606	md05c04.r1
c1366	32.2	5.0	552	8	AQ169993	AQ169993	HS_3175_B
1367	32.2	5.0	553	7	CF740778	CF740778	UI-M-HC0-
1368	32.2	5.0	554	6	CA976961	CA976961	AGENCOURT
1369	32.2	5.0	554	8	AQ038757	AQ038757	CIT-HSP-2
1370	32.2	5.0	558	2	BF577823	BF577823	602092128
c1371	32.2	5.0	563	6	CD314935	CD314935	StrPu621.
c1372	32.2	5.0	563	8	BZ532040	BZ532040	OGADQ56TC
1373	32.2	5.0	566	6	CB723469	CB723469	UI-M-GK0-
c1374	32.2	5.0	573	6	CA274096	CA274096	SCRLSD101
1375	32.2	5.0	574	7	CF750955	CF750955	UI-M-HK0-
1376	32.2	5.0	587	5	BP770790	BP770790	BP770790
1377	32.2	5.0	591	4	BI854748	BI854748	603381695
1378	32.2	5.0	591	6	CA450746	CA450746	UI-M-FV0-
c1379	32.2	5.0	593	5	BQ119844	BQ119844	EST605420
1380	32.2	5.0	594	7	CF173574	CF173574	B0925G06-
1381	32.2	5.0	601	7	CK793368	CK793368	AGENCOURT
c1382	32.2	5.0	602	4	BJ677080	BJ677080	BJ677080
c1383	32.2	5.0	610	2	BE991957	BE991957	UI-M-BZ1-
1384	32.2	5.0	616	7	CO182681	CO182681	EC23650.5
1385	32.2	5.0	616	9	CR312808	CR312808	Medicago
c1386	32.2	5.0	618	6	CA198491	CA198491	SCCCAM1C0
1387	32.2	5.0	619	5	BQ747992	BQ747992	UI-M-FA0-
1388	32.2	5.0	625	5	BQ748403	BQ748403	UI-M-FA0-
c1389	32.2	5.0	644	7	CK841315	CK841315	UI-R-BJ0p
1390	32.2	5.0	654	8	AZ843678	AZ843678	2M0142G12
1391	32.2	5.0	655	1	AL650954	AL650954	AL650954
1392	32.2	5.0	655	7	CK541591	CK541591	rswhb0_00
1393	32.2	5.0	673	5	BQ931217	BQ931217	AGENCOURT
c1394	32.2	5.0	675	5	BX254945	BX254945	BX254945
1395	32.2	5.0	676	7	CF174033	CF174033	B0932F07-
1396	32.2	5.0	676	7	CN412841	CN412841	170005325
1397	32.2	5.0	677	8	BZ325200	BZ325200	ic50c01.g
c1398	32.2	5.0	677	8	AQ624436	AQ624436	HS_2106_B
1399	32.2	5.0	680	6	CD401340	CD401340	Gm_ck2341
1400	32.2	5.0	681	4	BJ003202	BJ003202	BJ003202
1401	32.2	5.0	681	5	BU724840	BU724840	SJMBLD05
c1402	32.2	5.0	685	9	CL930299	CL930299	OA_ABa003
1403	32.2	5.0	688	7	CN857597	CN857597	000722AAA
c1404	32.2	5.0	696	7	CN970085	CN970085	17582_123
c1405	32.2	5.0	700	1	AL504376	AL504376	AL504376
1406	32.2	5.0	705	9	CG735091	CG735091	ZMMBBb029
c1407	32.2	5.0	707	6	CA074695	CA074695	SCEZAM108
1408	32.2	5.0	713	8	BZ375939	BZ375939	ie63d03.g
1409	32.2	5.0	714	5	BP169099	BP169099	BP169099
1410	32.2	5.0	744	5	BW011394	BW011394	BW011394
1411	32.2	5.0	763	9	CNS03IVO	AL246093	Tetraodon

c1412	32.2	5.0	772	8	BZ465091	BZ465091 BONAF53TR
1413	32.2	5.0	776	9	AG353237	AG353237 Mus muscu
c1414	32.2	5.0	788	7	CO878233	CO878233 BovGen_06
c1415	32.2	5.0	793	8	BZ728186	BZ728186 OGFCI95TM
1416	32.2	5.0	814	9	CNS009RZ	AL054161 Drosophil
1417	32.2	5.0	824	9	CG673362	CG673362 trs1094 t
c1418	32.2	5.0	826	5	BU245541	BU245541 603781905
1419	32.2	5.0	829	8	BZ179504	BZ179504 CH230-444
c1420	32.2	5.0	829	9	CC831110	CC831110 ZMMBBb018
1421	32.2	5.0	832	9	CC995873	CC995873 ZUACJ88TH
1422	32.2	5.0	841	8	BZ539071	BZ539071 OGADA09TC
1423	32.2	5.0	842	7	CN169157	CN169157 AGENCOURT
c1424	32.2	5.0	866	9	CG367461	CG367461 OGWBL75TH
1425	32.2	5.0	877	5	BU907959	BU907959 AGENCOURT
c1426	32.2	5.0	877	8	AZ531291	AZ531291 ENTBQ34TR
1427	32.2	5.0	888	7	CO799835	CO799835 AGENCOURT
1428	32.2	5.0	905	9	CL505217	CL505217 SAIL_747_
1429	32.2	5.0	925	7	CO063131	CO063131 est_k_bre
1430	32.2	5.0	934	9	CNS0134H	AL102395 Drosophil
1431	32.2	5.0	934	9	CG923618	CG923618 MBELC49TR
c1432	32.2	5.0	958	9	CC632418	CC632418 OGPAI69TV
1433	32.2	5.0	977	6	CA786606	CA786606 AGENCOURT
1434	32.2	5.0	999	9	CG738606	CG738606 ZMMBBc018
c1435	32.2	5.0	1080	8	CC301162	CC301162 CH261-9K2
1436	32.2	5.0	1087	8	CC285168	CC285168 CH261-34A
1437	32.2	5.0	1265	8	CC290844	CC290844 CH261-172
1438	32.2	5.0	1278	7	CK997193	CK997193 ip15f12.b
1439	32.2	5.0	1285	7	CK997269	CK997269 ip16e07.b
c1440	32.2	5.0	1310	9	AG338164	AG338164 Mus muscu
1441	32.2	5.0	1965	3	AK043080	AK043080 Mus muscu
c1442	32	5.0	108	9	CG426551	CG426551 01S0587-0
c1443	32	5.0	221	2	BB160215	BB160215
c1444	32	5.0	237	1	AV345651	AV345651 AV345651
c1445	32	5.0	277	2	BB072563	BB072563 BB072563
c1446	32	5.0	295	9	CC977260	CC977260 ZUAG181TH
1447	32	5.0	297	2	BE839487	BE839487 RC6-FN014
1448	32	5.0	328	5	BP940163	BP940163 BP940163
c1449	32	5.0	369	9	CE464580	CE464580 tigr-gss-
c1450	32	5.0	370	5	BP758272	BP758272 BP758272
1451	32	5.0	375	1	AA159946	AA159946 zo79d02.r
c1452	32	5.0	395	9	CR346039	CR346039 Medicago
c1453	32	5.0	409	4	BM752157	BM752157 K-EST0028
c1454	32	5.0	409	8	AQ422278	AQ422278 RPCI-11-1
1455	32	5.0	413	9	CG944450	CG944450 MBEEL17TF
c1456	32	5.0	415	9	CR351842	CR351842 Medicago
1457	32	5.0	430	9	CR508081	CR508081 Medicago
1458	32	5.0	430	9	CG421992	CG421992 ZMMBBc003
c1459	32	5.0	434	8	AQ363782	AQ363782 nbxb0059P
c1460	32	5.0	444	6	CA911913	CA911913 PCS00865X
1461	32	5.0	450	1	AI856886	AI856886 BSBmL3SZ1
c1462	32	5.0	461	8	AQ224147	AQ224147 HS_2003_A
1463	32	5.0	475	8	AZ121210	AZ121210 RPCI-23-1
1464	32	5.0	483	6	BY551890	BY551890 BY551890
c1465	32	5.0	496	5	BQ132615	BQ132615 fz61e02.y
1466	32	5.0	500	1	AU087417	AU087417 AU087417
c1467	32	5.0	510	8	AZ358336	AZ358336 1M0100A16
c1468	32	5.0	517	1	AA149674	AA149674 zo01e07.r
1469	32	5.0	521	8	BH685413	BH685413 BOMLU55TF
c1470	32	5.0	522	9	FR0027029	AL019858 F.rubripe
1471	32	5.0	524	6	C93209	C93209 C93209 Dict
c1472	32	5.0	526	2	AW780501	AW780501 sl71g04.y
c1473	32	5.0	528	4	BI178697	BI178697 EST519642
1474	32	5.0	530	9	CG962611	CG962611 MBEFX20TF
c1475	32	5.0	534	2	BF407502	BF407502 UI-R-BJ2-
1476	32	5.0	535	6	CB971311	CB971311 CAB10005_
1477	32	5.0	539	4	BJ124473	BJ124473 BJ124473_
1478	32	5.0	557	1	AI958896	AI958896 fd05e10.y
1479	32	5.0	571	9	CR493996	CR493996 Medicago
1480	32	5.0	572	6	CA514703	CA514703 KS09030A0
c1481	32	5.0	576	8	BH399600	BH399600 AG-ND-124
1482	32	5.0	579	8	AZ611857	AZ611857 1M0438N23
1483	32	5.0	583	5	BU498453	BU498453 PfESTOab9
c1484	32	5.0	589	9	AG199788	AG199788 Pan trogl
c1485	32	5.0	598	4	BM496402	BM496402 IpCGBr2_1
c1486	32	5.0	599	9	CR807408	CR807408 GR0AAA3DB
1487	32	5.0	600	7	CK689714	CK689714 ZF101-P00
c1488	32	5.0	607	9	CR349007	CR349007 Medicago
c1489	32	5.0	610	8	BZ906757	BZ906757 CH240_29N
1490	32	5.0	615	8	AZ162140	AZ162140 SP_0071_A
1491	32	5.0	618	9	CR513056	CR513056 Medicago
1492	32	5.0	620	4	BJ653230	BJ653230 BJ653230
c1493	32	5.0	622	8	B52372	B52372 CIT-HSP-200
1494	32	5.0	627	9	CR510496	CR510496 Medicago
c1495	32	5.0	632	4	BM496541	BM496541 IpCGBr2_3
1496	32	5.0	643	9	CR506233	CR506233 Medicago
1497	32	5.0	644	6	CB251704	CB251704 1030 Aede
1498	32	5.0	646	2	BB632347	BB632347 BB632347
1499	32	5.0	653	8	AZ696705	AZ696705 RPCI-23-2
1500	32	5.0	658	9	CL909497	CL909497 OA_ABa000

ALIGNMENTS

RESULT 1
AY399636
LOCUS AY399636 669 bp DNA linear GSS 12-DEC-2003
DEFINITION Homo sapiens HCM0290 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY399636
VERSION AY399636.1 GI:39755625
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 669)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 669)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES Location/Qualifiers
source 1. .669
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
gene <1. .>669
/locus_tag="HCM0290"
ORIGIN

Query Match 98.3%; Score 628; DB 9; Length 669;
Best Local Similarity 99.8%; Pred. No. 1.2e-174;
Matches 639; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
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Db          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
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Db         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
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Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
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Db        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
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Db        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
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Db        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
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Db        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
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Db        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
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Db        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
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Db        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGA 639
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Db        601 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGA 640
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RESULT 2
BI760941

LOCUS	BI760941 870 bp mRNA linear EST 25-SEP-2001
DEFINITION	603043142F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5183554 5', mRNA sequence.
ACCESSION	BI760941
VERSION	BI760941.1 GI:15752519
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 870)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM11458 row: c column: 11 High quality sequence stop: 844.

FEATURES	Location/Qualifiers
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	/mol_type="mRNA"
	/db_xref="taxon:9606"
	/clone="IMAGE:5183554"
	/lab_host="DH10B"
	/clone_lib="NIH_MGC_116"
	/note="Organ: pooled colon, kidney, stomach; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 97.7%; Score 624; DB 4; Length 870;
Best Local Similarity 99.8%; Pred. No. 2e-173;
Matches 635; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Qy          5 TGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGTGCAG 64
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Db         12 TGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGTGCAG 71

Qy         65 AAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATATGCCT 124
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Db         72 AAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATATGCCT 131

Qy        125 GGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAAGTTC 184
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Db        132 GGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAAGTTC 191

Qy        185 CCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGGGTAT 244
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Db        192 CCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGGGTAT 251

Qy        245 CATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAGGTGC 304
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Db        252 CATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAGGTGC 311

Qy        305 AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAA 364
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Db        312 AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAA 371

Qy        365 CTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCA 424
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Db        372 CTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCA 431

Qy        425 TCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGA 484
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Db        432 TCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGA 491

Qy        485 TTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGATGACG 544
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Db        492 TTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGATGACG 551

Qy        545 CTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCCCTGG 604
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Db        552 CTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCCCTGG 611

Qy        605 ACATGAAGGG-GGGCATATTAATGATGCCTTCATGA 639
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Db        612 ACATGAAGGGAGGGCATATTAATGATGCCTTCATGA 647
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RESULT 3
BG400845

LOCUS	BG400845 792 bp mRNA linear EST 12-MAR-2001
DEFINITION	602464068F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4592296 5', mRNA sequence.
ACCESSION	BG400845
VERSION	BG400845.1 GI:13294293
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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REFERENCE   1  (bases 1 to 792)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
             cDNA Library Preparation: CLONTECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1330  row: g  column: 17
            High quality sequence stop: 784.
FEATURES             Location/Qualifiers
     source          1. .792
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4592296"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_75"
                     /note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and
                     3' adaptors were used in cloning as follows: 5' adaptor
                     sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).  Average insert size 1.65
                     kb (range 0.5-4.0 kb). 15/15 colonies contained  inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech  Laboratories (Palo Alto,
                     CA). Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             97.4%;  Score 622.4;  DB 4;  Length 792;
  Best Local Similarity   99.4%;  Pred. No. 5.9e-173;
  Matches  636;  Conservative    0;  Mismatches    1;  Indels    3;  Gaps    1;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
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Db         32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
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Db         92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 271

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 331

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 451

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
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Db        452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        512 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 571

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        572 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 631

Qy        601 CTGGACATGAAGGG---GGGCATATTAATGATGCCTTCAT 637
              |||||||||||||   || ||||||||||||||||||||
Db        632 CTGGACATGAAGGGAGCGGCCATATTAATGATGCCTTCAT 671


RESULT 4
CB139945
LOCUS       CB139945                663 bp    mRNA    linear   EST 29-JAN-2003
DEFINITION  K-EST0193043 L4SNU368s1 Homo sapiens cDNA clone L4SNU368s1-5-H10
            5', mRNA sequence.
ACCESSION   CB139945
VERSION     CB139945.1  GI:28113403
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 663)
  AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
  TITLE     21C Frontier Korean EST Project 2001
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 5  row: H  column: 10
            High quality sequence stop: 663.
FEATURES             Location/Qualifiers
     source          1. .663
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="L4SNU368s1-5-H10"
                     /sex="M"
                     /tissue_type="Liver"
                     /cell_type="Polygonal"
                     /cell_line="SNU-368"
                     /lab_host="Top10F'"
                     /clone_lib="L4SNU368s1"
                     /note="Organ: Liver; Vector: pCNS-D2; Site_1: EcoRI;
                     Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
                     bacterial alkaline phosphatase (BAP) and then decapped
                     with tabacco acid pyrophosphatase (TAP). The decapped
                     intact mRNA was ligated with DNA-RNA linker including
                     EcoRI site by treatment of T4 RNA ligase and the first
                     strand cDNA was synthesized from oligo dT-selected mRNA by
                     priming with dT-tailed vector. The dT-tailed vector was
                     adjusted to have about 60nt. The cDNA vector was
                     circularized with E. coli DNA ligase after digestion of
                     EcoRI which site is also included in vector. An RNA strand
                     converted to a DNA strand by Okayama-Berg method. The
                     obtained cDNA vectors were used for transformation of
                     competent cells E. coli Top10F' by electroporation method.
                     The cDNA libraries constructed by this method are
                     full-length enriched cDNA library. After analyzing and
                     sequencing about 2,000 - 3,000 colonies in original cDNA
                     library, the abundant cDNAs were selected and amplified by
                     PCR reaction using vector region primer including T7
                     promotor as 5' primer and N(dT)14 as 3' primer. The PCR
                     products were used as template for synthesis of
                     biotinylated single stranded RNA by in vitro transcription
                     reaction. The synthesized RNA probes were hybridized with
```

antisense single stranded cDNAs prepared from original liberary and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformaion of the remaining DNA into competent cells E. coli Top10F' with electroporation method."

ORIGIN

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  Query Match             96.9%;  Score 619.4;  DB 6;  Length 663;
  Best Local Similarity   99.7%;  Pred. No. 4.3e-172;
  Matches  631;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
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Db         31 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 90

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 150

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 210

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 270

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 330

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 390

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 450

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 510

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 570

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        571 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 630

Qy        601 CTGGACATG-AAGGGGGGCATATTAATGATGCC 632
              ||||||||| |||| ||||||||||||||||||
Db        631 CTGGACATGAAAGGAGGGCATATTAATGATGCC 663
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RESULT 5
CV028808

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LOCUS       CV028808                629 bp    mRNA    linear   EST 20-AUG-2004
DEFINITION  7418 Full Length cDNA from the Mammalian Gene Collection Homo
            sapiens cDNA 5' similar to BC015099, mRNA sequence.
ACCESSION   CV028808
VERSION     CV028808.1  GI:51486911
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 629)
  AUTHORS   Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S.,
            Dricot,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O.,
            Clingingsmith,T.R., Hartley,J.L., Esposito,D., Cheo,D., Moore,T.,
            Simmons,B., Sequerra,R., Bosak,S., Doucette-Stamm,L., Le Peuch,C.,
            Vandenhaute,J., Cusick,M.E., Albala,J.S., Hill,D.E. and Vidal,M.
  TITLE     Human ORFeome Version 1.1: a Platform for Reverse Proteomics
  JOURNAL   Genome Res. (2004) In press
COMMENT     Contact: Vidal M
            Marc Vidal Laboratory
            Dana Farber Cancer Institute
            1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
            Tel: 617 632 5180
            Fax: 617 632 5739
            Email: Marc_Vidal@dfci.harvard.edu
            ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF
            results from a PCR reaction using an MGC full-length cDNA as
            template DNA and ORF specific primers
            PCR PRimers
            FORWARD: ATGTTGTGGCTGCTCTTTTTTCT
            BACKWARD: CAGAGAGGGGTGAGCCTCTCAT
            Insert Length: 629    Std Error: 50.00
            Plate: 11020  row: 02  column: A
            Seq primer: ACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAAC
            High quality sequence start: 99
            High quality sequence stop: 628
            POLYA=No.
FEATURES              Location/Qualifiers
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                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /tissue_type="mixed"
                      /clone_lib="Full Length cDNA from the Mammalian Gene
                      Collection"
                      /note="Vector: mixed; The ORFs were PCR amplified from the
                      MGC (Mammalian Gene Collection) as of April 2004 and
                      cloned by recombinational Gateway cloning into pDONR223
                      Donor vector. Reference : MGC (Mammalian Gene Collection)
                      Program Team, Generation and Initial Analysis of more than
                      15,000 Full-Length Human and Mouse cDNA Sequences. PNAS,
                      2002, 99(26), 16899-16903"
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ORIGIN

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  Query Match             96.2%;  Score 615;  DB 7;  Length 629;
  Best Local Similarity   99.5%;  Pred. No. 8.5e-171;
  Matches  626;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
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Db        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGANAATGGCATCCCCTCTGATCCC 600

Qy        601 CTGGACATGAAGGG-GGGCATATTAATGA 628
              ||||||||||||||| || ||||||||||
Db        601 CTGGACATGAAGGGAGGNCATATTAATGA 629


RESULT 6
CB137859
LOCUS       CB137859                639 bp    mRNA    linear   EST 29-JAN-2003
DEFINITION  K-EST0190636 L4SNU368s1 Homo sapiens cDNA clone L4SNU368s1-11-F08
            5', mRNA sequence.
ACCESSION   CB137859
VERSION     CB137859.1  GI:28108763
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 639)
  AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
  TITLE     21C Frontier Korean EST Project 2001
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 11  row: F  column: 08
            High quality sequence stop: 639.
FEATURES             Location/Qualifiers
     source          1. .639
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="L4SNU368s1-11-F08"
                     /sex="M"
                     /tissue_type="Liver"
                     /cell_type="Polygonal"
                     /cell_line="SNU-368"
                     /lab_host="Top10F'"
                     /clone_lib="L4SNU368s1"
                     /note="Organ: Liver; Vector: pCNS-D2; Site_1: EcoRI;
                     Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
                     bacterial alkaline phosphatase (BAP) and then decapped
                     with tabacco acid pyrophosphatase (TAP). The decapped
                     intact mRNA was ligated with DNA-RNA linker including
                     EcoRI site by treatment of T4 RNA ligase and the first
                     strand cDNA was synthesized from oligo dT-selected mRNA by
                     priming with dT-tailed vector. The dT-tailed vector was
                     adjusted to have about 60nt. The cDNA vector was
                     circularized with E. coli DNA ligase after digestion of
                     EcoRI which site is also included in vector. An RNA strand
                     converted to a DNA strand by Okayama-Berg method. The
                     obtained cDNA vectors were used for transformation of
                     competent cells E. coli Top10F' by electroporation method.
                     The cDNA libraries constructed by this method are
                     full-length enriched cDNA library. After analyzing and
                     sequencing about 2,000 - 3,000 colonies in original cDNA
                     library, the abundant cDNAs were selected and amplified by
                     PCR reaction using vector region primer including T7
                     promotor as 5' primer and N(dT)14 as 3' primer. The PCR
                     products were used as template for synthesis of
                     biotinylated single stranded RNA by in vitro transcription
                     reaction. The synthesized RNA probes were hybridized with
                     antisense single stranded cDNAs prepared from original
                     liberary and incubated with avidin-gel. After removing
                     DNA-RNA hybrids by centrifuge, the subtracted cDNA
                     libraries were constructed by transformaion of the
                     remaining DNA into competent cells E. coli Top10F' with
                     electroporation method."
ORIGIN

  Query Match             95.3%;  Score 609;  DB 6;  Length 639;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-169;
  Matches  609;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 90

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 150

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 210

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
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Db        211 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 270

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
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Db        271 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 330

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 390

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 450

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 510

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 570

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        571 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 630

Qy        601 CTGGACATG 609
              |||||||||
Db        631 CTGGACATG 639


RESULT 7
BG429618
LOCUS       BG429618                866 bp    mRNA    linear   EST 14-MAR-2001
DEFINITION  602501304F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4614937 5',
            mRNA sequence.
ACCESSION   BG429618
VERSION     BG429618.1  GI:13336124
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 866)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
             cDNA Library Preparation: CLONTECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1367  row: g  column: 02
            High quality sequence stop: 707.
FEATURES             Location/Qualifiers
     source          1. .866
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4614937"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_75"
                     /note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and
                     3' adaptors were used in cloning as follows: 5' adaptor
                     sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).  Average insert size 1.65
                     kb (range 0.5-4.0 kb). 15/15 colonies contained  inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech  Laboratories (Palo Alto,
                     CA). Note: this is a NIH_MGC Library."
ORIGIN

  Query Match           94.9%;  Score 606.2;  DB 4;  Length 866;
  Best Local Similarity   99.1%;  Pred. No. 3.8e-168;
  Matches  631;  Conservative    0;  Mismatches    3;  Indels    3;  Gaps    2;

Qy          5 TGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGTGCAG 64
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         35 TGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGTGCAG 94

Qy         65 AAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATATGCCT 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         95 AAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATATGCCT 154

Qy        125 GGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAAGTTC 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        155 GGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAAGTTC 214

Qy        185 CCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGGGTAT 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        215 CCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGGGTAT 274

Qy        245 CATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAGGTGC 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        275 CATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAGGTGC 334

Qy        305 AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        335 AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAA 394

Qy        365 CTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCA 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        395 CTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCA 454

Qy        425 TCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        455 TCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGA 514

Qy        485 TTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGATGACG 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        515 TTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGATGACG 574

Qy        545 CTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCCCTGG 604
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db        575 CTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGAT-CCCTGG 633

Qy        605 ACATGAAGGG--GGGCATATTAATGATGCCTTCATGA 639
              |||||| |||  |||||||||| ||||| ||||||||
Db        634 ACATGACGGGCAGGGCATATTATTGATGGCTTCATGA 670


RESULT 8
BG427247
LOCUS       BG427247                855 bp    mRNA    linear   EST 14-MAR-2001
DEFINITION  602494304F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4608048 5',
            mRNA sequence.
ACCESSION   BG427247
VERSION     BG427247.1  GI:13333753
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 855)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
             cDNA Library Preparation: CLONTECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1349  row: h  column: 01
            High quality sequence stop: 735.
FEATURES             Location/Qualifiers
     source          1. .855
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:4608048"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_75"
                     /note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and
                     3' adaptors were used in cloning as follows: 5' adaptor
                     sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).  Average insert size 1.65
                     kb (range 0.5-4.0 kb). 15/15 colonies contained  inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech  Laboratories (Palo Alto,
                     CA). Note: this is a NIH_MGC Library."
ORIGIN

  Query Match           94.7%;  Score 605;  DB 4;  Length 855;
  Best Local Similarity   99.5%;  Pred. No. 8.7e-168;
  Matches  638;  Conservative    0;  Mismatches    0;  Indels    3;  Gaps    3;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         33 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 92

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 152

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        153 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 212

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 272

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        273 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 332

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        333 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 392

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 452

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 512

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAAC-AAAGAACCATCTGAAGTGGA 539
              |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        513 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAAGAACCATCTGAAGTGGA 572

Qy        540 TGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCC 599
              |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        573 TGACGCTGAAGAT-AGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCC 631

Qy        600 CCTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGA 639
              ||||||||||||||| ||||||||||||||||||||||||
Db        632 CCTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGA 672
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RESULT 9
BG429705
LOCUS       BG429705                804 bp    mRNA    linear   EST 14-MAR-2001
DEFINITION  602493709F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4607499 5',
            mRNA sequence.
ACCESSION   BG429705
VERSION     BG429705.1  GI:13336211
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 804)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
             cDNA Library Preparation: CLONTECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1348  row: a  column: 04
            High quality sequence stop: 731.
FEATURES             Location/Qualifiers
     source          1. .804
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4607499"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_75"
                     /note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and
                     3' adaptors were used in cloning as follows: 5' adaptor
                     sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).  Average insert size 1.65
                     kb (range 0.5-4.0 kb). 15/15 colonies contained  inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech  Laboratories (Palo Alto,
                     CA). Note: this is a NIH_MGC Library."
ORIGIN

  Query Match            94.0%;  Score 600.8;  DB 4;  Length 804;
  Best Local Similarity  97.2%;  Pred. No. 1.5e-166;
  Matches  622;  Conservative    0;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 271

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 331

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 451

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAG-AAAGAACAAAGAACCATCTGAAGTGGA 539
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db        512 CTGATTTTATCAGGGATCTGGCAACGTAGAAGCAAAGAACAAAGAACCATCTGAAGTGGA 571

Qy        540 TGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCC 599
              |||||||||||||||||||||||||||||||||||||| ||  |    ||||||||||||
Db        572 TGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGACAAATGGCATCCCTCTGATCC 631

Qy        600 CCTGGACATGAAGGGGGGCATATTAATGATGCCTTCATGA 639
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Db        632 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGA 671
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RESULT 10
BG429174
LOCUS       BG429174                780 bp    mRNA    linear   EST 14-MAR-2001
DEFINITION  602498032F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4612062 5',
            mRNA sequence.
ACCESSION   BG429174
VERSION     BG429174.1  GI:13335680
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 780)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
```

```
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
             cDNA Library Preparation: CLONTECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1359  row: o  column: 07
            High quality sequence stop: 718.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4612062"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_75"
                     /note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and
                     3' adaptors were used in cloning as follows: 5' adaptor
                     sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).  Average insert size 1.65
                     kb (range 0.5-4.0 kb). 15/15 colonies contained  inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech  Laboratories (Palo Alto,
                     CA). Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             93.7%;  Score 599;  DB 4;  Length 780;
  Best Local Similarity   99.8%;  Pred. No. 5.1e-166;
  Matches  610;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy         30 TGCCATTCATGCTGAACTCTGTCAACCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAG 89
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TGCCATTCATGCTGAACTCTGTCAACCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAG 60

Qy         90 TATCAGAACAGCTCTGGGAGATAAAGCATATGCCTGGGATACCAATGAAGAATACCTCTT 149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TATCAGAACAGCTCTGGGAGATAAAGCATATGCCTGGGATACCAATGAAGAATACCTCTT 120

Qy        150 CAAAGCGATGGTAGCTTTCTCCATGAGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTC 209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CAAAGCGATGGTAGCTTTCTCCATGAGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTC 180

Qy        210 CCATGTCCTACTTTGCAATGTAACCCAGAGGGTATCATTCTGGTTTGTGGTTACAGACCC 269
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCATGTCCTACTTTGCAATGTAACCCAGAGGGTATCATTCTGGTTTGTGGTTACAGACCC 240

Qy        270 TTCAAAAAATCACACCCTTCCTGCTGTTGAGGTGCAATCAGCCATAAGAATGAACAAGAA 329
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TTCAAAAAATCACACCCTTCCTGCTGTTGAGGTGCAATCAGCCATAAGAATGAACAAGAA 300

Qy        330 CCGGATCAACAATGCCTTCTTTCTAAATGACCAAACTCTGGAATTTTTAAAAATCCCTTC 389
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCGGATCAACAATGCCTTCTTTCTAAATGACCAAACTCTGGAATTTTTAAAAATCCCTTC 360

Qy        390 CACACTTGCACCACCCATGGACCCATCTGTGCCCATCTGGATTATTATATTTGGTGTGAT 449
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CACACTTGCACCACCCATGGACCCATCTGTGCCCATCTGGATTATTATATTTGGTGTGAT 420

Qy        450 ATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTATCAGGGATCTGGCAACGTAG 509
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Db        421 ATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTATCAGGGATCTGGCAACGTAG 480

Qy        510 AAGAAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGATAAGTGTGAAAACATGAT 569
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Db        481 AAGAAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGATAAGTGTGAAAACATGAT 540

Qy        570 CACAATTGAAAATGGCATCCCCTCTGATCCCCTGGACATGAAGGG-GGGCATATTAATGA 628
              ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        541 CACAATTGAAAATGGCATCCCCTCTGATCCCCTGGACATGAAGGGAGGGCATATTAATGA 600

Qy        629 TGCCTTCATGA 639
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Db        601 TGCCTTCATGA 611


RESULT 11
BG400319
LOCUS       BG400319                 791 bp    mRNA    linear   EST 12-MAR-2001
DEFINITION  602464526F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4592575 5',
            mRNA sequence.
ACCESSION   BG400319
VERSION     BG400319.1  GI:13293767
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 791)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
             cDNA Library Preparation: CLONTECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1331  row: c  column: 08
            High quality sequence stop: 711.
FEATURES             Location/Qualifiers
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                     /clone="IMAGE:4592575"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_75"
                     /note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and
                     3' adaptors were used in cloning as follows: 5' adaptor
                     sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).  Average insert size 1.65
                     kb (range 0.5-4.0 kb). 15/15 colonies contained  inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech  Laboratories (Palo Alto,
                     CA). Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             93.0%;  Score 594;  DB 4;  Length 791;
  Best Local Similarity   99.4%;  Pred. No. 1.5e-164;
  Matches  638;  Conservative    0;  Mismatches    0;  Indels    4;  Gaps    4;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 90

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 150

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 210

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        211 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 270

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 330

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 390

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 450

Qy        421 CCCATCTGGATTATTATATTT-GGTGTGATATTTTGCATCATCATAGTTGCAATTGCACT 479
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        451 CCCATCTGGATTATTATATTTCGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACT 510

Qy        480 ACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGA 539
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 ACTGA-TTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGA 569

Qy        540 TGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCC 599
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        570 TGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCC 629

Qy        600 CCTGGACATGAAGGG-GGGCATATTAA-TGATGCCTTCATGA 639
              ||||||||||||||| |||||||||| ||||||||||||||
Db        630 CCTGGACATGAAGGGAGGGCATATTAAGTGATGCCTTCATGA 671
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RESULT 12
BG430955
LOCUS       BG430955                850 bp    mRNA    linear   EST 14-MAR-2001
DEFINITION  602500255F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4613965 5',
            mRNA sequence.
ACCESSION   BG430955
VERSION     BG430955.1  GI:13337461
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 850)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
             cDNA Library Preparation: CLONTECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1364  row: n  column: 14
            High quality sequence stop: 681.
FEATURES             Location/Qualifiers
     source          1. .850
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4613965"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_75"
                     /note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and
                     3' adaptors were used in cloning as follows: 5' adaptor
                     sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).  Average insert size 1.65
                     kb (range 0.5-4.0 kb). 15/15 colonies contained  inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech  Laboratories (Palo Alto,
                     CA). Note: this is a NIH_MGC Library."
ORIGIN
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  Query Match             92.7%;  Score 592.6;  DB 4;  Length 850;
  Best Local Similarity   97.5%;  Pred. No. 4.1e-164;
  Matches  623;  Conservative    0;  Mismatches   14;  Indels    2;  Gaps    2;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         36 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 95

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 155

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 215

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 275

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        276 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 335

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 395

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 455

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 515

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 575

Qy        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600
              |||||||||||| |||||||||||||||||||||||||||||  | || ||||||||||||
Db        576 GACGCTGAAGAT-AGTGTGAAAACATGATCACAATTGAAAAATGGAT-CCCTCTGATCCC 633

Qy        601 CTGGACATGAAGGGGGGCATATTAATGATGCCTTCATGA 639
                  |     | || |||||||||| ||||||||||||||
Db        634 TGGACATGAAGGGAGGGCATATTACTGATGCCTTCATGA 672
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RESULT 13
BG399473
LOCUS       BG399473                808 bp    mRNA    linear   EST 12-MAR-2001
DEFINITION  602441206F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4557073 5',
            mRNA sequence.
ACCESSION   BG399473
VERSION     BG399473.1  GI:13293021
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 808)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
```

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            cDNA Library Preparation: CLONTECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLCM1260  row: l  column: 02
           High quality sequence stop: 637.
FEATURES             Location/Qualifiers
     source          1. .808
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4557073"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_75"
                     /note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and
                     3' adaptors were used in cloning as follows: 5' adaptor
                     sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).  Average insert size 1.65
                     kb (range 0.5-4.0 kb). 15/15 colonies contained  inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech  Laboratories (Palo Alto,
                     CA). Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             91.7%;  Score 586;  DB 4;  Length 808;
  Best Local Similarity   96.5%;  Pred. No. 3.7e-162;
  Matches  610;  Conservative    0;  Mismatches   20;  Indels    2;  Gaps    1;

Qy          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91

Qy         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 271

Qy        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 331

Qy        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 451

Qy        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        512 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACCAAGAACCATCTGAAGTGGAT 571

Qy        541 GACGCTGAAGATAAGT--GTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATC 598
              ||||||||||||||||   |||||||||||| ||||   ||||||  | ||||||||||
Db        572 GACGCTGAAGATAAGTTGTTGAAAACATGATCCCAATCTGAAATGGGCTTCCCTCTGATC 631

Qy        599 CCCTGGACATGAAGGGGGGCATATTAATGATG 630
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              |||||||| ||||| || |    |   | |||
Db        632 CCCTGGACCTGAAGAGGAGGGCCTATTTAATG 663


RESULT 14
BG399402
LOCUS       BG399402                 736 bp    mRNA    linear   EST 12-MAR-2001
DEFINITION  602441161F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4557015 5',
            mRNA sequence.
ACCESSION   BG399402
VERSION     BG399402.1  GI:13292850
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 736)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
             cDNA Library Preparation: CLONTECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1260  row: i  column: 16
            High quality sequence stop: 661.
FEATURES             Location/Qualifiers
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                     /clone="IMAGE:4557015"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_75"
                     /note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and
                     3' adaptors were used in cloning as follows: 5' adaptor
                     sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).  Average insert size 1.65
                     kb (range 0.5-4.0 kb). 15/15 colonies contained  inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech  Laboratories (Palo Alto,
                     CA). Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             91.7%;  Score 585.8;  DB 4;  Length 736;
  Best Local Similarity   99.2%;  Pred. No. 4.1e-162;
  Matches  620;  Conservative    0;  Mismatches    2;  Indels    3;  Gaps    3;

Qy         12 GCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGTGCAGAAAATGC 71
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 GCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGTGCAGAAAATGC 62

Qy         72 TTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATATGCCTGGGATAC 131
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 TTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATATGCCTGGGATAC 122

Qy        132 CAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAAGTTCCCAACAG 191
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 CAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAAGTTCCCAACAG 182

Qy        192 AGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGGGTATCATTCTG 251
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 AGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGGGTATCATTCTG 242

Qy        252 GTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAGGTGCAATCAGC 311
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        243 GTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAGGTGCAATCAGC 302

Qy        312 CATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAACTCTGGA 371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 CATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAACTCTGGA 362

Qy        372 ATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCATCTGGAT 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 ATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCATCTGGAT 422

Qy        432 TATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTATC 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 TATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTATC 482

Qy        492 AGGGATCTGGCAACGTAGAAG-AAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAG 550
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        483 AGGGATCTGGCAACGTAGAAGAAAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAG 542

Qy        551 ATAAGTGTGAAAACATGATCACAA-TTGAAAATGGCATCCCCTCTGATCCCCTGGACATG 609
              |||||||||||||||||||||||| |||||||||||||||||||| ||||||||||||
Db        543 ATAAGTGTGAAAACATGATCACAATTTGAAAATGGCATCCCCTCTGAT-CCCTGGACATG 601

Qy        610 AAGGGGGGCATATTAATGATGCCTT 634
              | || ||||||||||||||||||||
Db        602 AGGGAGGGCATATTAATGATGCCTT 626
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RESULT 15
BG427745
LOCUS       BG427745                677 bp    mRNA    linear   EST 14-MAR-2001
DEFINITION  602497114F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4610834 5',
            mRNA sequence.
ACCESSION   BG427745
VERSION     BG427745.1  GI:13334251
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 677)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
            cDNA Library Preparation: CLONTECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1356  row: l  column: 03
            High quality sequence stop: 677.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4610834"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_75"
                     /note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and
                     3' adaptors were used in cloning as follows: 5' adaptor
                     sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).  Average insert size 1.65
                     kb (range 0.5-4.0 kb). 15/15 colonies contained  inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech  Laboratories (Palo Alto,
                     CA). Note: this is a NIH_MGC Library."
ORIGIN
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  Query Match             91.6%;  Score 585.4;  DB 4;  Length 677;
  Best Local Similarity   99.1%;  Pred. No. 5.2e-162;
  Matches  630;  Conservative    0;  Mismatches    2;  Indels    4;  Gaps    4;

Qy          5 TGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGTGCAG 64
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         36 TGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGTGCAG 95

Qy         65 AAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATATGCCT 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 AAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATATGCCT 155

Qy        125 GGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAAGTTC 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 GGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAAGTTC 215

Qy        185 CCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGGGTAT 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 CCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGGGTAT 275

Qy        245 CATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAGGTGC 304
              ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        276 CATTCTGGTNTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAGGTGC 335

Qy        305 AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAA 395

Qy        365 CTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCA 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 CTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCA 455

Qy        425 TCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGA 484
              |||||||||||||||| ||||||||| ||||||||||||||||||||||||||||||||
Db        456 TCTGGATTATTATATTCGGTGTGATA-TTTGCATCATCATAGTTGCAATTGCACTACTGA 514

Qy        485 TTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGATGACG 544
              |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db        515 TTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAA-CATCTGAAGTGGATGACG 573

Qy        545 CTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCCCTGG 604
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        574 CTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGG-ATCCCCTCTGATCCCCTGG 632

Qy        605 ACATGAAGGG-GGGCATATTAATGATGCCTTCATGA 639
              |||||||||| ||||||||||||||||||||||||||
Db        633 ACATGAAGGGAGGGCATATTAATGATGCCTTCATGA 668
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Search completed: February 24, 2005, 22:28:53
Job time : 2179.33 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 24, 2005, 19:24:31 ; Search time 5859.34 Seconds
(without alignments)
11131.073 Million cell updates/sec

Title: US-09-989-724-386
Perfect score: 1346
Sequence: 1 gaaagaatgttgtggctgct.....aaaaaaaaaaaaaaaaaaa 1346

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1346	100.0	1346	6	AR252633	AR252633 Sequence
2	1346	100.0	1346	6	AR528692	AR528692 Sequence
3	1346	100.0	1346	6	AX403499	AX403499 Sequence
4	1346	100.0	1346	6	AX464348	AX464348 Sequence
5	1346	100.0	1346	9	AY359060	AY359060 Homo sapi
6	1328.6	98.7	1605	9	BC014317	BC014317 Homo sapi
7	1325.4	98.5	1377	9	BC050606	BC050606 Homo sapi
8	1325.4	98.5	1440	9	BC015099	BC015099 Homo sapi
9	1324.6	98.4	1447	6	BD205644	BD205644 97 human
10	1321.8	98.2	1401	6	BD083420	BD083420 Secreted
11	1309.4	97.3	1347	6	AX083392	AX083392 Sequence
12	1307.8	97.2	1345	9	AF229179	AF229179 Homo sapi
13	1305	97.0	1356	6	BD135300	BD135300 110 human
14	845.2	62.8	862	6	BD270445	BD270445 Genes ass
15	799.4	59.4	848	6	AR177334	AR177334 Sequence
16	799.4	59.4	848	6	BD139270	BD139270 Extended
17	799.4	59.4	848	6	BD203799	BD203799 5'EST and
18	799.4	59.4	848	6	BD247957	BD247957 5' ESTs f
19	799.4	59.4	848	6	CQ771919	CQ771919 Sequence
20	799.4	59.4	848	6	AR340701	AR340701 Sequence
21	799.4	59.4	848	6	AR412373	AR412373 Sequence
22	799.4	59.4	848	6	AX884142	AX884142 Sequence
23	799.4	59.4	848	6	AX939008	AX939008 Sequence
24	799.4	59.4	848	6	AX968599	AX968599 Sequence
25	799.4	59.4	848	6	AX969202	AX969202 Sequence
26	799.4	59.4	848	6	BD023757	BD023757 Sequence
27	799.4	59.4	848	6	BD073618	BD073618 5'EST of
28	799.4	59.4	848	6	BD075896	BD075896 5' EST of
29	799.4	59.4	848	6	BD076074	BD076074 5' EST of
30	799.4	59.4	848	6	BD076775	BD076775 5' EST of
31	799.4	59.4	848	6	BD077436	BD077436 5'EST of
32	799.4	59.4	848	6	BD077737	BD077737 5'EST of
33	799.4	59.4	848	6	BD085880	BD085880 Elongatio
34	799.4	59.4	848	6	BD107926	BD107926 EST and e
35	799.4	59.4	848	6	BD131408	BD131408 cDNA enco
c 36	793.4	58.9	159446	9	AC003669	AC003669 Homo sapi
37	793.4	58.9	165730	2	AC061988	AC061988 Homo sapi
38	654	48.6	666	6	AX083382	AX083382 Sequence
39	614.4	45.6	1222	10	BC049912	BC049912 Mus muscu
40	589.8	43.8	1262	10	AF178085	AF178085 Mus muscu
41	551.4	41.0	1266	10	BC078838	BC078838 Rattus no
42	545	40.5	545	6	CQ714932	CQ714932 Sequence
43	539.6	40.1	1181	10	AF178086	AF178086 Rattus no
44	409.4	30.4	439	6	AX939025	AX939025 Sequence
45	409.4	30.4	439	6	BD077452	BD077452 5'EST of
46	405	30.1	462	6	BD058424	BD058424 Secreted
47	232.6	17.3	355	6	CQ458858	CQ458858 Sequence
c 48	197.4	14.7	213	6	CQ111904	CQ111904 Sequence
c 49	197.4	14.7	213	6	CQ150704	CQ150704 Sequence
c 50	197.4	14.7	213	6	CQ184910	CQ184910 Sequence
c 51	197.4	14.7	213	6	CQ234037	CQ234037 Sequence
c 52	197.4	14.7	213	6	CQ271795	CQ271795 Sequence
c 53	197.4	14.7	213	6	CQ309364	CQ309364 Sequence
c 54	197.4	14.7	213	6	CQ346012	CQ346012 Sequence
55	191.2	14.2	112893	10	AL732294	AL732294 Mouse DNA
56	191.2	14.2	234105	10	AC091606	AC091606 Mus Muscu
c 57	188.2	14.0	464	6	CQ098839	CQ098839 Sequence
c 58	188.2	14.0	464	6	CQ137751	CQ137751 Sequence
c 59	188.2	14.0	464	6	CQ175049	CQ175049 Sequence
c 60	188.2	14.0	464	6	CQ221115	CQ221115 Sequence
c 61	188.2	14.0	464	6	CQ259275	CQ259275 Sequence
c 62	188.2	14.0	464	6	CQ296932	CQ296932 Sequence
c 63	188.2	14.0	464	6	CQ333335	CQ333335 Sequence
64	182.6	13.6	1131	5	BC058203	BC058203 Xenopus l
c 65	157.4	11.7	225558	2	AC103066	AC103066 Rattus no
66	157.4	11.7	226820	2	AC118872	AC118872 Rattus no
67	144.2	10.7	2415	6	AX047760	AX047760 Sequence
68	126.8	9.4	1877	5	BC065470	BC065470 Danio rer
69	125.6	9.3	2415	6	AX047764	AX047764 Sequence
70	125	9.3	2415	6	AR135178	AR135178 Sequence
71	125	9.3	2415	6	BD274685	BD274685 Angiotens
72	125	9.3	2415	6	E43987	E43987 ACE-analogo
73	125	9.3	2415	6	AR382342	AR382342 Sequence
74	125	9.3	2415	6	AX418984	AX418984 Sequence
75	125	9.3	2418	6	E39033	E39033 MPROT15 pol
76	125	9.3	2418	9	AY623811	AY623811 Homo sapi
77	125	9.3	2599	6	E43988	E43988 ACE-analogo
78	125	9.3	3325	9	AF291820	AF291820 Homo sapi
79	125	9.3	3334	6	AX047758	AX047758 Sequence
80	125	9.3	3339	9	BC048094	BC048094 Homo sapi
81	125	9.3	3341	9	HSM800880	AL110224 Homo sapi
82	125	9.3	3348	9	BC039902	BC039902 Homo sapi
83	125	9.3	3375	9	BC059378	BC059378 Homo sapi
84	125	9.3	3396	6	AR135177	AR135177 Sequence
85	125	9.3	3396	6	BD274684	BD274684 Angiotens
86	125	9.3	3396	6	AR353104	AR353104 Sequence
87	125	9.3	3396	6	AR382341	AR382341 Sequence
88	125	9.3	3396	6	AX418982	AX418982 Sequence
89	125	9.3	3396	6	AX431513	AX431513 Sequence
90	125	9.3	3405	6	CQ754222	CQ754222 Sequence
91	125	9.3	3405	9	AF241254	AF241254 Homo sapi
92	123.4	9.2	2599	9	AB046569	AB046569 Homo sapi

	93	119.8	8.9	3732	6	AR528488 AR528488 Sequence
	94	119.8	8.9	3732	6	AX463938 AX463938 Sequence
	95	119.8	8.9	3732	9	AY358714 AY358714 Homo sapi
	96	118	8.8	1879	5	BC053284 BC053284 Danio rer
	97	117	8.7	2920	6	AR353103 AR353103 Sequence
c	98	111.4	8.3	435	6	CQ458859 CQ458859 Sequence
	99	111.4	8.3	2638	6	AX047762 AX047762 Sequence
	100	109.6	8.1	2760	10	AB053181 AB053181 Mus muscu
	101	108.6	8.1	1993	10	AB053182 AB053182 Mus muscu
	102	108.2	8.0	2638	6	AX047765 AX047765 Sequence
	103	108.2	8.0	2739	6	CQ754224 CQ754224 Sequence
	104	108.2	8.0	2739	10	BC026801 BC026801 Mus muscu
	105	96.8	7.2	2134	6	CQ714933 CQ714933 Sequence
	106	96.8	7.2	2262	6	E39034 E39034 MPROT15 pol
	107	94.8	7.0	1013	9	AK026461 AK026461 Homo sapi
	108	77.4	5.8	41572	9	AY217547 AY217547 Homo sapi
c	109	77.4	5.8	194492	9	AC097625 AC097625 Homo sapi
	110	73.4	5.5	84550	3	PFMAL1P2_3 Continuation (4 of
c	111	69.4	5.2	2350	6	AR263862 AR263862 Sequence
	112	69.4	5.2	216259	2	CR749761 CR749761 Danio rer
	113	69.2	5.1	202661	2	CR556715 CR556715 Danio rer
	114	69.2	5.1	250029	3	AE014830 AE014830 Plasmodiu
	115	69	5.1	287510	2	CR753823 CR753823 Danio rer
	116	68.6	5.1	348034	3	CR382400 CR382400 Plasmodiu
	117	68.4	5.1	1119	5	BX935959 BX935959 Gallus ga
c	118	68.2	5.1	164979	2	CR847573 CR847573 Danio rer
	119	68	5.1	110000	3	PFMAL1P2_2 Continuation (3 of
	120	67.8	5.0	167245	2	CR626882 CR626882 Danio rer
	121	67.6	5.0	209719	2	CR847825 CR847825 Danio rer
	122	67.2	5.0	110000	2	PFMAL7P1_12 Continuation (13 o
	123	67.2	5.0	172464	2	CR792425 CR792425 Danio rer
	124	67	5.0	8056	6	AX599046 AX599046 Sequence
	125	67	5.0	55372	2	CR759965 CR759965 Danio rer
c	126	67	5.0	348034	3	CR382400 CR382400 Plasmodiu
	127	66.8	5.0	348600	1	AB063521 AB063521 Wiggleswo
c	128	66.6	4.9	55372	2	CR759965 CR759965 Danio rer
	129	66.6	4.9	251448	3	AE014819 AE014819 Plasmodiu
c	130	66.2	4.9	58697	2	AC144975 AC144975 Xenopus t
c	131	66.2	4.9	110000	3	PFMAL1P2_0 AL031745 Plasmodiu
c	132	66.2	4.9	165988	2	CR626888 CR626888 Danio rer
c	133	66.2	4.9	171427	9	AC021590 AC021590 Homo sapi
	134	66.2	4.9	198627	5	AL845168 AL845168 Zebrafish
c	135	66	4.9	93133	9	AC022140 AC022140 Homo sapi
	136	66	4.9	109975	9	AC112497 AC112497 Homo sapi
	137	66	4.9	148878	2	CR759816 CR759816 Danio rer
c	138	66	4.9	174402	9	AC016991 AC016991 Homo sapi
c	139	65.8	4.9	60604	2	AC023466 AC023466 Homo sapi
c	140	65.8	4.9	172578	2	CR812468 CR812468 Danio rer
	141	65.6	4.9	186147	2	CR626891 CR626891 Danio rer
c	142	65.4	4.9	116197	2	AC135614 AC135614 Pan trogl
c	143	65.4	4.9	158085	2	CR388149 CR388149 Danio rer
	144	65.2	4.8	170920	9	AC138627 AC138627 Homo sapi
	145	65.2	4.8	181515	2	CR759824 CR759824 Danio rer
	146	65.2	4.8	227073	2	CR846086 CR846086 Danio rer
	147	65	4.8	7448	3	AF465305 AF465305 Dictyoste
	148	65	4.8	192581	2	PFMAL13P1 AL049180 Plasmodiu
c	149	65	4.8	222825	2	CR628387 CR628387 Danio rer
c	150	65	4.8	228609	2	CR759885 CR759885 Danio rer
c	151	64.8	4.8	167124	2	CR812482 CR812482 Danio rer
c	152	64.8	4.8	171382	2	CR392331 CR392331 Danio rer
	153	64.8	4.8	172399	2	CR762388 CR762388 Danio rer
	154	64.8	4.8	192676	10	AL671706 AL671706 Mouse DNA
	155	64.8	4.8	204662	2	CR753838 CR753838 Danio rer
	156	64.8	4.8	234796	2	CR318626 CR318626 Danio rer
c	157	64.8	4.8	245165	2	CR383660 CR383660 Danio rer
	158	64.4	4.8	76568	3	MBREV AF538053 Monosiga
	159	64.4	4.8	174012	2	CR847512 CR847512 Danio rer
	160	64.4	4.8	174198	2	CR762438 CR762438 Danio rer
	161	64.4	4.8	250793	2	CR388030 CR388030 Danio rer
	162	64.2	4.8	5477	3	PFCAATPAS X71765 P. falcipar
c	163	64.2	4.8	167872	2	CR792455 CR792455 Danio rer
c	164	64.2	4.8	187144	2	BX957353 BX957353 Danio rer
c	165	64	4.8	110000	2	PFMAL7P1_07 Continuation (8 of
c	166	64	4.8	138964	2	BX950176 BX950176 Danio rer
c	167	64	4.8	250029	3	AE014830 AE014830 Plasmodiu
c	168	64	4.8	250029	3	AE014838 AE014838 Plasmodiu
c	169	63.8	4.7	110000	2	PFMAL13_11 Continuation (12 o
	170	63.8	4.7	173234	2	CR550306 CR550306 Danio rer
c	171	63.8	4.7	180660	2	BX255894 BX255894 Danio rer
	172	63.8	4.7	202533	2	CR392031 CR392031 Danio rer
	173	63.8	4.7	245072	2	CR381551 CR381551 Danio rer
c	174	63.8	4.7	330050	3	PFA929355 AL929355 Plasmodiu
	175	63.6	4.7	164755	2	BX927094 BX927094 Danio rer
	176	63.6	4.7	183844	2	CR753873 CR753873 Danio rer
c	177	63.6	4.7	186005	2	BX927412 BX927412 Danio rer
c	178	63.6	4.7	202533	2	CR392031 CR392031 Danio rer
	179	63.6	4.7	226108	2	CR759967 CR759967 Danio rer
c	180	63.6	4.7	250029	3	AE014820 AE014820 Plasmodiu
c	181	63.4	4.7	67970	3	PFMAL1P3 AL031746 Plasmodiu
c	182	63.4	4.7	110000	2	PFMAL13_05 Continuation (6 of
	183	63.4	4.7	110000	3	AC116305_0 AC116305 Dictyoste
c	184	63.4	4.7	170276	9	AL353143 AL353143 Human DNA
	185	63.2	4.7	200260	2	CR753814 CR753814 Danio rer
c	186	63.2	4.7	206042	2	CR753794 CR753794 Danio rer
	187	63	4.7	3030	3	PFAMRNA L12043 Plasmodium
	188	63	4.7	3474	6	AX576256 AX576256 Sequence
	189	63	4.7	164668	9	AC091925 AC091925 Homo sapi
	190	63	4.7	175016	2	CR759867 CR759867 Danio rer
	191	63	4.7	188663	2	CR457449 CR457449 Danio rer
c	192	63	4.7	250663	3	AE014826 AE014826 Plasmodiu
	193	63	4.7	327236	2	CR385026 CR385026 Danio rer
	194	62.8	4.7	5286	6	CQ806844 CQ806844 Sequence
	195	62.8	4.7	5286	6	CQ807118 CQ807118 Sequence
	196	62.8	4.7	5286	6	AX795782 AX795782 Sequence
	197	62.8	4.7	5286	6	AX795898 AX795898 Sequence
	198	62.8	4.7	100925	9	AC012627 AC012627 Homo sapi
c	199	62.8	4.7	142514	2	CR790361 CR790361 Danio rer
	200	62.8	4.7	154901	2	CR751231 CR751231 Danio rer
c	201	62.8	4.7	181557	2	CR847945 CR847945 Danio rer
c	202	62.8	4.7	192187	3	AC117072 AC117072 Dictyoste
	203	62.8	4.7	208116	2	CR555302 CR555302 Danio rer
c	204	62.8	4.7	214709	2	CR749183 CR749183 Danio rer
c	205	62.8	4.7	235532	9	AC008739 AC008739 Homo sapi
	206	62.6	4.7	153947	2	CR788315 CR788315 Danio rer
	207	62.6	4.7	168389	9	AC110015 AC110015 Homo sapi
c	208	62.6	4.7	196859	9	AC087277 AC087277 Homo sapi
	209	62.6	4.7	209852	2	AC151363 AC151363 Gasterost
c	210	62.4	4.6	5413	6	AX251450 AX251450 Sequence
c	211	62.4	4.6	9810	6	AX345328 AX345328 Sequence
	212	62.4	4.6	149831	2	CR847943 CR847943 Danio rer
	213	62.4	4.6	174001	2	BX927081 BX927081 Danio rer
	214	62.4	4.6	250029	3	AE014816 AE014816 Plasmodiu
c	215	62.4	4.6	253151	3	AE014842 AE014842 Plasmodiu
	216	62.4	4.6	335050	3	PFA929356 AL929356 Plasmodiu
	217	62.2	4.6	8056	6	AX598900 AX598900 Sequence
c	218	62.2	4.6	72243	9	AL731858 AL731858 Human DNA
	219	62.2	4.6	124114	9	HSJ858M22 AL118510 Human DNA
c	220	62.2	4.6	165797	2	CR847851 CR847851 Danio rer
	221	62.2	4.6	186857	2	CR735109 CR735109 Danio rer
	222	62.2	4.6	195319	2	CR388410 CR388410 Danio rer
	223	62.2	4.6	196420	2	BX908771 BX908771 Danio rer
	224	62	4.6	121958	2	CR759861 CR759861 Danio rer
c	225	62	4.6	134799	2	CR352285 CR352285 Danio rer
c	226	62	4.6	182223	2	CR790384 CR790384 Danio rer
	227	62	4.6	210718	2	CR589941 CR589941 Danio rer
c	228	61.8	4.6	110000	2	PFMAL13_22 Continuation (23 o
	229	61.8	4.6	133877	2	AC120883 AC120883 Homo sapi
	230	61.8	4.6	159448	2	CR627500 CR627500 Danio rer
	231	61.8	4.6	166820	2	CR388213 CR388213 Danio rer
	232	61.8	4.6	168103	2	CR751601 CR751601 Danio rer
	233	61.8	4.6	172285	2	CR381538 CR381538 Danio rer
c	234	61.8	4.6	230976	2	BX927201 BX927201 Danio rer
c	235	61.8	4.6	261134	2	CR318600 CR318600 Danio rer
c	236	61.8	4.6	335050	3	PFA929356 AL929356 Plasmodiu
c	237	61.6	4.6	2706	1	AF268053 AF268053 Candidatu
c	238	61.6	4.6	129240	9	AC084128 AC084128 Homo sapi

239	61.6	4.6	156395	2	CR387986	CR387986 Danio rer
240	61.6	4.6	163735	9	AC027277	AC027277 Homo sapi
c 241	61.6	4.6	182518	9	AC131649	AC131649 Homo sapi
242	61.6	4.6	185085	2	CR762404	CR762404 Danio rer
243	61.6	4.6	196762	2	CR759796	CR759796 Danio rer
c 244	61.6	4.6	218909	2	CR626875	CR626875 Danio rer
c 245	61.4	4.6	961	3	AY351412	AY351412 Arethusan
c 246	61.4	4.6	110000	2	PFMAL8P1_04	Continuation (5 of
c 247	61.4	4.6	110000	2	PFMAL8P1_07	Continuation (8 of
c 248	61.4	4.6	135121	9	AC069525	AC069525 Homo sapi
249	61.4	4.6	163443	2	AC006280	AC006280 Plasmodiu
250	61.4	4.6	165959	2	CR792429	CR792429 Danio rer
c 251	61.4	4.6	195863	2	CR847978	CR847978 Danio rer
c 252	61.4	4.6	243513	2	CR753817	CR753817 Danio rer
c 253	61.4	4.6	252650	3	AE014847	AE014847 Plasmodiu
c 254	61.2	4.5	935	3	AY351413	AY351413 Arethusan
c 255	61.2	4.5	173288	2	AC138859	AC138859 Homo sapi
c 256	61.2	4.5	175605	2	CR450746	CR450746 Danio rer
c 257	61.2	4.5	188638	2	CR759889	CR759889 Danio rer
258	61.2	4.5	264232	2	CR626890	CR626890 Danio rer
259	61	4.5	162977	2	CR631122	CR631122 Danio rer
c 260	61	4.5	174001	2	BX927081	BX927081 Danio rer
261	61	4.5	192187	3	AC117072	AC117072 Dictyoste
c 262	61	4.5	196759	2	CR788226	CR788226 Danio rer
263	61	4.5	246611	2	AC111404	AC111404 Rattus no
c 264	61	4.5	254449	3	AE014817	AE014817 Plasmodiu
c 265	61	4.5	333321	3	AC116986	AC116986 Dictyoste
266	60.8	4.5	165048	2	CR790371	CR790371 Danio rer
267	60.8	4.5	175235	2	CR790380	CR790380 Danio rer
c 268	60.8	4.5	180540	2	CR847859	CR847859 Danio rer
c 269	60.8	4.5	186040	2	CR391974	CR391974 Danio rer
270	60.8	4.5	210050	2	CR376844	CR376844 Danio rer
271	60.6	4.5	57941	9	BX323827	BX323827 Human DNA
272	60.6	4.5	72143	9	AC131094	AC131094 Homo sapi
273	60.6	4.5	81147	9	AL606504	AL606504 Human DNA
c 274	60.6	4.5	83391	6	AX458577	AX458577 Sequence
275	60.6	4.5	146613	2	CR786569	CR786569 Danio rer
c 276	60.6	4.5	146850	2	CR394559	CR394559 Danio rer
c 277	60.6	4.5	156141	2	CR749777	CR749777 Danio rer
278	60.6	4.5	169894	2	CR762466	CR762466 Danio rer
c 279	60.6	4.5	186175	2	CR318664	CR318664 Danio rer
c 280	60.6	4.5	194561	2	CR450706	CR450706 Danio rer
281	60.6	4.5	205475	2	CR762392	CR762392 Danio rer
282	60.6	4.5	205544	2	CR847834	CR847834 Danio rer
c 283	60.6	4.5	210218	2	CR555304	CR555304 Danio rer
c 284	60.6	4.5	349751	3	PFMAL4P3	AL035476 Plasmodiu
c 285	60.4	4.5	113955	9	AC068291	AC068291 Homo sapi
286	60.4	4.5	142402	2	CR847574	CR847574 Danio rer
287	60.4	4.5	144202	2	CR628391	CR628391 Danio rer
c 288	60.4	4.5	185162	9	AC140132	AC140132 Homo sapi
c 289	60.4	4.5	190163	2	CR354398	CR354398 Danio rer
c 290	60.4	4.5	199128	9	AC091946	AC091946 Homo sapi
c 291	60.4	4.5	224175	2	CR812957	CR812957 Danio rer
c 292	60.4	4.5	346940	2	AC107420	AC107420 Homo sapi
293	60.4	4.5	349418	3	CR382398	CR382398 Plasmodiu
294	60.4	4.5	349751	3	PFMAL4P3	AL035476 Plasmodiu
c 295	60.2	4.5	39575	3	AC116925	AC116925 Dictyoste
c 296	60.2	4.5	93288	9	AC020926	AC020926 Homo sapi
297	60.2	4.5	110000	2	PFMAL13_23	Continuation (24 o
c 298	60.2	4.5	110000	2	PFMAL13P2_0	AL049185 Plasmodiu
c 299	60.2	4.5	155609	2	BX927284	BX927284 Danio rer
300	60.2	4.5	162445	9	AL158151	AL158151 Human DNA
301	60.2	4.5	168069	2	CR812470	CR812470 Danio rer
302	60.2	4.5	181213	2	AC141431	AC141431 Homo sapi
303	60.2	4.5	190482	2	CR450828	CR450828 Danio rer
304	60.2	4.5	210548	2	CR751608	CR751608 Danio rer
c 305	60.2	4.5	213541	9	HUAC004381	AC004381 Homo sapi
c 306	60.2	4.5	217838	2	BX901955	BX901955 Danio rer
307	60.2	4.5	239166	2	BX950179	BX950179 Danio rer
c 308	60.2	4.5	250743	3	AE014836	AE014836 Plasmodiu
c 309	60.2	4.5	251762	3	AE014851	AE014851 Plasmodiu
310	60	4.5	60	6	CQ539130	CQ539130 Sequence
311	60	4.5	82453	9	AC004558	AC004558 Homo sapi
c 312	60	4.5	110000	2	PFMAL7P1_08	Continuation (9 of
c 313	60	4.5	143903	5	BX247887	BX247887 Zebrafish
c 314	60	4.5	158548	3	PFMAL3P2	AL034558 Plasmodiu
c 315	60	4.5	170627	2	AC125567	AC125567 Rattus no
316	60	4.5	172556	2	CR762400	CR762400 Danio rer
317	60	4.5	183318	2	CR376728	CR376728 Danio rer
c 318	60	4.5	187277	9	AC022968	AC022968 Homo sapi
319	60	4.5	205013	2	AY269187	AY269187 Homo sapi
c 320	60	4.5	221924	2	CR388047	CR388047 Danio rer
c 321	60	4.5	233769	2	CR631124	CR631124 Danio rer
c 322	60	4.5	234796	2	CR318626	CR318626 Danio rer
323	60	4.5	250621	2	CR792433	CR792433 Danio rer
324	59.8	4.4	137594	2	CR812464	CR812464 Danio rer
c 325	59.8	4.4	159610	5	BX088559	BX088559 Zebrafish
c 326	59.8	4.4	162075	9	HS127D3	AL021026 Human DNA
c 327	59.8	4.4	167518	9	CNS05TEK	AL359233 Human chr
c 328	59.8	4.4	174832	2	CR293499	CR293499 Danio rer
329	59.8	4.4	194559	2	CR628365	CR628365 Danio rer
c 330	59.8	4.4	196149	2	AC004709	AC004709 Plasmodiu
331	59.8	4.4	251797	2	BX890543	BX890543 Danio rer
332	59.8	4.4	252632	3	AE014818	AE014818 Plasmodiu
c 333	59.8	4.4	256879	3	AC116982	AC116982 Dictyoste
334	59.6	4.4	148385	2	CR749764	CR749764 Danio rer
335	59.6	4.4	155758	2	CR792441	CR792441 Danio rer
336	59.6	4.4	163724	2	CR788299	CR788299 Danio rer
337	59.6	4.4	164443	2	CR751221	CR751221 Danio rer
338	59.6	4.4	167229	9	AC006269	AC006269 Homo sapi
c 339	59.6	4.4	172285	2	CR381538	CR381538 Danio rer
c 340	59.6	4.4	182748	2	CR388066	CR388066 Danio rer
341	59.6	4.4	194513	2	CR524482	CR524482 Danio rer
c 342	59.6	4.4	210343	2	CR753890	CR753890 Danio rer
c 343	59.6	4.4	210548	2	CR751608	CR751608 Danio rer
c 344	59.6	4.4	225861	2	CR628381	CR628381 Danio rer
345	59.6	4.4	239941	2	CR749176	CR749176 Danio rer
346	59.4	4.4	47573	3	AF030694	AF030694 Plasmodiu
347	59.4	4.4	167548	2	CR759878	CR759878 Danio rer
c 348	59.4	4.4	169448	2	CR385039	CR385039 Danio rer
349	59.4	4.4	170929	2	CR759865	CR759865 Danio rer
350	59.4	4.4	171441	2	BX950202	BX950202 Danio rer
c 351	59.4	4.4	181515	2	CR759824	CR759824 Danio rer
c 352	59.4	4.4	186165	9	AC112187	AC112187 Homo sapi
353	59.4	4.4	198349	2	CR788292	CR788292 Danio rer
354	59.4	4.4	199145	2	CR759742	CR759742 Danio rer
355	59.4	4.4	204430	2	CR792453	CR792453 Danio rer
356	59.4	4.4	243513	2	CR753817	CR753817 Danio rer
c 357	59.2	4.4	110000	2	PFMAL13_25	Continuation (26 o
c 358	59.2	4.4	115952	9	AL772267	AL772267 Human DNA
c 359	59.2	4.4	148394	2	CR753884	CR753884 Danio rer
360	59.2	4.4	159835	2	CR387984	CR387984 Danio rer
c 361	59.2	4.4	165574	2	CR847571	CR847571 Danio rer
c 362	59.2	4.4	170534	2	CR391918	CR391918 Danio rer
c 363	59.2	4.4	172816	9	AC093899	AC093899 Homo sapi
364	59.2	4.4	180109	2	BX294164	BX294164 Danio rer
365	59.2	4.4	189149	2	AC046171	AC046171 Homo sapi
c 366	59.2	4.4	251448	3	AE014819	AE014819 Plasmodiu
c 367	59.2	4.4	266335	2	CR762497	CR762497 Danio rer
c 368	59	4.4	128338	2	CR774177	CR774177 Danio rer
c 369	59	4.4	153947	2	CR788315	CR788315 Danio rer
370	59	4.4	154044	2	CR786570	CR786570 Danio rer
c 371	59	4.4	159603	2	CR762422	CR762422 Danio rer
c 372	59	4.4	168389	9	AC110015	AC110015 Homo sapi
c 373	59	4.4	169562	2	CR394565	CR394565 Danio rer
c 374	59	4.4	169794	2	AC004688	AC004688 Plasmodiu
375	59	4.4	173927	2	CR812798	CR812798 Danio rer
c 376	59	4.4	176704	2	CR628364	CR628364 Danio rer
377	59	4.4	199230	2	CR762470	CR762470 Danio rer
378	59	4.4	211748	2	CR392346	CR392346 Danio rer
c 379	59	4.4	217621	2	BX901924	BX901924 Danio rer
380	59	4.4	221953	2	BX928743	BX928743 Danio rer
381	59	4.4	246940	2	CR628329	CR628329 Danio rer
382	58.8	4.4	2503	6	AX033851	AX033851 Sequence
c 383	58.8	4.4	9997	6	AX281374	AX281374 Sequence
c 384	58.8	4.4	9997	6	AX345271	AX345271 Sequence

c 385	58.8	4.4	29993	6	AX825169	AX825169 Sequence
c 386	58.8	4.4	29993	6	AX825171	AX825171 Sequence
c 387	58.8	4.4	38342	6	AX251504	AX251504 Sequence
c 388	58.8	4.4	38342	6	AX344503	AX344503 Sequence
c 389	58.8	4.4	125632	2	CR753868	CR753868 Danio rer
390	58.8	4.4	135803	2	CR762395	CR762395 Danio rer
c 391	58.8	4.4	149189	5	AL845366	AL845366 Zebrafish
392	58.8	4.4	162554	2	CR626901	CR626901 Danio rer
393	58.8	4.4	168936	2	CR735127	CR735127 Danio rer
c 394	58.8	4.4	169494	9	AL450083	AL450083 Human DNA
c 395	58.8	4.4	177623	2	CR394571	CR394571 Danio rer
396	58.8	4.4	179399	2	BX890603	BX890603 Danio rer
c 397	58.8	4.4	185989	2	CR407587	CR407587 Danio rer
c 398	58.8	4.4	190058	2	CR628384	CR628384 Danio rer
399	58.8	4.4	191191	2	CR847965	CR847965 Danio rer
400	58.8	4.4	209866	2	BX546466	BX546466 Danio rer
c 401	58.8	4.4	213636	2	CR559931	CR559931 Danio rer
402	58.8	4.4	237931	9	AC022098	AC022098 Homo sapi
c 403	58.8	4.4	239613	2	CR790367	CR790367 Danio rer
c 404	58.8	4.4	250022	3	AE014824	AE014824 Plasmodiu
405	58.8	4.4	253764	2	BX855620	BX855620 Danio rer
406	58.8	4.4	257757	3	AE014837	AE014837 Plasmodiu
407	58.6	4.4	9810	6	AX345329	AX345329 Sequence
c 408	58.6	4.4	110000	2	PFMAL13_01	Continuation (2 of
c 409	58.6	4.4	110000	2	PFMAL7P1_12	Continuation (13 o
410	58.6	4.4	113515	6	AX347076	AX347076 Sequence
411	58.6	4.4	126999	9	AL513328	AL513328 Human DNA
412	58.6	4.4	137564	2	CR762439	CR762439 Danio rer
413	58.6	4.4	149223	2	CR382382	CR382382 Danio rer
c 414	58.6	4.4	153459	2	CR847994	CR847994 Danio rer
415	58.6	4.4	163651	2	CR790381	CR790381 Danio rer
416	58.6	4.4	165012	5	BX005274	BX005274 Zebrafish
417	58.6	4.4	175544	2	AC117342	AC117342 Rattus no
c 418	58.6	4.4	176122	2	CR628401	CR628401 Danio rer
419	58.6	4.4	180096	2	CR626872	CR626872 Danio rer
c 420	58.6	4.4	205479	2	CR847506	CR847506 Danio rer
c 421	58.6	4.4	209561	2	CR383669	CR383669 Danio rer
c 422	58.6	4.4	210954	2	CR545461	CR545461 Danio rer
423	58.6	4.4	212683	2	CR388029	CR388029 Danio rer
c 424	58.6	4.4	213402	2	BX901895	BX901895 Danio rer
c 425	58.6	4.4	215231	2	CR385085	CR385085 Danio rer
c 426	58.6	4.4	234347	2	CR847960	CR847960 Danio rer
c 427	58.6	4.4	242324	2	CR759863	CR759863 Danio rer
c 428	58.6	4.4	310779	2	AC005140	AC005140 Plasmodiu
429	58.6	4.4	340552	3	PFA929354	AL929354 Plasmodiu
c 430	58.4	4.3	99003	2	AL390756	AL390756 Homo sapi
431	58.4	4.3	110000	2	PFMAL8P1_09	Continuation (10 o
c 432	58.4	4.3	122168	9	AC127383	AC127383 Homo sapi
c 433	58.4	4.3	124871	2	CR735110	CR735110 Danio rer
434	58.4	4.3	130349	9	AC011593	AC011593 Homo sapi
c 435	58.4	4.3	135203	9	AC025278	AC025278 Homo sapi
436	58.4	4.3	148486	2	CR753871	CR753871 Danio rer
c 437	58.4	4.3	166565	2	CR589947	CR589947 Danio rer
c 438	58.4	4.3	171887	2	CR788232	CR788232 Danio rer
c 439	58.4	4.3	183614	2	CR847995	CR847995 Danio rer
c 440	58.4	4.3	196567	2	CR318605	CR318605 Danio rer
441	58.4	4.3	209515	2	BX571687	BX571687 Danio rer
442	58.4	4.3	229331	2	CR759914	CR759914 Danio rer
443	58.2	4.3	64394	9	AL928596	AL928596 Human DNA
444	58.2	4.3	86826	3	PFMAL3P5	AL034556 Plasmodiu
c 445	58.2	4.3	90550	9	AL592166	AL592166 Human DNA
c 446	58.2	4.3	110000	2	PFMAL13_02	Continuation (3 of
447	58.2	4.3	110000	2	PFMAL13P2_1	Continuation (2 of
448	58.2	4.3	110000	3	AC116305_1	Continuation (2 of
449	58.2	4.3	143037	2	CR735143	CR735143 Danio rer
c 450	58.2	4.3	159635	9	AC142351	AC142351 Pan trogl
c 451	58.2	4.3	160534	2	CR450837	CR450837 Danio rer
452	58.2	4.3	176034	2	CR524826	CR524826 Danio rer
c 453	58.2	4.3	194513	2	CR524482	CR524482 Danio rer
454	58.2	4.3	196490	2	AC005507	AC005507 Plasmodiu
455	58.2	4.3	198666	2	CR847504	CR847504 Danio rer
c 456	58.2	4.3	210050	2	CR376844	CR376844 Danio rer
457	58.2	4.3	213792	2	BX927177	BX927177 Danio rer
c 458	58.2	4.3	228285	2	CR391925	CR391925 Danio rer
c 459	58.2	4.3	244097	2	CR354394	CR354394 Danio rer
460	58.2	4.3	249943	3	AE014823	AE014823 Plasmodiu
c 461	58	4.3	65644	9	AL590364	AL590364 Human DNA
c 462	58	4.3	110000	2	PFMAL7P1_03	Continuation (4 of
c 463	58	4.3	153702	9	AL645730	AL645730 Human DNA
c 464	58	4.3	156849	2	CR405684	CR405684 Danio rer
465	58	4.3	170536	9	AC093914	AC093914 Homo sapi
c 466	58	4.3	172036	9	AC046181	AC046181 Homo sapi
467	58	4.3	178687	2	AC148722	AC148722 Ictalurus
468	58	4.3	181792	2	CR388184	CR388184 Danio rer
c 469	58	4.3	197061	2	CR759830	CR759830 Danio rer
c 470	58	4.3	202169	2	AC149549	AC149549 Gorilla g
471	58	4.3	205907	2	CR388065	CR388065 Danio rer
c 472	58	4.3	236119	2	CR788254	CR788254 Danio rer
c 473	58	4.3	239323	2	CR788304	CR788304 Danio rer
c 474	58	4.3	253001	3	AE014834	AE014834 Plasmodiu
475	58	4.3	254436	3	AE014827	AE014827 Plasmodiu
476	58	4.3	273994	2	CR792438	CR792438 Danio rer
c 477	57.8	4.3	109391	9	AL160031	AL160031 Human DNA
478	57.8	4.3	142655	2	CR762428	CR762428 Danio rer
c 479	57.8	4.3	145925	5	BX842571	BX842571 Zebrafish
c 480	57.8	4.3	163443	2	AC006280	AC006280 Plasmodiu
481	57.8	4.3	165933	1	AP004174	AP004174 Mycoplasm
482	57.8	4.3	177199	5	BX547933	BX547933 Zebrafish
c 483	57.8	4.3	180164	2	CR759818	CR759818 Danio rer
484	57.8	4.3	180366	2	CR753867	CR753867 Danio rer
c 485	57.8	4.3	189144	2	CR559945	CR559945 Danio rer
486	57.8	4.3	204509	2	CR792449	CR792449 Danio rer
c 487	57.8	4.3	205429	2	AC005506	AC005506 Plasmodiu
488	57.8	4.3	253132	3	AE014846	AE014846 Plasmodiu
c 489	57.6	4.3	14591	3	AE001406	AE001406 Plasmodiu
c 490	57.6	4.3	105940	9	AC010606	AC010606 Homo sapi
491	57.6	4.3	110000	3	AC116984_2	Continuation (3 of
492	57.6	4.3	150962	2	CR847546	CR847546 Danio rer
c 493	57.6	4.3	167068	2	BX323866	BX323866 Danio rer
c 494	57.6	4.3	169357	2	CR847871	CR847871 Danio rer
495	57.6	4.3	171295	2	CR388131	CR388131 Danio rer
496	57.6	4.3	171867	2	CR628361	CR628361 Danio rer
497	57.6	4.3	175014	2	BX942825	BX942825 Danio rer
c 498	57.6	4.3	180450	3	AE014835	AE014835 Plasmodiu
499	57.6	4.3	186979	2	CR631129	CR631129 Danio rer
500	57.6	4.3	195602	2	CR388375	CR388375 Danio rer
c 501	57.6	4.3	198970	2	BX470255	BX470255 Danio rer
c 502	57.6	4.3	204478	2	CR450778	CR450778 Danio rer
503	57.6	4.3	210343	2	CR753890	CR753890 Danio rer
504	57.6	4.3	227896	2	BX545909	BX545909 Mus muscu
505	57.6	4.3	228285	2	CR391925	CR391925 Danio rer
c 506	57.6	4.3	234081	3	PFMAL4P2	AL035475 Plasmodiu
507	57.6	4.3	250029	3	AE014820	AE014820 Plasmodiu
508	57.6	4.3	251376	2	CR628341	CR628341 Danio rer
509	57.6	4.3	251382	2	CR626924	CR626924 Danio rer
510	57.6	4.3	254733	3	AC117075	AC117075 Dictyoste
511	57.4	4.3	12029	3	AE001401	AE001401 Plasmodiu
c 512	57.4	4.3	17839	3	AE001384	AE001384 Plasmodiu
c 513	57.4	4.3	52704	2	AC151519	AC151519 Danio rer
514	57.4	4.3	103344	9	HS1100E15	AL035551 Human DNA
c 515	57.4	4.3	105238	9	AC011458	AC011458 Homo sapi
516	57.4	4.3	110000	2	PFMAL13_08	Continuation (9 of
517	57.4	4.3	111861	9	AC069435	AC069435 Homo sapi
518	57.4	4.3	144784	9	AC009224	AC009224 Homo sapi
c 519	57.4	4.3	154071	3	AC115598	AC115598 Dictyoste
c 520	57.4	4.3	155954	2	CR752653	CR752653 Danio rer
521	57.4	4.3	169520	2	CR753882	CR753882 Danio rer
c 522	57.4	4.3	169800	2	CR847821	CR847821 Danio rer
523	57.4	4.3	174311	2	CR678065	CR678065 Danio rer
524	57.4	4.3	175287	2	CR450738	CR450738 Danio rer
525	57.4	4.3	180450	3	AE014835	AE014835 Plasmodiu
526	57.4	4.3	182871	3	AC117176	AC117176 Dictyoste
c 527	57.4	4.3	183584	9	AC012492	AC012492 Homo sapi
c 528	57.4	4.3	185640	5	AL772314	AL772314 Zebrafish
c 529	57.4	4.3	191707	2	CR847971	CR847971 Danio rer
c 530	57.4	4.3	227073	2	CR846086	CR846086 Danio rer

	531	57.4	4.3	250078	3	AE014829 AE014829 Plasmodiu
	532	57.4	4.3	252420	3	AE014841 AE014841 Plasmodiu
	533	57.4	4.3	253151	3	AE014842 AE014842 Plasmodiu
	534	57.4	4.3	259474	9	HUAC004605 AC004605 Homo sapi
c	535	57.4	4.3	259474	9	HUAC004605 AC004605 Homo sapi
	536	57.2	4.2	5000	3	AF482397 AF482397 Dictyoste
c	537	57.2	4.2	8056	6	AX599046 AX599046 Sequence
c	538	57.2	4.2	39984	3	AC114258 AC114258 Dictyoste
c	539	57.2	4.2	110000	2	PFMAL8P1_03 Continuation (4 of
c	540	57.2	4.2	110000	3	AC116984_4 Continuation (5 of
	541	57.2	4.2	142514	2	CR790361 CR790361 Danio rer
c	542	57.2	4.2	149106	2	CR762407 CR762407 Danio rer
c	543	57.2	4.2	157042	2	CR759826 CR759826 Danio rer
	544	57.2	4.2	157194	5	BX005475 BX005475 Zebrafish
	545	57.2	4.2	160982	2	CR786564 CR786564 Danio rer
	546	57.2	4.2	162954	2	BX548252 BX548252 Danio rer
c	547	57.2	4.2	165979	2	CR376741 CR376741 Danio rer
	548	57.2	4.2	168054	2	BX936460 BX936460 Danio rer
	549	57.2	4.2	170823	2	AC133549 AC133549 Homo sapi
	550	57.2	4.2	170974	2	CR751545 CR751545 Danio rer
c	551	57.2	4.2	172464	2	CR792425 CR792425 Danio rer
c	552	57.2	4.2	173637	2	CR376735 CR376735 Danio rer
c	553	57.2	4.2	180004	2	CR352247 CR352247 Danio rer
c	554	57.2	4.2	180346	9	AC092615 AC092615 Homo sapi
c	555	57.2	4.2	181792	9	AC098822 AC098822 Homo sapi
c	556	57.2	4.2	186369	2	CR388151 CR388151 Danio rer
	557	57.2	4.2	188777	2	CR774179 CR774179 Danio rer
	558	57.2	4.2	189598	2	BX957347 BX957347 Danio rer
	559	57.2	4.2	200953	2	CR762483 CR762483 Danio rer
c	560	57.2	4.2	202863	2	BX927344 BX927344 Danio rer
c	561	57.2	4.2	210077	2	CR450750 CR450750 Danio rer
	562	57.2	4.2	211376	2	CR762437 CR762437 Danio rer
	563	57.2	4.2	223198	2	CR762426 CR762426 Danio rer
c	564	57.2	4.2	224514	2	CR376802 CR376802 Danio rer
c	565	57.2	4.2	226108	2	CR759967 CR759967 Danio rer
	566	57.2	4.2	241048	2	CR753832 CR753832 Danio rer
	567	57.2	4.2	250029	3	AE014839 AE014839 Plasmodiu
	568	57.2	4.2	250195	3	AE014831 AE014831 Plasmodiu
	569	57.2	4.2	254050	3	PFA929358 AL929358 Plasmodiu
	570	57.2	4.2	293431	2	PFMAL13P4 AL049181 Plasmodiu
	571	57.2	4.2	297798	2	CR396591 CR396591 Danio rer
c	572	57.2	4.2	347050	3	PFA929351 AL929351 Plasmodiu
c	573	57.2	4.2	349980	6	AX344555 AX344555 Sequence
	574	57.2	4.2	349980	6	AX951695 AX951695 Sequence
	575	57	4.2	14001	3	PFCOMPIRB X95276 P.falciparu
	576	57	4.2	110000	2	BX539337_2 Continuation (3 of
c	577	57	4.2	114276	9	AC011355 AC011355 Homo sapi
c	578	57	4.2	145496	2	CR545470 CR545470 Danio rer
	579	57	4.2	155106	9	AC104069 AC104069 Homo sapi
	580	57	4.2	156657	2	CR769763 CR769763 Danio rer
	581	57	4.2	157467	2	CR792423 CR792423 Danio rer
	582	57	4.2	166486	2	CR812469 CR812469 Danio rer
	583	57	4.2	169546	2	AC004157 AC004157 Plasmodiu
	584	57	4.2	176704	2	CR628364 CR628364 Danio rer
	585	57	4.2	180861	2	CR391970 CR391970 Danio rer
	586	57	4.2	181430	2	CR407555 CR407555 Danio rer
c	587	57	4.2	187294	2	CR735107 CR735107 Danio rer
	588	57	4.2	199138	2	CR450798 CR450798 Danio rer
c	589	57	4.2	199296	2	CR753895 CR753895 Danio rer
	590	57	4.2	204486	2	CR752655 CR752655 Danio rer
	591	57	4.2	219074	2	CR769779 CR769779 Danio rer
c	592	57	4.2	228327	2	CR536612 CR536612 Danio rer
	593	57	4.2	233878	2	AC098146 AC098146 Rattus no
c	594	57	4.2	250707	3	AE014848 AE014848 Plasmodiu
c	595	57	4.2	251376	2	CR628341 CR628341 Danio rer
c	596	57	4.2	255459	2	CR382321 CR382321 Danio rer
	597	57	4.2	266335	2	CR762497 CR762497 Danio rer
c	598	57	4.2	287510	2	CR753823 CR753823 Danio rer
	599	57	4.2	326441	2	CR812467 CR812467 Danio rer
c	600	57	4.2	347582	3	PFMAL4P1 AL034557 Plasmodiu
c	601	56.8	4.2	18166	2	PFMAL8PE AL929364 Plasmodiu
	602	56.8	4.2	60582	2	AC008576_3 Continuation (4 of
c	603	56.8	4.2	86826	3	PFMAL3P5 AL034556 Plasmodiu
c	604	56.8	4.2	110000	2	PFMAL13_18 Continuation (19 o
	605	56.8	4.2	151143	2	AC141740 AC141740 Apis mell
	606	56.8	4.2	151544	9	AC013509 AC013509 Homo sapi
c	607	56.8	4.2	152661	3	AC010577 AC010577 Drosophil
	608	56.8	4.2	157314	2	CR352289 CR352289 Danio rer
c	609	56.8	4.2	157630	9	AC135012 AC135012 Homo sapi
	610	56.8	4.2	158249	5	BX470154 BX470154 Zebrafish
c	611	56.8	4.2	159910	9	AC009235 AC009235 Homo sapi
	612	56.8	4.2	163448	2	CR846088 CR846088 Danio rer
	613	56.8	4.2	164399	3	PFMAL3P6 Z98551 Plasmodium
	614	56.8	4.2	164772	2	CR382291 CR382291 Danio rer
	615	56.8	4.2	173395	2	CR762393 CR762393 Danio rer
c	616	56.8	4.2	174397	9	AC067773 AC067773 Homo sapi
	617	56.8	4.2	180279	2	BX901957 BX901957 Danio rer
c	618	56.8	4.2	181468	2	CR762391 CR762391 Danio rer
c	619	56.8	4.2	185048	2	CR392021 CR392021 Danio rer
	620	56.8	4.2	187415	2	CR759968 CR759968 Danio rer
c	621	56.8	4.2	187708	2	CR788293 CR788293 Danio rer
	622	56.8	4.2	192389	2	CR751229 CR751229 Danio rer
c	623	56.8	4.2	201556	2	CR847570 CR847570 Danio rer
	624	56.8	4.2	213948	2	CR792432 CR792432 Danio rer
c	625	56.8	4.2	227211	2	CR847561 CR847561 Danio rer
c	626	56.8	4.2	238266	2	CR392026 CR392026 Danio rer
	627	56.8	4.2	250029	3	AE014838 AE014838 Plasmodiu
	628	56.8	4.2	281723	3	PFA929359 AL929359 Plasmodiu
	629	56.6	4.2	104853	9	AC117444 AC117444 Homo sapi
	630	56.6	4.2	120192	2	AC093220 AC093220 Homo sapi
c	631	56.6	4.2	132254	3	AC116330 AC116330 Dictyoste
c	632	56.6	4.2	135848	2	CR394521 CR394521 Danio rer
	633	56.6	4.2	140231	2	BX901943 BX901943 Danio rer
c	634	56.6	4.2	142275	2	CR788316 CR788316 Danio rer
c	635	56.6	4.2	154995	9	AC011979 Homo sapi
c	636	56.6	4.2	156395	2	CR387986 CR387986 Danio rer
	637	56.6	4.2	156851	2	CR751546 CR751546 Danio rer
	638	56.6	4.2	161641	9	AC109464 Homo sapi
c	639	56.6	4.2	163475	2	CR628390 CR628390 Danio rer
	640	56.6	4.2	166014	2	CR762396 CR762396 Danio rer
	641	56.6	4.2	169194	2	CR788297 CR788297 Danio rer
	642	56.6	4.2	170276	9	AL353143 AL353143 Human DNA
c	643	56.6	4.2	171302	2	CR762414 CR762414 Danio rer
c	644	56.6	4.2	173570	2	CR457484 CR457484 Danio rer
	645	56.6	4.2	177462	2	CR749767 CR749767 Danio rer
	646	56.6	4.2	178025	2	CR752654 CR752654 Danio rer
c	647	56.6	4.2	179213	2	CR792414 CR792414 Danio rer
c	648	56.6	4.2	179571	2	CR361569 CR361569 Danio rer
c	649	56.6	4.2	188797	9	AC150210 AC150210 Pan trogl
	650	56.6	4.2	199874	2	CR626878 CR626878 Danio rer
c	651	56.6	4.2	202825	2	BX927088 BX927088 Danio rer
	652	56.6	4.2	206042	2	CR753794 CR753794 Danio rer
	653	56.6	4.2	209903	2	CR376757 CR376757 Danio rer
c	654	56.6	4.2	212365	2	CR589876 CR589876 Danio rer
	655	56.6	4.2	225861	2	CR628381 CR628381 Danio rer
c	656	56.6	4.2	235760	2	CR556713 CR556713 Danio rer
	657	56.6	4.2	237005	2	CR749168 CR749168 Danio rer
	658	56.6	4.2	243096	2	CR388362 CR388362 Danio rer
c	659	56.6	4.2	257570	2	CR354431 CR354431 Danio rer
c	660	56.6	4.2	273275	3	AE014828 AE014828 Plasmodiu
c	661	56.6	4.2	285490	2	CR391920 CR391920 Danio rer
	662	56.6	4.2	319520	2	BX936378 BX936378 Danio rer
c	663	56.4	4.2	5286	6	CQ806574 CQ806574 Sequence
c	664	56.4	4.2	5286	6	AX795682 AX795682 Sequence
c	665	56.4	4.2	8633	3	PFPFMDR1 X56851 P.falciparu
c	666	56.4	4.2	40611	3	AC116987 AC116987 Dictyoste
	667	56.4	4.2	99263	2	CNS01DX9 AL139177 Homo sapi
	668	56.4	4.2	119483	5	BX470158 BX470158 Zebrafish
	669	56.4	4.2	125632	2	CR753868 CR753868 Danio rer
c	670	56.4	4.2	156404	2	CR626908 CR626908 Danio rer
c	671	56.4	4.2	159726	2	CR356246 CR356246 Danio rer
c	672	56.4	4.2	163795	9	AP000356 AP000356 Homo sapi
c	673	56.4	4.2	166281	2	CR790386 CR790386 Danio rer
	674	56.4	4.2	169215	2	CR318593 CR318593 Danio rer
c	675	56.4	4.2	169979	2	BX901942 BX901942 Danio rer
c	676	56.4	4.2	171424	2	CR749743 CR749743 Danio rer

	677	56.4	4.2	175058	2	CR753843 CR753843 Danio rer
	678	56.4	4.2	175223	9	AC004617 AC004617 Homo sapi
c	679	56.4	4.2	181002	2	BX957288 BX957288 Danio rer
c	680	56.4	4.2	183373	2	CR381594 CR381594 Danio rer
	681	56.4	4.2	187010	2	CR627498 CR627498 Danio rer
	682	56.4	4.2	187155	2	CR388186 CR388186 Danio rer
	683	56.4	4.2	188406	2	CR381547 CR381547 Danio rer
c	684	56.4	4.2	196722	2	CR352307 CR352307 Danio rer
	685	56.4	4.2	199296	2	CR753895 CR753895 Danio rer
	686	56.4	4.2	210579	2	CR792427 CR792427 Danio rer
c	687	56.4	4.2	211723	2	CR749164 CR749164 Danio rer
c	688	56.4	4.2	218311	2	CR749741 CR749741 Danio rer
	689	56.4	4.2	227211	2	CR847561 CR847561 Danio rer
c	690	56.4	4.2	228431	2	CR788237 CR788237 Danio rer
	691	56.4	4.2	243006	2	BX927082 BX927082 Danio rer
c	692	56.4	4.2	245802	2	AC006279 AC006279 Plasmodiu
	693	56.4	4.2	248167	2	CR627491 CR627491 Danio rer
	694	56.4	4.2	252394	3	AE014833 AE014833 Plasmodiu
c	695	56.4	4.2	252450	2	CR753861 CR753861 Danio rer
	696	56.4	4.2	260929	3	AE014852 AE014852 Plasmodiu
	697	56.2	4.2	2009	6	AX457067 AX457067 Sequence
	698	56.2	4.2	57304	9	AC004802 AC004802 Homo sapi
c	699	56.2	4.2	100925	9	AC012627 AC012627 Homo sapi
c	700	56.2	4.2	110000	2	CR318630_0 CR318630 Danio rer
	701	56.2	4.2	110000	2	CR555291_1 Continuation (2 of
c	702	56.2	4.2	110000	2	CR555291_2 Continuation (3 of
c	703	56.2	4.2	110000	3	AC116305_1 Continuation (2 of
c	704	56.2	4.2	110000	3	AC116305_2 Continuation (3 of
	705	56.2	4.2	134972	2	CR388177 CR388177 Danio rer
	706	56.2	4.2	153701	2	AC147533 AC147533 Macropus
c	707	56.2	4.2	157467	2	CR792423 CR792423 Danio rer
	708	56.2	4.2	158950	9	AL391425 AL391425 Human DNA
	709	56.2	4.2	159300	2	CR759813 CR759813 Danio rer
	710	56.2	4.2	159603	2	CR762422 CR762422 Danio rer
c	711	56.2	4.2	160276	2	CR376832 CR376832 Danio rer
	712	56.2	4.2	166281	2	CR790386 CR790386 Danio rer
	713	56.2	4.2	167320	2	CR450810 CR450810 Danio rer
	714	56.2	4.2	169098	2	CR678488 CR678488 Danio rer
	715	56.2	4.2	169257	2	CR626961 CR626961 Danio rer
	716	56.2	4.2	185618	2	CR847796 CR847796 Danio rer
	717	56.2	4.2	187478	2	BX927379 BX927379 Danio rer
c	718	56.2	4.2	192772	2	CR735144 CR735144 Danio rer
	719	56.2	4.2	193505	2	CR628366 CR628366 Danio rer
	720	56.2	4.2	208710	2	CR788244 CR788244 Danio rer
	721	56.2	4.2	215231	2	CR385085 CR385085 Danio rer
	722	56.2	4.2	235532	9	AC008739 AC008739 Homo sapi
	723	56.2	4.2	236582	2	CR388102 CR388102 Danio rer
c	724	56.2	4.2	252394	3	AE014833 AE014833 Plasmodiu
	725	56.2	4.2	260850	2	CR628328 CR628328 Danio rer
c	726	56.2	4.2	310003	1	AE014016 AE014016 Buchnera
c	727	56.2	4.2	349980	6	AX344572 AX344572 Sequence
	728	56	4.2	2724	1	AF268055 AF268055 Candidatu
	729	56	4.2	28150	9	AC137733 AC137733 Homo sapi
	730	56	4.2	40611	3	AC116987 AC116987 Dictyoste
c	731	56	4.2	72487	5	BX294109 BX294109 Zebrafish
c	732	56	4.2	76354	9	AC048340 AC048340 Homo sapi
	733	56	4.2	89665	9	AC063976 AC063976 Homo sapi
c	734	56	4.2	120007	9	AF064864 AF064864 Homo sapi
c	735	56	4.2	120609	9	AF165176 AF165176 Homo sapi
c	736	56	4.2	127277	9	AC010175 AC010175 Homo sapi
	737	56	4.2	135203	9	AC025278 AC025278 Homo sapi
c	738	56	4.2	144314	2	CR751232 CR751232 Danio rer
	739	56	4.2	148856	2	BX942828 BX942828 Danio rer
	740	56	4.2	149603	9	AC022100 AC022100 Homo sapi
c	741	56	4.2	151951	2	CR762429 CR762429 Danio rer
	742	56	4.2	152356	2	CR762406 CR762406 Danio rer
	743	56	4.2	157605	2	CR450752 CR450752 Danio rer
c	744	56	4.2	162666	9	AC125796 AC125796 Homo sapi
c	745	56	4.2	163660	2	AC046165 AC046165 Homo sapi
	746	56	4.2	163930	2	CR847885 CR847885 Danio rer
	747	56	4.2	167396	2	CR352259 CR352259 Danio rer
c	748	56	4.2	167592	2	CR847845 CR847845 Danio rer
c	749	56	4.2	170606	2	BX957335 BX957335 Danio rer
	750	56	4.2	175919	2	CR786574 CR786574 Danio rer
	751	56	4.2	178388	9	AC079630 AC079630 Homo sapi
c	752	56	4.2	185596	9	AC021553 AC021553 Homo sapi
c	753	56	4.2	187415	2	CR759968 CR759968 Danio rer
	754	56	4.2	187962	2	CR759825 CR759825 Danio rer
c	755	56	4.2	196613	2	CR735105 CR735105 Danio rer
c	756	56	4.2	198349	2	CR788292 CR788292 Danio rer
	757	56	4.2	206832	2	CR759927 CR759927 Danio rer
c	758	56	4.2	213184	2	CR749750 CR749750 Danio rer
	759	56	4.2	222081	2	CR759875 CR759875 Danio rer
	760	56	4.2	239323	2	CR788304 CR788304 Danio rer
c	761	56	4.2	239941	2	CR749176 CR749176 Danio rer
	762	56	4.2	245802	2	AC006279 AC006279 Plasmodiu
c	763	56	4.2	250621	2	CR792433 CR792433 Danio rer
c	764	56	4.2	260929	3	AE014852 AE014852 Plasmodiu
	765	56	4.2	320170	2	CR792440 CR792440 Danio rer
c	766	56	4.2	338224	2	CR749766 CR749766 Danio rer
c	767	56	4.2	340000	9	HS21C083 AL163283 Homo sapi
	768	56	4.2	349174	1	AB063522 AB063522 Wiggleswo
	769	55.8	4.1	67970	3	PFMAL1P3 AL031746 Plasmodiu
c	770	55.8	4.1	103344	9	HS1100E15 AL035551 Human DNA
	771	55.8	4.1	108908	3	PFMAL3P8 AL034560 Plasmodiu
c	772	55.8	4.1	110000	2	PFMAL13_04 Continuation (5 of
	773	55.8	4.1	110000	2	PFMAL8P1_08 Continuation (9 of
c	774	55.8	4.1	111861	9	AC069435 AC069435 Homo sapi
c	775	55.8	4.1	120346	5	BX548060 BX548060 Zebrafish
c	776	55.8	4.1	127820	9	HSJ612B15 AL049597 Human DNA
c	777	55.8	4.1	139760	2	CR388023 CR388023 Danio rer
	778	55.8	4.1	141986	2	CR792459 CR792459 Danio rer
c	779	55.8	4.1	149238	2	CR847833 CR847833 Danio rer
	780	55.8	4.1	151482	9	AC068765 AC068765 Homo sapi
	781	55.8	4.1	152359	9	AC093790 AC093790 Homo sapi
c	782	55.8	4.1	154680	2	CR788243 CR788243 Danio rer
	783	55.8	4.1	161474	2	AC144356 AC144356 Danio rer
c	784	55.8	4.1	172777	2	CR847809 CR847809 Danio rer
c	785	55.8	4.1	173234	2	CR550306 CR550306 Danio rer
c	786	55.8	4.1	175235	2	CR790380 CR790380 Danio rer
	787	55.8	4.1	175260	2	CR786568 CR786568 Danio rer
c	788	55.8	4.1	176196	2	CR762444 CR762444 Danio rer
	789	55.8	4.1	179607	2	CR388084 CR388084 Danio rer
	790	55.8	4.1	185272	2	CR751602 CR751602 Danio rer
c	791	55.8	4.1	187636	2	CR376762 CR376762 Danio rer
c	792	55.8	4.1	189476	2	AC009893 AC009893 Homo sapi
	793	55.8	4.1	190890	9	AC087385 AC087385 Homo sapi
c	794	55.8	4.1	195319	2	CR388410 CR388410 Danio rer
c	795	55.8	4.1	195942	2	CR394542 CR394542 Danio rer
	796	55.8	4.1	209215	2	CR751543 CR751543 Danio rer
	797	55.8	4.1	210338	2	CR753862 CR753862 Danio rer
	798	55.8	4.1	213184	2	CR749750 CR749750 Danio rer
	799	55.8	4.1	223166	2	CR790362 CR790362 Danio rer
c	800	55.8	4.1	228732	2	CR391929 CR391929 Danio rer
c	801	55.8	4.1	251956	2	CR626889 CR626889 Danio rer
c	802	55.6	4.1	5500	3	PFAMDF M29154 P.falciparu
c	803	55.6	4.1	14867	3	AE001398 AE001398 Plasmodiu
c	804	55.6	4.1	28150	9	AC137733 AC137733 Homo sapi
c	805	55.6	4.1	34956	5	CR547122 CR547122 Zebrafish
	806	55.6	4.1	47601	9	AC078802 AC078802 Homo sapi
c	807	55.6	4.1	58891	2	AC021479 AC021479 Mus muscu
c	808	55.6	4.1	103457	2	CR762416 CR762416 Danio rer
	809	55.6	4.1	110000	2	PFMAL13_11 Continuation (12 o
	810	55.6	4.1	110000	2	PFMAL13_12 Continuation (13 o
c	811	55.6	4.1	110000	3	PFMAL1P2_1 Continuation (2 of
	812	55.6	4.1	131149	2	CR626939 CR626939 Danio rer
	813	55.6	4.1	146667	2	CR555294 CR555294 Danio rer
	814	55.6	4.1	151032	9	AC105201 AC105201 Homo sapi
	815	55.6	4.1	151802	3	AC114263 AC114263 Dictyoste
c	816	55.6	4.1	157405	2	CR790377 CR790377 Danio rer
	817	55.6	4.1	158548	3	PFMAL3P2 AL034558 Plasmodiu
	818	55.6	4.1	161449	2	CR752652 CR752652 Danio rer
	819	55.6	4.1	162325	2	CR774195 CR774195 Danio rer
	820	55.6	4.1	162892	5	BX004873 BX004873 Zebrafish
c	821	55.6	4.1	167245	2	CR626882 CR626882 Danio rer
c	822	55.6	4.1	172706	2	AL391135 AL391135 Homo sapi

c 823	55.6	4.1	175260	2	CR786568	CR786568 Danio rer
824	55.6	4.1	175842	9	AL731547	Human DNA
c 825	55.6	4.1	178427	2	CR392006	CR392006 Danio rer
826	55.6	4.1	180095	2	BX901961	BX901961 Danio rer
c 827	55.6	4.1	181223	2	CR376799	CR376799 Danio rer
828	55.6	4.1	181557	2	CR847945	CR847945 Danio rer
c 829	55.6	4.1	182681	2	CR627485	CR627485 Danio rer
c 830	55.6	4.1	182871	3	AC117176	Dictyoste
831	55.6	4.1	184260	2	AC144594	AC144594 Danio rer
c 832	55.6	4.1	185618	2	CR847796	CR847796 Danio rer
c 833	55.6	4.1	199230	2	CR762470	Danio rer
c 834	55.6	4.1	199551	2	AC006281	AC006281 Plasmodiu
835	55.6	4.1	199567	2	CR759921	CR759921 Danio rer
c 836	55.6	4.1	207198	2	CR376829	Danio rer
837	55.6	4.1	210077	2	CR450750	CR450750 Danio rer
838	55.6	4.1	213698	2	CR788262	CR788262 Danio rer
839	55.6	4.1	223939	2	CR788309	Danio rer
840	55.6	4.1	228609	2	CR759885	CR759885 Danio rer
841	55.6	4.1	229740	2	CR790370	CR790370 Danio rer
c 842	55.6	4.1	233552	2	CR769784	Danio rer
c 843	55.6	4.1	239484	2	CR759895	CR759895 Danio rer
c 844	55.6	4.1	243235	2	CR318614	CR318614 Danio rer
845	55.6	4.1	250531	3	AE014845	Plasmodiu
c 846	55.6	4.1	251382	2	CR626924	CR626924 Danio rer
c 847	55.6	4.1	282240	2	CR753865	CR753865 Danio rer
848	55.6	4.1	291781	2	CR792436	Danio rer
849	55.6	4.1	313050	3	PFA929352	AL929352 Plasmodiu
c 850	55.6	4.1	337203	3	CR382401	CR382401 Plasmodiu
c 851	55.6	4.1	349980	6	AX344550	Sequence
c 852	55.4	4.1	5286	6	CQ806844	Sequence
c 853	55.4	4.1	5286	6	CQ807118	Sequence
c 854	55.4	4.1	5286	6	AX795782	Sequence
c 855	55.4	4.1	5286	6	AX795898	Sequence
c 856	55.4	4.1	10328	6	AX346446	Sequence
c 857	55.4	4.1	110000	2	PFMAL13_13	Continuation (14 o
858	55.4	4.1	110000	2	PFMAL7P1_00	AL844506 Plasmodiu
c 859	55.4	4.1	114226	2	AC004710	AC004710 Plasmodiu
860	55.4	4.1	144765	2	CR759966	Danio rer
c 861	55.4	4.1	148937	2	CR361568	CR361568 Danio rer
c 862	55.4	4.1	152209	9	HS1108D11	AL034419 Human DNA
863	55.4	4.1	168202	2	CR759804	Danio rer
c 864	55.4	4.1	171272	2	CR450726	CR450726 Danio rer
c 865	55.4	4.1	172399	2	CR762388	Danio rer
866	55.4	4.1	172777	2	CR847809	Danio rer
867	55.4	4.1	172811	9	AC066608	AC066608 Homo sapi
c 868	55.4	4.1	178273	2	AC005308	AC005308 Plasmodiu
869	55.4	4.1	180540	2	CR847859	Danio rer
870	55.4	4.1	182223	2	CR790384	Danio rer
c 871	55.4	4.1	192751	2	BX927366	BX927366 Danio rer
c 872	55.4	4.1	196490	2	AC005507	Plasmodiu
c 873	55.4	4.1	197199	2	CR536605	CR536605 Danio rer
874	55.4	4.1	197951	2	CR392343	CR392343 Danio rer
c 875	55.4	4.1	213790	2	CR678465	Danio rer
876	55.4	4.1	233658	2	CR354421	CR354421 Danio rer
877	55.4	4.1	250421	3	AE014849	AE014849 Plasmodiu
878	55.4	4.1	250743	3	AE014836	AE014836 Plasmodiu
c 879	55.4	4.1	251551	3	AE014844	AE014844 Plasmodiu
880	55.4	4.1	347582	3	PFMAL4P1	AL034557 Plasmodiu
881	55.4	4.1	348174	3	CR382399	CR382399 Plasmodiu
882	55.2	4.1	84274	5	BX470141	BX470141 Zebrafish
883	55.2	4.1	110000	2	PFMAL7P1_11	Continuation (12 o
884	55.2	4.1	133016	2	CR749774	Danio rer
885	55.2	4.1	134708	9	AC147046	AC147046 Pan trogl
c 886	55.2	4.1	136657	9	AC068600	AC068600 Homo sapi
887	55.2	4.1	138604	9	AC104826	Homo sapi
888	55.2	4.1	147948	2	CR381577	CR381577 Danio rer
c 889	55.2	4.1	148525	2	AC016675	AC016675 Homo sapi
c 890	55.2	4.1	150495	2	CR513781	Danio rer
c 891	55.2	4.1	155010	2	CR524821	CR524821 Danio rer
c 892	55.2	4.1	156978	2	CR339045	CR339045 Danio rer
c 893	55.2	4.1	162435	2	CR759820	Danio rer
c 894	55.2	4.1	162977	2	CR631122	CR631122 Danio rer
c 895	55.2	4.1	163724	2	CR788299	CR788299 Danio rer
896	55.2	4.1	166132	2	CR759748	CR759748 Danio rer
c 897	55.2	4.1	167437	2	CR450713	Danio rer
c 898	55.2	4.1	171233	2	CR626886	CR626886 Danio rer
899	55.2	4.1	171537	2	CR762390	Danio rer
c 900	55.2	4.1	175433	2	CR786578	Danio rer
901	55.2	4.1	180506	2	BX005403	BX005403 Danio rer
c 902	55.2	4.1	183318	2	CR376728	Danio rer
903	55.2	4.1	201659	2	AC146419	AC146419 Pan trogl
c 904	55.2	4.1	204486	2	CR752655	CR752655 Danio rer
c 905	55.2	4.1	208116	2	CR555302	CR555302 Danio rer
906	55.2	4.1	211185	2	CR769766	Danio rer
907	55.2	4.1	223904	2	CR759864	CR759864 Danio rer
908	55.2	4.1	239484	2	CR759895	CR759895 Danio rer
909	55.2	4.1	248767	2	CR769782	Danio rer
c 910	55.2	4.1	250078	3	AE014829	AE014829 Plasmodiu
c 911	55.2	4.1	250195	3	AE014831	AE014831 Plasmodiu
912	55.2	4.1	269242	2	CR388212	Danio rer
c 913	55.2	4.1	272698	3	PFMAL4P4	AL035477 Plasmodiu
914	55	4.1	1806	3	AY135378	AY135378 Plasmodiu
915	55	4.1	2000	6	AX655393	Sequence
916	55	4.1	4382	3	PFSC04084	AL010254 Plasmodiu
c 917	55	4.1	5286	6	CQ806843	Sequence
c 918	55	4.1	5286	6	CQ807117	Sequence
c 919	55	4.1	5286	6	AX795781	Sequence
c 920	55	4.1	5286	6	AX795897	Sequence
921	55	4.1	6181	6	AX251970	Sequence
922	55	4.1	6181	6	AX344362	Sequence
923	55	4.1	6181	6	AX348755	Sequence
c 924	55	4.1	16217	6	AX345527	Sequence
c 925	55	4.1	47577	3	AF396436	AF396436 Tetrahyme
c 926	55	4.1	80803	9	AC133522	AC133522 Homo sapi
c 927	55	4.1	102314	2	BX571814	BX571814 Danio rer
928	55	4.1	110000	2	AC139803_1	Continuation (2 of
c 929	55	4.1	113812	8	AC149135	AC149135 Medicago
c 930	55	4.1	131378	9	AC112653	AC112653 Homo sapi
931	55	4.1	142372	9	AC132152	AC132152 Homo sapi
932	55	4.1	143244	9	AC091997	AC091997 Homo sapi
933	55	4.1	153459	2	CR847994	CR847994 Danio rer
c 934	55	4.1	155091	2	CR759783	CR759783 Danio rer
935	55	4.1	159862	2	CR788253	CR788253 Danio rer
c 936	55	4.1	163070	2	CR774194	CR774194 Danio rer
c 937	55	4.1	173585	9	AC090527	AC090527 Homo sapi
938	55	4.1	176898	9	AC117569	AC117569 Homo sapi
c 939	55	4.1	178474	2	CR792417	CR792417 Danio rer
940	55	4.1	178785	9	AC068139	AC068139 Homo sapi
c 941	55	4.1	178840	2	BX936414	BX936414 Danio rer
c 942	55	4.1	181480	2	CR628393	CR628393 Danio rer
943	55	4.1	183285	2	BX899180	BX899180 Danio rer
c 944	55	4.1	185748	2	AC137308	AC137308 Rattus no
c 945	55	4.1	194028	2	AC111077	AC111077 Homo sapi
c 946	55	4.1	199874	2	CR626878	CR626878 Danio rer
c 947	55	4.1	200752	2	CR548622	CR548622 Danio rer
c 948	55	4.1	201312	2	AC067900	AC067900 Homo sapi
c 949	55	4.1	204804	2	CR354372	CR354372 Danio rer
c 950	55	4.1	210338	2	CR753862	CR753862 Danio rer
c 951	55	4.1	210384	2	CR556714	CR556714 Danio rer
952	55	4.1	216023	2	BX957254	BX957254 Danio rer
953	55	4.1	235069	2	BX936448	BX936448 Danio rer
c 954	55	4.1	253924	3	AE014822	AE014822 Plasmodiu
955	54.8	4.1	961	3	AY351412	AY351412 Arethusan
956	54.8	4.1	2718	1	AF268062	AF268062 Candidatu
957	54.8	4.1	2982	3	DDISGSPA	M33862 Dictyosteli
c 958	54.8	4.1	14459	3	AE001383	AE001383 Plasmodiu
c 959	54.8	4.1	105842	9	AC107387	AC107387 Homo sapi
c 960	54.8	4.1	110000	3	AC116984_1	Continuation (2 of
961	54.8	4.1	110000	3	PFMAL1P2_0	AL031745 Plasmodiu
962	54.8	4.1	146917	2	CR450801	CR450801 Danio rer
c 963	54.8	4.1	149563	2	CR376750	CR376750 Danio rer
964	54.8	4.1	149816	2	CR812918	CR812918 Danio rer
c 965	54.8	4.1	154486	2	CR847972	CR847972 Danio rer
c 966	54.8	4.1	154601	2	CR759745	CR759745 Danio rer
967	54.8	4.1	157090	2	CR786573	CR786573 Danio rer
c 968	54.8	4.1	160892	2	CR381637	CR381637 Danio rer

969	54.8	4.1	161056	2	CR388093	CR388093 Danio rer
970	54.8	4.1	165140	2	CR759821	CR759821 Danio rer
971	54.8	4.1	167953	2	AC010948	AC010948 Homo sapi
c 972	54.8	4.1	170141	2	AL611928	AL611928 Homo sapi
c 973	54.8	4.1	170325	2	CR788305	CR788305 Danio rer
974	54.8	4.1	170703	2	BX897681	BX897681 Danio rer
c 975	54.8	4.1	172206	2	CR788323	CR788323 Danio rer
c 976	54.8	4.1	180279	2	BX901957	BX901957 Danio rer
977	54.8	4.1	182681	2	CR627485	CR627485 Danio rer
c 978	54.8	4.1	185085	2	CR762404	CR762404 Danio rer
c 979	54.8	4.1	186431	2	AC022281	AC022281 Homo sapi
c 980	54.8	4.1	188414	2	CR388091	CR388091 Danio rer
c 981	54.8	4.1	190165	2	AC012344	AC012344 Homo sapi
982	54.8	4.1	191689	2	BX957320	BX957320 Danio rer
c 983	54.8	4.1	194392	2	CR788233	CR788233 Danio rer
c 984	54.8	4.1	200260	2	CR753814	CR753814 Danio rer
c 985	54.8	4.1	205339	2	CR388181	CR388181 Danio rer
986	54.8	4.1	208029	2	CR318659	CR318659 Danio rer
c 987	54.8	4.1	210310	2	CR749177	CR749177 Danio rer
988	54.8	4.1	212499	2	CR626887	CR626887 Danio rer
c 989	54.8	4.1	215966	2	CR558305	CR558305 Danio rer
990	54.8	4.1	218659	2	BX942812	BX942812 Danio rer
991	54.8	4.1	222133	2	CR762487	CR762487 Danio rer
992	54.8	4.1	243066	2	AC120999	AC120999 Rattus no
c 993	54.8	4.1	249995	3	AE014840	AE014840 Plasmodiu
994	54.8	4.1	253924	3	AE014822	AE014822 Plasmodiu
c 995	54.8	4.1	281723	3	PFA929359	AL929359 Plasmodiu
996	54.8	4.1	312724	3	AE003846	AE003846 Drosophil
c 997	54.8	4.1	322588	2	CR385047	CR385047 Danio rer
998	54.8	4.1	347050	3	PFA929351	AL929351 Plasmodiu
999	54.6	4.1	8622	8	YSCMTCYTOC	M97514 Saccharomyc
c1000	54.6	4.1	78578	2	PFMAL13P9	AL096783 Plasmodiu
1001	54.6	4.1	79018	9	AL627107	AL627107 Human DNA
c1002	54.6	4.1	79018	9	AL627107	AL627107 Human DNA
c1003	54.6	4.1	86258	5	BX842699	BX842699 Zebrafish
1004	54.6	4.1	90373	3	AC115680	AC115680 Dictyoste
1005	54.6	4.1	105320	3	AC116920	AC116920 Dictyoste
c1006	54.6	4.1	110000	2	PFMAL13_15	Continuation (16 o
c1007	54.6	4.1	120025	9	AC146384	AC146384 Pan trogl
1008	54.6	4.1	133218	9	AC008410	AC008410 Homo sapi
c1009	54.6	4.1	152971	2	CR769777	CR769777 Danio rer
c1010	54.6	4.1	156657	2	CR769763	CR769763 Danio rer
c1011	54.6	4.1	165284	2	CR759767	CR759767 Danio rer
c1012	54.6	4.1	167396	2	CR352259	CR352259 Danio rer
1013	54.6	4.1	169794	2	AC004688	AC004688 Plasmodiu
1014	54.6	4.1	173671	9	AC100778	AC100778 Homo sapi
1015	54.6	4.1	175471	2	CR678388	CR678388 Danio rer
c1016	54.6	4.1	177301	9	AC103949	AC103949 Homo sapi
c1017	54.6	4.1	178045	2	CR762472	CR762472 Danio rer
1018	54.6	4.1	183137	2	CR759797	CR759797 Danio rer
c1019	54.6	4.1	183158	2	CR759872	CR759872 Danio rer
c1020	54.6	4.1	183293	2	CR769781	CR769781 Danio rer
c1021	54.6	4.1	183580	2	CR555299	CR555299 Danio rer
1022	54.6	4.1	186007	2	CR847530	CR847530 Danio rer
1023	54.6	4.1	186723	2	AC027752	AC027752 Homo sapi
1024	54.6	4.1	188529	2	BX927370	BX927370 Danio rer
c1025	54.6	4.1	188963	2	CR762411	CR762411 Danio rer
c1026	54.6	4.1	192139	9	AC021955	AC021955 Homo sapi
1027	54.6	4.1	195585	2	CR735129	CR735129 Danio rer
1028	54.6	4.1	196149	2	AC004709	AC004709 Plasmodiu
1029	54.6	4.1	196888	2	CR456627	CR456627 Danio rer
1030	54.6	4.1	197455	9	AC005701	AC005701 Homo sapi
1031	54.6	4.1	198572	2	CR792413	CR792413 Danio rer
c1032	54.6	4.1	199931	2	CR589877	CR589877 Danio rer
1033	54.6	4.1	203320	2	AC136933	AC136933 Homo sapi
1034	54.6	4.1	219461	2	BX842685	BX842685 Danio rer
c1035	54.6	4.1	223166	2	CR790362	CR790362 Danio rer
c1036	54.6	4.1	224393	2	CR749751	CR749751 Danio rer
1037	54.6	4.1	232824	2	CR759946	CR759946 Danio rer
c1038	54.6	4.1	234009	2	CR383672	CR383672 Danio rer
1039	54.6	4.1	247684	2	BX901883	BX901883 Danio rer
c1040	54.6	4.1	252632	3	AE014818	AE014818 Plasmodiu
1041	54.6	4.1	252650	3	AE014847	AE014847 Plasmodiu
c1042	54.6	4.1	260850	2	CR628328	CR628328 Danio rer
c1043	54.6	4.1	340552	3	PFA929354	AL929354 Plasmodiu
1044	54.6	4.1	341050	3	PFA929357	AL929357 Plasmodiu
c1045	54.4	4.0	500	6	CQ398760	CQ398760 Sequence
c1046	54.4	4.0	500	6	CQ405041	CQ405041 Sequence
1047	54.4	4.0	700	6	AX183285	AX183285 Sequence
1048	54.4	4.0	2710	1	AF250388	AF250388 Carsonell
c1049	54.4	4.0	6109	6	AX346632	AX346632 Sequence
c1050	54.4	4.0	6631	6	AX323725	AX323725 Sequence
c1051	54.4	4.0	7490	6	AX345185	AX345185 Sequence
1052	54.4	4.0	57203	3	AC115581	AC115581 Dictyoste
c1053	54.4	4.0	75523	9	AL627233	AL627233 Human DNA
c1054	54.4	4.0	80150	9	AC134620	AC134620 Homo sapi
c1055	54.4	4.0	105686	9	AC012072	AC012072 Homo sapi
c1056	54.4	4.0	110000	2	PFMAL8P1_05	Continuation (6 of
1057	54.4	4.0	110000	3	AC116984_3	Continuation (4 of
1058	54.4	4.0	125685	9	AC073310	AC073310 Homo sapi
1059	54.4	4.0	132254	3	AC116330	AC116330 Dictyoste
c1060	54.4	4.0	139409	9	AC069181	AC069181 Homo sapi
1061	54.4	4.0	148937	2	CR361568	CR361568 Danio rer
1062	54.4	4.0	152724	2	CR769778	CR769778 Danio rer
1063	54.4	4.0	153702	9	AL645730	AL645730 Human DNA
c1064	54.4	4.0	154850	2	CR376747	CR376747 Danio rer
1065	54.4	4.0	159621	9	AC083801	AC083801 Homo sapi
c1066	54.4	4.0	159862	2	CR788253	CR788253 Danio rer
1067	54.4	4.0	161444	2	BX897740	BX897740 Danio rer
c1068	54.4	4.0	162098	2	CR847881	CR847881 Danio rer
1069	54.4	4.0	163814	5	AL953863	AL953863 Zebrafish
c1070	54.4	4.0	164117	2	CR792430	CR792430 Danio rer
c1071	54.4	4.0	164300	2	CR450717	CR450717 Danio rer
1072	54.4	4.0	164376	2	AC135317	AC135317 Medicago
1073	54.4	4.0	167124	2	CR812482	CR812482 Danio rer
1074	54.4	4.0	170569	2	CR792421	CR792421 Danio rer
1075	54.4	4.0	170796	2	AC069416	AC069416 Homo sapi
1076	54.4	4.0	171233	2	CR626886	CR626886 Danio rer
c1077	54.4	4.0	171255	9	AL691447	AL691447 Human DNA
c1078	54.4	4.0	171317	9	AC020941	AC020941 Homo sapi
1079	54.4	4.0	172828	2	CR790379	CR790379 Danio rer
c1080	54.4	4.0	177462	2	CR749767	CR749767 Danio rer
c1081	54.4	4.0	178363	2	AC148615	AC148615 Ictalurus
c1082	54.4	4.0	178733	9	AC026003	AC026003 Homo sapi
c1083	54.4	4.0	181069	2	CR762471	CR762471 Danio rer
c1084	54.4	4.0	185142	2	CR678384	CR678384 Danio rer
c1085	54.4	4.0	188777	2	CR774179	CR774179 Danio rer
c1086	54.4	4.0	195742	2	AC151362	AC151362 Ictalurus
1087	54.4	4.0	196613	2	CR735105	CR735105 Danio rer
c1088	54.4	4.0	208848	2	AC139608	AC139608 Rattus no
1089	54.4	4.0	211855	2	CR753866	CR753866 Danio rer
1090	54.4	4.0	214310	2	CR847982	CR847982 Danio rer
1091	54.4	4.0	216831	2	CR627490	CR627490 Danio rer
c1092	54.4	4.0	222489	2	CR847953	CR847953 Danio rer
1093	54.4	4.0	226728	2	CR318596	CR318596 Danio rer
1094	54.4	4.0	239613	2	CR790367	CR790367 Danio rer
1095	54.4	4.0	273275	3	AE014828	AE014828 Plasmodiu
c1096	54.4	4.0	291781	2	CR792436	CR792436 Danio rer
c1097	54.2	4.0	859	9	AF385609	AF385609 Homo sapi
c1098	54.2	4.0	1987	3	DDIRAP1A	L09750 Dictyosteli
c1099	54.2	4.0	9180	6	AX346866	AX346866 Sequence
c1100	54.2	4.0	15980	3	CCA242872	AJ242872 Ceratitis
c1101	54.2	4.0	17443	3	AC024806	AC024806 Caenorhab
c1102	54.2	4.0	33651	3	AC114261	AC114261 Dictyoste
1103	54.2	4.0	59051	9	AC144547	AC144547 Homo sapi
c1104	54.2	4.0	110000	2	PFMAL13_23	Continuation (24 o
1105	54.2	4.0	110000	2	PFMAL7P1_02	Continuation (3 of
1106	54.2	4.0	110000	2	PFMAL7P1_03	Continuation (4 of
c1107	54.2	4.0	110000	2	PFMAL8P1_06	Continuation (7 of
c1108	54.2	4.0	115933	9	AC015842	AC015842 Homo sapi
c1109	54.2	4.0	125685	9	AC073310	AC073310 Homo sapi
1110	54.2	4.0	131734	2	CR792420	CR792420 Danio rer
c1111	54.2	4.0	136713	9	AC112255	AC112255 Homo sapi
c1112	54.2	4.0	140580	2	CR628334	CR628334 Danio rer
1113	54.2	4.0	143996	9	AC016912	AC016912 Homo sapi
1114	54.2	4.0	144228	9	AC068599	AC068599 Homo sapi

1115	54.2	4.0	152878	3	CEY18D10A	AL034393	Caenorhab
c1116	54.2	4.0	156060	2	AC004153	AC004153	Plasmodiu
1117	54.2	4.0	156578	2	CR786577	CR786577	Danio rer
c1118	54.2	4.0	160654	2	CR788241	CR788241	Danio rer
c1119	54.2	4.0	162810	2	CR392028	CR392028	Danio rer
c1120	54.2	4.0	163280	2	AC141308	AC141308	Homo sapi
1121	54.2	4.0	163437	9	AC092606	AC092606	Homo sapi
1122	54.2	4.0	163475	2	CR628390	CR628390	Danio rer
c1123	54.2	4.0	164402	2	CR407571	CR407571	Danio rer
1124	54.2	4.0	164910	2	CR792457	CR792457	Danio rer
c1125	54.2	4.0	167376	5	BX004803	BX004803	Zebrafish
c1126	54.2	4.0	174041	9	AL356423	AL356423	Human DNA
c1127	54.2	4.0	174070	9	AC146092	AC146092	Pan trogl
1128	54.2	4.0	178095	2	CR753874	CR753874	Danio rer
c1129	54.2	4.0	179603	6	CQ870485	CQ870485	Sequence
1130	54.2	4.0	185596	9	AC021553	AC021553	Homo sapi
1131	54.2	4.0	191745	5	AL929309	AL929309	Zebrafish
1132	54.2	4.0	193626	2	CR391971	CR391971	Danio rer
c1133	54.2	4.0	194354	2	BX908786	BX908786	Danio rer
1134	54.2	4.0	194392	2	CR788233	CR788233	Danio rer
c1135	54.2	4.0	196049	2	CR388037	CR388037	Danio rer
c1136	54.2	4.0	201838	2	CR752642	CR752642	Danio rer
c1137	54.2	4.0	203320	2	AC136933	AC136933	Homo sapi
c1138	54.2	4.0	204272	2	CR762441	CR762441	Danio rer
1139	54.2	4.0	205048	2	CR589944	CR589944	Danio rer
c1140	54.2	4.0	205954	2	BX470257	BX470257	Danio rer
c1141	54.2	4.0	205980	2	CR788301	CR788301	Danio rer
1142	54.2	4.0	207592	2	CR847888	CR847888	Danio rer
c1143	54.2	4.0	216899	2	CR759846	CR759846	Danio rer
1144	54.2	4.0	222859	2	AC119799	AC119799	Pan trogl
c1145	54.2	4.0	257109	3	AC116963	AC116963	Dictyoste
1146	54.2	4.0	343050	3	PFA929353	AL929353	Plasmodiu
c1147	54	4.0	5513	9	AC098796	AC098796	Homo sapi
c1148	54	4.0	6106	6	AX251184	AX251184	Sequence
c1149	54	4.0	6106	6	AX346375	AX346375	Sequence
c1150	54	4.0	6106	6	AX348419	AX348419	Sequence
1151	54	4.0	9424	8	SDO404228	AJ404228	Saccharom
c1152	54	4.0	11288	6	AR134885	AR134885	Sequence
c1153	54	4.0	11288	6	AR182304	AR182304	Sequence
c1154	54	4.0	11288	6	AR370519	AR370519	Sequence
c1155	54	4.0	11288	6	AR479027	AR479027	Sequence
c1156	54	4.0	11288	6	AX269130	AX269130	Sequence
c1157	54	4.0	11288	9	HSCRCANTA	Z21818	H.sapiens c
c1158	54	4.0	15056	6	BD195539	BD195539	Adenoviru
c1159	54	4.0	15056	6	BD224258	BD224258	Adenoviru
c1160	54	4.0	15056	6	AR266427	AR266427	Sequence
c1161	54	4.0	15056	6	AR474484	AR474484	Sequence
c1162	54	4.0	15056	6	AX259954	AX259954	Sequence
c1163	54	4.0	15056	6	AX262359	AX262359	Sequence
c1164	54	4.0	43337	5	BX511016	BX511016	Zebrafish
c1165	54	4.0	105570	9	HS49E3	AL160451	Homo sapi
c1166	54	4.0	106763	9	AP002091	AP002091	Homo sapi
1167	54	4.0	110000	2	CR555291_2	Continuation (3 of	
c1168	54	4.0	110000	2	PFMAL13_26	Continuation (27 o	
1169	54	4.0	120026	2	CR388420	CR388420	Danio rer
1170	54	4.0	124871	2	CR735110	CR735110	Danio rer
c1171	54	4.0	131550	2	CR548629	CR548629	Danio rer
1172	54	4.0	132943	9	AC011287	AC011287	Homo sapi
1173	54	4.0	142025	2	CR792461	CR792461	Danio rer
1174	54	4.0	143117	2	CR762399	CR762399	Danio rer
1175	54	4.0	145992	9	AC134919	AC134919	Homo sapi
1176	54	4.0	148491	2	CR626866	CR626866	Danio rer
1177	54	4.0	153943	2	AC027417	AC027417	Homo sapi
1178	54	4.0	157544	9	AC098590	AC098590	Homo sapi
c1179	54	4.0	161699	9	AC107300	AC107300	Homo sapi
c1180	54	4.0	163835	9	AC136488	AC136488	Homo sapi
c1181	54	4.0	164468	9	AC136489	AC136489	Homo sapi
c1182	54	4.0	164481	2	CR759908	CR759908	Danio rer
c1183	54	4.0	164515	2	BX000440	BX000440	Danio rer
1184	54	4.0	165574	2	CR847571	CR847571	Danio rer
c1185	54	4.0	166014	2	CR762396	CR762396	Danio rer
1186	54	4.0	166284	9	AC108485	AC108485	Homo sapi
1187	54	4.0	170189	2	BX957358	BX957358	Danio rer
c1188	54	4.0	170536	9	AC093914	AC093914	Homo sapi
c1189	54	4.0	172243	9	AC016730	AC016730	Homo sapi
1190	54	4.0	174162	2	CR759781	CR759781	Danio rer
c1191	54	4.0	174198	2	CR762438	CR762438	Danio rer
1192	54	4.0	174574	2	CR759746	CR759746	Danio rer
c1193	54	4.0	175722	2	CR762417	CR762417	Danio rer
1194	54	4.0	175959	2	AL450429	AL450429	Homo sapi
1195	54	4.0	177164	9	AL365202	AL365202	Human DNA
c1196	54	4.0	178207	9	AC140172	AC140172	Homo sapi
c1197	54	4.0	179026	2	CR352332	CR352332	Danio rer
c1198	54	4.0	179483	9	AC019230	AC019230	Homo sapi
1199	54	4.0	180652	2	CR762436	CR762436	Danio rer
1200	54	4.0	183984	2	CR361550	CR361550	Danio rer
1201	54	4.0	187054	2	CR762421	CR762421	Danio rer
c1202	54	4.0	194745	2	BX936315	BX936315	Danio rer
c1203	54	4.0	196420	2	BX908771	BX908771	Danio rer
1204	54	4.0	200557	9	AC009052	AC009052	Homo sapi
1205	54	4.0	201838	2	CR752642	CR752642	Danio rer
1206	54	4.0	202169	2	AC149549	AC149549	Gorilla g
c1207	54	4.0	202676	2	CR788311	CR788311	Danio rer
c1208	54	4.0	207281	2	CR847891	CR847891	Danio rer
1209	54	4.0	214339	2	CR762403	CR762403	Danio rer
1210	54	4.0	218311	2	CR749741	CR749741	Danio rer
c1211	54	4.0	220158	2	CR678095	CR678095	Danio rer
1212	54	4.0	220874	2	CR376848	CR376848	Danio rer
c1213	54	4.0	223966	2	CR318666	CR318666	Danio rer
1214	54	4.0	244683	2	CR392363	CR392363	Danio rer
1215	54	4.0	250022	3	AE014824	AE014824	Plasmodiu
1216	54	4.0	251762	3	AE014851	AE014851	Plasmodiu
c1217	54	4.0	254436	3	AE014827	AE014827	Plasmodiu
c1218	54	4.0	266544	3	AC116956	AC116956	Dictyoste
1219	54	4.0	310779	2	AC005140	AC005140	Plasmodiu
c1220	54	4.0	341050	3	PFA929357	AL929357	Plasmodiu
c1221	54	4.0	343050	3	PFA929353	AL929353	Plasmodiu
c1222	54	4.0	349418	3	CR382398	CR382398	Plasmodiu
1223	53.8	4.0	935	3	AY351413	AY351413	Arethusan
1224	53.8	4.0	1141	6	AX083744	AX083744	Sequence
c1225	53.8	4.0	14433	3	AE001369	AE001369	Plasmodiu
1226	53.8	4.0	16324	3	AY630340	AY630340	Philaenus
1227	53.8	4.0	68843	9	AL450427	AL450427	Human DNA
c1228	53.8	4.0	83728	2	BX927234_3	Continuation (4 of	
1229	53.8	4.0	90550	9	AL592166	AL592166	Human DNA
1230	53.8	4.0	101955	9	AC099759	AC099759	Homo sapi
1231	53.8	4.0	110621	2	CR762468	CR762468	Danio rer
1232	53.8	4.0	130117	9	AC004907	AC004907	Homo sapi
c1233	53.8	4.0	137564	2	CR762439	CR762439	Danio rer
c1234	53.8	4.0	141861	2	CR318612	CR318612	Danio rer
1235	53.8	4.0	148337	2	AC021509	AC021509	Homo sapi
c1236	53.8	4.0	148348	2	AC104074	AC104074	Homo sapi
c1237	53.8	4.0	148484	2	CR450693	CR450693	Danio rer
c1238	53.8	4.0	149603	9	AC022100	AC022100	Homo sapi
c1239	53.8	4.0	152956	2	CR762485	CR762485	Danio rer
1240	53.8	4.0	159763	2	CR751547	CR751547	Danio rer
1241	53.8	4.0	165988	2	CR626888	CR626888	Danio rer
1242	53.8	4.0	166949	2	CR352321	CR352321	Danio rer
c1243	53.8	4.0	170237	9	AL137070	AL137070	Human DNA
1244	53.8	4.0	170534	2	CR391918	CR391918	Danio rer
1245	53.8	4.0	171887	2	CR788232	CR788232	Danio rer
1246	53.8	4.0	172880	9	AC027419	AC027419	Homo sapi
c1247	53.8	4.0	174363	9	AC009133	AC009133	Homo sapi
c1248	53.8	4.0	178025	2	CR752654	CR752654	Danio rer
c1249	53.8	4.0	180430	9	AC096768	AC096768	Homo sapi
c1250	53.8	4.0	180941	9	AC092373	AC092373	Homo sapi
1251	53.8	4.0	181165	2	BX908767	BX908767	Danio rer
1252	53.8	4.0	183951	2	CR318651	CR318651	Danio rer
1253	53.8	4.0	184039	9	AC099327	AC099327	Homo sapi
1254	53.8	4.0	184431	2	CR628331	CR628331	Danio rer
1255	53.8	4.0	185111	9	AL845331	AL845331	Human DNA
1256	53.8	4.0	187636	2	CR376762	CR376762	Danio rer
c1257	53.8	4.0	189598	2	BX957347	BX957347	Danio rer
1258	53.8	4.0	189662	9	AC015468	AC015468	Homo sapi
c1259	53.8	4.0	198143	2	CR759948	CR759948	Danio rer
c1260	53.8	4.0	199240	2	BX936447	BX936447	Danio rer

1261	53.8	4.0	202324	2	AC144712	AC144712 Danio rer
1262	53.8	4.0	204223	2	CR759958	CR759958 Danio rer
c1263	53.8	4.0	204509	2	CR792449	CR792449 Danio rer
c1264	53.8	4.0	210718	2	CR589941	CR589941 Danio rer
1265	53.8	4.0	213056	9	AC103590	AC103590 Homo sapi
c1266	53.8	4.0	214147	2	CR769774	CR769774 Danio rer
1267	53.8	4.0	221501	2	CR762440	CR762440 Danio rer
1268	53.8	4.0	227440	2	CR626904	CR626904 Danio rer
1269	53.8	4.0	229435	2	CR457452	CR457452 Danio rer
1270	53.8	4.0	240437	2	CR391961	CR391961 Danio rer
1271	53.8	4.0	246785	2	CR790385	CR790385 Danio rer
c1272	53.8	4.0	248167	2	CR627491	CR627491 Danio rer
1273	53.8	4.0	250663	3	AE014826	AE014826 Plasmodiu
1274	53.8	4.0	258645	2	CR555295	CR555295 Danio rer
c1275	53.8	4.0	348174	3	CR382399	CR382399 Plasmodiu
1276	53.6	4.0	3586	5	BC070012	BC070012 Danio rer
c1277	53.6	4.0	30157	9	AC073242	AC073242 Homo sapi
c1278	53.6	4.0	32036	9	AL645638	AL645638 Human DNA
c1279	53.6	4.0	67885	2	CR339061_4	Continuation (5 of
c1280	53.6	4.0	116256	9	AL139101	AL139101 Human DNA
c1281	53.6	4.0	134798	5	AL954697	AL954697 Zebrafish
1282	53.6	4.0	142275	2	CR788316	CR788316 Danio rer
c1283	53.6	4.0	144563	2	BX928742	BX928742 Danio rer
c1284	53.6	4.0	145856	2	CR759812	CR759812 Danio rer
c1285	53.6	4.0	148385	2	CR749764	CR749764 Danio rer
c1286	53.6	4.0	148878	2	CR759816	CR759816 Danio rer
1287	53.6	4.0	149122	2	BX927105	BX927105 Danio rer
c1288	53.6	4.0	152358	2	CR628402	CR628402 Danio rer
1289	53.6	4.0	152594	2	CR759923	CR759923 Danio rer
c1290	53.6	4.0	156630	9	BS000087	BS000087 Pan trogl
1291	53.6	4.0	156849	2	CR405684	CR405684 Danio rer
c1292	53.6	4.0	163651	2	CR790381	CR790381 Danio rer
c1293	53.6	4.0	168103	2	CR751601	CR751601 Danio rer
c1294	53.6	4.0	169397	2	CR774191	CR774191 Danio rer
c1295	53.6	4.0	170179	2	CR555290	CR555290 Danio rer
1296	53.6	4.0	170832	2	CR376769	CR376769 Danio rer
1297	53.6	4.0	171514	2	CR759903	CR759903 Danio rer
1298	53.6	4.0	179354	2	CR354588	CR354588 Danio rer
1299	53.6	4.0	179798	2	BX927244	BX927244 Danio rer
c1300	53.6	4.0	180629	2	CR388025	CR388025 Danio rer
1301	53.6	4.0	182390	2	BX927075	BX927075 Danio rer
1302	53.6	4.0	184470	9	AL589823	AL589823 Human DNA
c1303	53.6	4.0	184630	2	CR548632	CR548632 Danio rer
1304	53.6	4.0	185162	9	AC140132	AC140132 Homo sapi
1305	53.6	4.0	185748	2	AC137308	AC137308 Rattus no
1306	53.6	4.0	199128	9	AC091946	AC091946 Homo sapi
1307	53.6	4.0	206964	5	BX664610	BX664610 Zebrafish
1308	53.6	4.0	207325	2	CR376835	CR376835 Danio rer
1309	53.6	4.0	210873	2	CR753899	CR753899 Danio rer
1310	53.6	4.0	224150	9	AC135783	AC135783 Homo sapi
1311	53.6	4.0	232822	2	AC120204	AC120204 Pan trogl
1312	53.6	4.0	233659	2	CR545476	CR545476 Danio rer
c1313	53.6	4.0	236120	14	AF063866	AF063866 Melanoplu
1314	53.6	4.0	249995	3	AE014840	AE014840 Plasmodiu
c1315	53.6	4.0	250029	3	AE014839	AE014839 Plasmodiu
1316	53.6	4.0	253755	2	CR812465	CR812465 Danio rer
c1317	53.6	4.0	254050	3	PFA929358	AL929358 Plasmodiu
1318	53.6	4.0	258658	3	AE014832	AE014832 Plasmodiu
c1319	53.4	4.0	6641	6	AX281294	AX281294 Sequence
c1320	53.4	4.0	6641	6	AX345217	AX345217 Sequence
c1321	53.4	4.0	9642	6	AX345258	AX345258 Sequence
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1323	53.4	4.0	27491	9	AC010284	AC010284 Homo sapi
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1325	53.4	4.0	111998	9	AC011509	AC011509 Homo sapi
c1326	53.4	4.0	114576	9	AC074397	AC074397 Homo sapi
c1327	53.4	4.0	116061	9	AL732324	AL732324 Human DNA
1328	53.4	4.0	136240	3	AC117070	AC117070 Dictyoste
c1329	53.4	4.0	137889	9	AC073269	AC073269 Homo sapi
1330	53.4	4.0	147792	2	CR457463	CR457463 Danio rer
1331	53.4	4.0	150209	2	CR759744	CR759744 Danio rer
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1334	53.4	4.0	163382	6	CQ869778	CQ869778 Sequence
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1338	53.4	4.0	169562	2	CR394565	CR394565 Danio rer
c1339	53.4	4.0	170703	2	BX897681	BX897681 Danio rer
c1340	53.4	4.0	170920	9	AC138627	AC138627 Homo sapi
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c1344	53.4	4.0	180290	9	AC005081	AC005081 Homo sapi
1345	53.4	4.0	184954	2	CR376796	CR376796 Danio rer
1346	53.4	4.0	190535	2	CR735130	CR735130 Danio rer
1347	53.4	4.0	192994	2	CR318588	CR318588 Danio rer
c1348	53.4	4.0	195488	2	CR753885	CR753885 Danio rer
c1349	53.4	4.0	195602	2	CR388375	CR388375 Danio rer
1350	53.4	4.0	197225	9	AC093835	AC093835 Homo sapi
c1351	53.4	4.0	199533	2	CR450834	CR450834 Danio rer
1352	53.4	4.0	201656	2	CR786582	CR786582 Danio rer
1353	53.4	4.0	203216	2	AC097328	AC097328 Pan trogl
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1357	53.4	4.0	223509	2	CR388007	CR388007 Danio rer
c1358	53.4	4.0	227441	2	CR589875	CR589875 Danio rer
1359	53.4	4.0	233769	2	CR631124	CR631124 Danio rer
c1360	53.4	4.0	248925	2	CR749745	CR749745 Danio rer
1361	53.4	4.0	250053	3	AE014825	AE014825 Plasmodiu
c1362	53.4	4.0	250823	3	AE014821	AE014821 Plasmodiu
c1363	53.4	4.0	301450	1	AP003185	AP003185 Clostridi
1364	53.4	4.0	331039	3	AC116979	AC116979 Dictyoste
c1365	53.4	4.0	341153	2	BX914212	BX914212 Danio rer
1366	53.2	4.0	434	8	AY021974	AY021974 Oryza sat
1367	53.2	4.0	1509	3	LFAJ5426	AJ005426 Lysiphleb
1368	53.2	4.0	2710	1	AF250387	AF250387 Carsonell
c1369	53.2	4.0	11469	3	AE001411	AE001411 Plasmodiu
1370	53.2	4.0	12029	3	AE001373	AE001373 Plasmodiu
c1371	53.2	4.0	53932	2	AC023371	AC023371 Homo sapi
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1373	53.2	4.0	86020	5	CR556723	CR556723 Zebrafish
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1381	53.2	4.0	123589	9	AC104790	AC104790 Homo sapi
1382	53.2	4.0	132112	2	CR626862	CR626862 Danio rer
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1384	53.2	4.0	138278	2	CR790373	CR790373 Danio rer
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c1386	53.2	4.0	145650	2	CR762412	CR762412 Danio rer
1387	53.2	4.0	145856	2	CR759812	CR759812 Danio rer
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1397	53.2	4.0	164300	2	CR450717	CR450717 Danio rer
c1398	53.2	4.0	168069	2	CR812470	CR812470 Danio rer
1399	53.2	4.0	169227	2	CR788248	CR788248 Danio rer
c1400	53.2	4.0	169546	2	AC004157	AC004157 Plasmodiu
1401	53.2	4.0	171424	2	CR749743	CR749743 Danio rer
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1404	53.2	4.0	172164	2	CR387936	CR387936 Danio rer
1405	53.2	4.0	172758	2	AC022553	AC022553 Homo sapi
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c1412	53.2	4.0	187962	2	CR759825	CR759825 Danio rer
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c1417	53.2	4.0	198899	9	AC090192	AC090192 Homo sapi
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1420	53.2	4.0	210207	2	CR457459	CR457459 Danio rer
1421	53.2	4.0	210218	2	CR555304	CR555304 Danio rer
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c1433	53.2	4.0	263169	2	BX927111	BX927111 Danio rer
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c1436	53	3.9	530	6	CQ398223	CQ398223 Sequence
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1476	53	3.9	184884	2	CR774187	CR774187 Danio rer
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ALIGNMENTS

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RESULT 1
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LOCUS       AR252633               1346 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 386 from patent US 6478825.
ACCESSION   AR252633
VERSION     AR252633.1  GI:27300541
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1346)
  AUTHORS   Winterbottom,J.M., Shimp,L., Boyce,T.M. and Kaes,D.
  TITLE     Implant, method of making same and use of the implant for the
            treatment of bone defects
  JOURNAL   Patent: US 6478825-A 386 12-NOV-2002;
FEATURES             Location/Qualifiers
     source          1. .1346
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             100.0%;  Score 1346;  DB 6;  Length 1346;
  Best Local Similarity   100.0%;  Pred. No. 7.5e-266;
  Matches 1346;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60
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Db          1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60

Qy         61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
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Db         61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120

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Qy        721 GTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCTT 780
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Qy        781 CTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAAC 840
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Qy       1201 GTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCATT 1260
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Qy       1321 AAAAAAAAAAAAAAAAAAAAAAAAA 1346
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Db       1321 AAAAAAAAAAAAAAAAAAAAAAAAA 1346
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RESULT 2
AR528692

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LOCUS       AR528692                1346 bp    DNA     linear   PAT 08-OCT-2004
DEFINITION  Sequence 481 from patent US 6725730.
ACCESSION   AR528692
VERSION     AR528692.1  GI:53916770
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1346)
  AUTHORS   Bollinger,C.L. Jr.
  TITLE     Crane test weight assembly and method
  JOURNAL   Patent: US 6725730-A 481 27-APR-2004;
FEATURES             Location/Qualifiers
     source          1. .1346
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match           100.0%;  Score 1346;  DB 6;  Length 1346;
  Best Local Similarity  100.0%;  Pred. No. 7.5e-266;
  Matches 1346;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60
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Db          1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60

Qy         61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
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Db         61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120

Qy        121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
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Qy        181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
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Qy        241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300
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Qy        301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360
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Db        301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360

Qy        361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
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Db        661 TCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTGT 720

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Db        841 ACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGTA 900

Qy        901 TAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAATA 960
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Db        901 TAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAATA 960

Qy        961 AGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCCA 1020
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Db        961 AGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCCA 1020

Qy       1021 GTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATCA 1080
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Qy       1321 AAAAAAAAAAAAAAAAAAAAAAAAAA 1346
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Db       1321 AAAAAAAAAAAAAAAAAAAAAAAAAA 1346
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RESULT 3
AX403499
LOCUS       AX403499                1346 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 386 from Patent WO0073454.
ACCESSION   AX403499
VERSION     AX403499.1  GI:21436987
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ashkenazi,A.J., Baker,K.P., Botstein,D., Desnoyers,L., Eaton,D.,
            Ferrara,N., Gerber,H., Gerritsen,M., Goddard,A., Godowski,P.,
            Grimaldi,C.J., Gurney,A.L., Kljavin,I., Napier,M.A., Pan,J.,
            Paoni,N.F., Roy,M., Stewart,T.A., Tumas,D., Watanabe,C.K.,
            Williams,P., Wood,W.I. and Zhang,Z.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
            the same
  JOURNAL   Patent: WO 0073454-A 386 07-DEC-2000;
            Genentech Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1346
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match           100.0%;  Score 1346;  DB 6;  Length 1346;
  Best Local Similarity  100.0%;  Pred. No. 7.5e-266;
  Matches 1346;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60
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Db       1261 TCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTTT 1320

Qy       1321 AAAAAAAAAAAAAAAAAAAAAAAAAA 1346
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Db       1321 AAAAAAAAAAAAAAAAAAAAAAAAAA 1346
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RESULT 4
AX464348
LOCUS AX464348 1346 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 481 from Patent WO0140466.
ACCESSION AX464348
VERSION AX464348.1 GI:21899190
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Baker,K.P., Beresini,M., Deforge,L., Desnoyers,L., Filvaroff,E., Gao,W.Q., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L., Sherwood,S., Smith,V., Stewart,T.A., Tumas,D., Watanabe,C.K., Wood,W.L. and Zhang,Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding same
JOURNAL Patent: WO 0140466-A 481 07-JUN-2001;
Genentech Inc. (US)
FEATURES Location/Qualifiers
source 1. .1346
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN

Query Match 100.0%; Score 1346; DB 6; Length 1346;
Best Local Similarity 100.0%; Pred. No. 7.5e-266;
Matches 1346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db        661 TCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTGT 720

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Qy       1321 AAAAAAAAAAAAAAAAAAAAAAAAAA 1346
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Db       1321 AAAAAAAAAAAAAAAAAAAAAAAAAA 1346
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RESULT 5

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AY359060
LOCUS       AY359060                1346 bp    mRNA    linear   PRI 03-OCT-2003
DEFINITION  Homo sapiens clone DNA61873 NX-17 (UNQ678) mRNA, complete cds.
ACCESSION   AY359060
VERSION     AY359060.1  GI:37183237
KEYWORDS    FLI_CDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1346)
  AUTHORS   Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
            Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
            Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
            Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
            Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,
            Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,
            Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K.,
            Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
            Goddard,A., Wood,W.I. and Godowski,P.
  TITLE     The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
            Effort to Identify Novel Human Secreted and Transmembrane Proteins:
            A Bioinformatics Assessment
  JOURNAL   Genome Res. 13 (10), 2265-2270 (2003)
   PUBMED   12975309
REFERENCE   2  (bases 1 to 1346)
  AUTHORS   Clark,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
            Inc., 1 DNA Way, South San Francisco, CA 94080, USA
FEATURES             Location/Qualifiers
     source          1. .1346
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     CDS             7. .645
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                     /note="PRO1312"
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                     NEEYLFKAMVAFSMRKVPNREATEISHVLLCNVTQRVSFWFVVTDPSKNHTLPAVEVQ
                     SAIRMNKNRINNAFFLNDQTLEFLKIPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIAL
                     LILSGIWQRRRKNKEPSEVDDAEDKCENMITIENGIPSDPLDMKGGILMMPS"
ORIGIN

  Query Match           100.0%;  Score 1346;  DB 9;  Length 1346;
  Best Local Similarity  100.0%;  Pred. No. 7.5e-266;
  Matches 1346;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60

Qy         61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
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Db         61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120

Qy        121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
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Qy        181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
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Qy        241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300
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Qy        301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360
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Db        301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360

Qy        361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
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Db        361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420

Qy        421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
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Qy        481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540
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Db        481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540

Qy        541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 600
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Qy        601 GATCCCCTGGACATGAAGGGGGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGGC 660
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Qy        661 TCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTGT 720
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Db        841 ACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGTA 900

Qy        901 TAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAATA 960
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Db        901 TAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAATA 960

Qy        961 AGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCCA 1020
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Db        961 AGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCCA 1020

Qy       1021 GTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATCA 1080
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Qy       1081 CTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGGA 1140
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Qy       1141 TGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAACA 1200
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Qy       1201 GTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCATT 1260
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Qy       1261 TCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTTT 1320
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Qy       1321 AAAAAAAAAAAAAAAAAAAAAAAAAA 1346
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Db       1321 AAAAAAAAAAAAAAAAAAAAAAAAAA 1346
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RESULT 6
BC014317
LOCUS       BC014317               1605 bp    mRNA    linear   PRI 29-JUN-2004
DEFINITION  Homo sapiens transmembrane protein 27, mRNA (cDNA clone MGC:22707
            IMAGE:4048217), complete cds.
ACCESSION   BC014317
VERSION     BC014317.1  GI:15680012
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1605)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1605)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-SEP-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: CLONTECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Institute for Systems Biology
            http://www.systemsbiology.org
            contact: amadan@systemsbiology.org
            Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
            Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 31 Row: n Column: 3
            This clone was selected for full length sequencing because it
            passed the following selection criteria: Hexamer frequency ORF
            analysis, Similarity but not identity to protein.
FEATURES             Location/Qualifiers
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                     /clone="MGC:22707 IMAGE:4048217"
                     /tissue_type="Bone marrow, chronic myelogenous leukemia"
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                     /lab_host="DH10B"
                     /note="Vector: pDNR-LIB"
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                     LTPL"
ORIGIN

  Query Match             98.7%;  Score 1328.6;  DB 9;  Length 1605;
  Best Local Similarity   99.6%;  Pred. No. 2.7e-262;
  Matches 1342;  Conservative    0;  Mismatches    4;  Indels    1;  Gaps    1;

Qy          1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60
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Db        255 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 314

Qy         61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
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Db        315 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 374

Qy        121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
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Db        375 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 434

Qy        181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
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Db        435 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 494

Qy        241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300
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Qy        301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360
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Qy        361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
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Qy        421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
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Qy        481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540
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Db        735 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 794

Qy        541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 600
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Db        795 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 854

Qy        601 GATCCCCTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 659
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Db        855 GATCCCCTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 914

Qy        660 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 719
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Db        915 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 974

Qy        720 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 779
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Qy        780 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 839
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Qy        840 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 899
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Db       1095 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 1154

Qy        900 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 959
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Db       1155 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 1214

Qy        960 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1019
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Db       1215 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1274

Qy       1020 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1079
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Db       1275 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1334

Qy       1080 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1139
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Qy       1140 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1199
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Qy       1260 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1319
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Qy       1320 TAAAAAAAAAAAAAAAAAAAAAAAAAAA 1346
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Db       1575 GTAAAAAAAAAAAAAAAAAAAAAAAAA 1601
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RESULT 7
BC050606
LOCUS       BC050606                1377 bp    mRNA    linear   PRI 30-JUN-2004
DEFINITION  Homo sapiens transmembrane protein 27, mRNA (cDNA clone MGC:60059
            IMAGE:5183554), complete cds.
ACCESSION   BC050606
VERSION     BC050606.1  GI:30047080
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1377)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
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            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1377)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-APR-2003) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA  94305
            Web site:       http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 110 Row: c Column: 4
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 21361864.
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                     LTPL"
ORIGIN

  Query Match             98.5%;  Score 1325.4;  DB 9;  Length 1377;
  Best Local Similarity   99.5%;  Pred. No. 1.3e-261;
  Matches 1340;  Conservative    0;  Mismatches    6;  Indels    1;  Gaps    1;

Qy          1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60
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Db          3 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 62

Qy         61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
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Db         63 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 122

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Qy        361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
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Qy        960 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1019
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Qy       1020 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1079
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RESULT 8
BC015099

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LOCUS       BC015099               1440 bp    mRNA    linear   PRI 29-JUN-2004
DEFINITION  Homo sapiens transmembrane protein 27, mRNA (cDNA clone MGC:22827
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ACCESSION   BC015099
VERSION     BC015099.1  GI:15929328
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1440)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
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            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
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            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1440)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-OCT-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: CLONTECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Institute for Systems Biology
            http://www.systemsbiology.org
            contact: amadan@systemsbiology.org
            Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
            Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 31 Row: d Column: 11
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                     LTPL"
ORIGIN

  Query Match            98.5%;  Score 1325.4;  DB 9;  Length 1440;
  Best Local Similarity  99.5%;  Pred. No. 1.3e-261;
  Matches 1340;  Conservative    0;  Mismatches    6;  Indels    1;  Gaps    1;

Qy          1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60
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Qy        181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
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Qy        780 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 839
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Db        923 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 982

Qy        900 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 959
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Qy        960 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1019
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Qy       1080 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1139
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RESULT 9
BD205644
LOCUS       BD205644               1447 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  97 human secreted proteins.
ACCESSION   BD205644
VERSION     BD205644.1  GI:33015414
KEYWORDS    JP 2002533058-A/21.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1447)
  AUTHORS   Ruben,S.M., Florence,K., Ni,J., Rosen,C.A., Carter,K.C.,
            Moore,P.A., Olsen,H.S., Shi,Y., Young,P.E., Wei,F.F., Brewer,L.A.,
            Soppet,D.R., Lafleur,D.W., Endress,G.A. and Ebner,R.
  TITLE     97 human secreted proteins
  JOURNAL   Patent: JP 2002533058-A 21 08-OCT-2002;
            HUMAN GENOME SCIENCES INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002533058-A/21
            PD   08-OCT-2002
            PF   06-MAY-1999 JP 2000548451
            PR   12-MAY-1998 US    60/085093,12-MAY-1998 US    60/085094 PR
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            PI   C CARTER,
            PI   PAUL A MOORE,HENRIK S OLSEN,YANGGU SHI,PAUL E YOUNG,FING FEI
            PI   WEI,
            PI   LAURIE A BREWER,DANIEL R SOPPET,DAVID W LAFLEUR,GREGORY A  PI
             ENDRESS,
            PI   REINHARD EBNER
            PC   C12N15/09,C07K14/00,C07K14/435,C07K16/18,C12N1/15,C12N1/19, PC
              C12N1/21,
            PC   C12N5/10,C12P21/02,C12N15/00,C12N5/00
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            FT                   /organism='Homo sapiens (human)'.
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ORIGIN

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  Best Local Similarity   99.3%;  Pred. No. 1.8e-261;
  Matches 1338;  Conservative    2;  Mismatches    6;  Indels    1;  Gaps    1;

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Db        131 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 190

Qy        121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        191 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 250

Qy        181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 310

Qy        241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 370

Qy        301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        371 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 430

Qy        361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
              ||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        431 AATGMCCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 490

Qy        421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
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Db        491 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 550

Qy        481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540
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Db        551 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 610

Qy        541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 670

Qy        601 GATCCCCTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 659
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        671 GATCCCCTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 730

Qy        660 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 719
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        731 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 790

Qy        720 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 779
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Db        791 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 850

Qy        780 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 839
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Db        851 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 910

Qy        840 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 899
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        911 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 970

Qy        900 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 959
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        971 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 1030

Qy        960 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1019
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1031 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1090

Qy       1020 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1079
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1091 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1150

Qy       1080 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1139
              ||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||
Db       1151 ACTTATATCACTCTGKATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1210

Qy       1140 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1211 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1270

Qy       1200 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1271 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1330

Qy       1260 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1319
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1331 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1390

Qy       1320 TAAAAAAAAAAAAAAAAAAAAAAAAA 1346
              | |     ||||||||||||||||||||
Db       1391 TGATTGTGAAAAAAAAAAAAAAAAAA 1417


RESULT 10
BD083420
LOCUS       BD083420                1401 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Secreted proteins and polynucleotides encoding them.
ACCESSION   BD083420
VERSION     BD083420.1  GI:22629030
KEYWORDS    JP 2001523950-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 1401)
  AUTHORS   Jacobs,K., Mccoy,J.M., Lavallie,E.R., Racie,L.A., Merberg,D.,
            Treacy,M., Spaulding,V. and Agostino,M.J.
  TITLE     Secreted proteins and polynucleotides encoding them
  JOURNAL   Patent: JP 2001523950-A 2 27-NOV-2001;
            GENETICS INSTITUTE INC
COMMENT     PN   JP 2001523950-A/2
            PD   27-NOV-2001
            PF   23-JAN-1998 JP 1998532177
            PR   24-JAN-1997 US    08/788789
            PI   KENNETH JACOBS,JOHN M MCCOY,EDWARD R LAVALLIE,LISA A RACIE, PI
              DAVID MERBERG,
            PI   MAURICE TREACY,VIKKI SPAULDING,MICHAEL J AGOSTINO PC
            C12N15/12,C12N5/10,C07K14/47,C12Q1/68,A61K38/17 CC   Strandedness:
            Double;
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          CC   Topology: Linear;
          FH   Key             Location/Qualifiers.
FEATURES              Location/Qualifiers
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                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"
ORIGIN

  Query Match            98.2%;  Score 1321.8;  DB 6;  Length 1401;
  Best Local Similarity  99.8%;  Pred. No. 6.9e-261;
  Matches 1334;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         65 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 124

Qy         61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
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Db        125 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 184

Qy        121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
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Db        185 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 244

Qy        181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 304

Qy        241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        305 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 364

Qy        301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        365 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTGTA 424

Qy        361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        425 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 484

Qy        421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
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Db        485 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 544

Qy        481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        545 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 604

Qy        541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        605 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 664

Qy        601 GATCCCCTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 659
              |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db        665 GATCCCCTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 724

Qy        660 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 719
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        725 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 784

Qy        720 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 779
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Qy        780 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 839
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Db        845 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 904

Qy        840 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 899
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Db        905 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 964

Qy        900 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 959
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        965 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 1024

Qy        960 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1019
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1025 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1084

Qy       1020 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1079
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Db       1085 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1144

Qy       1080 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1139
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Db       1145 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1204

Qy       1140 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1199
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Db       1205 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1264

Qy       1200 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1259
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Db       1265 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1324

Qy       1260 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1319
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Db       1325 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1384

Qy       1320 TAAAAAAAAAAAAAAAA 1336
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Db       1385 AAAAAAAAAAAAAAAAA 1401


RESULT 11
AX083392
LOCUS       AX083392               1347 bp    DNA     linear   PAT 28-FEB-2001
DEFINITION  Sequence 84 from Patent WO0112660.
ACCESSION   AX083392
VERSION     AX083392.1  GI:13185232
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kato,S. and Kimura,T.
  TITLE     Human proteins having hydrophobic domains and dnas encoding these
            proteins
  JOURNAL   Patent: WO 0112660-A 84 22-FEB-2001;
            SAGAMI CHEMICAL RESEARCH CENTER (JP) ; Protegene Inc. (JP)
FEATURES              Location/Qualifiers
     source           1. .1347
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     CDS              26. .694
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                      /db_xref="GI:13185233"
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                      LTPL"
ORIGIN

  Query Match            97.3%;  Score 1309.4;  DB 6;  Length 1347;
  Best Local Similarity  99.8%;  Pred. No. 2.4e-258;
  Matches 1321;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60
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Db        20 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 79

Qy        61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
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Db        80 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 139

Qy       121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       140 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 199

Qy       181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       200 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 259

Qy       241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300
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Qy       301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360
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Qy       361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
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Db       380 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 439

Qy       421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
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Db       440 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 499

Qy       481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540
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Db       500 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 559

Qy       541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 600
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Db       560 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 619

Qy       601 GATCCCCTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 659
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Db       680 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 739

Qy       720 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 779
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Db       740 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 799

Qy       780 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 839
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Db       800 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAA 859

Qy       840 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 899
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Db       860 CACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGACAGT 919

Qy       900 ATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAAT 959
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Qy       960 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1019
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Qy      1020 AGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATC 1079
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Qy      1080 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1139
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Qy      1140 ATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTATCACACCAAC 1199
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Qy      1200 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1259
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Qy      1260 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1319
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Db      1280 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1339

Qy      1320 TAA 1322
             ||| 
Db      1340 TGA 1342
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RESULT 12
AF229179
LOCUS AF229179 1345 bp mRNA linear PRI 05-APR-2002
DEFINITION Homo sapiens collectrin mRNA, complete cds.
ACCESSION AF229179
VERSION AF229179.1 GI:9957753
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1345)
AUTHORS Zhang,H., Wada,J., Hida,K., Tsuchiyama,Y., Hiragushi,K., Shikata,K., Wang,H., Lin,S., Kanwar,Y.S. and Makino,H.
TITLE Collectrin, a collecting duct-specific transmembrane glycoprotein, is a novel homolog of ACE2 and is developmentally regulated in embryonic kidneys
JOURNAL J. Biol. Chem. 276 (20), 17132-17139 (2001)
MEDLINE 21264468
PUBMED 11278314
REFERENCE 2 (bases 1 to 1345)
AUTHORS Zhang,H., Wada,J. and Makino,H.
TITLE Human kidney specific membrane protein (NX-17)
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 1345)
AUTHORS Zhang,H., Wada,J. and Makino,H.
TITLE Direct Submission
JOURNAL Submitted (28-JAN-2000) Department of Medicine III, Okayama University Medical School, 2-5-1 Shikata-cho, Okayama 700-8558, Japan

FEATURES Location/Qualifiers
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CDS 24. .692
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ORIGIN

Query Match 97.2%; Score 1307.8; DB 9; Length 1345;
Best Local Similarity 99.8%; Pred. No. 5.2e-258;
Matches 1320; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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RESULT 13
BD135300

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LOCUS       BD135300                1356 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  110 human secretory proteins.
ACCESSION   BD135300
VERSION     BD135300.1  GI:23230245
KEYWORDS    JP 2002508167-A/51.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1356)
  AUTHORS   Moore,P.A., Ruben,S.M., Carter,K.C., Shi,Y., Rosen,C.A.,
            Soppet,D.R., Caou,H., Wei,Y.F., Florence,K., Duan,R.D.,
            Florence,C., Greene,J.M., Feng,P., Ferrie,A.M., Yu,G.L., Janat,F.
            and Ni,J.
  TITLE     110 human secretory proteins
  JOURNAL   Patent: JP 2002508167-A 51 19-MAR-2002;
            HUMAN GENOME SCIENCES INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002508167-A/51
            PD   19-MAR-2002
            PF   17-DEC-1998 JP 2000539040
            PR   18-DEC-1997 US   60/070 923,18-DEC-1997 US   60/068 007 PR
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            PI   PAUL A MOORE,STEVEN M RUBEN,KENNETH C CARTER,YANGGU SHI,CRAIG
            PI   A ROSEN,
            PI   DANIEL R SOPPET,HARA CAOU,YING FEI WEI,KIMBERLY FLORENCE, PI
            ROSANNE D DUAN,
            PI   CHARLES FLORENCE,JOHN M GREENE,PING FENG,ANN M FERRIE,GUO  PI
             LIANG YU,
            PI   FORD JANAT,JIAN NI
            PC   C12N15/09,A61K38/00,A61K48/00,A61P9/00,A61P9/10,A61P15/00, PC
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Qy        960 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1019
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Db        971 AAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCC 1030

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Qy       1080 ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1139
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Db       1151 ATGGATAAAATTGGAATTACTCATATACAGGGTGGGATTTTATCCTGTTATCACACCAAC 1210

Qy       1200 AGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1259
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Db       1211 AGTTGATTATATATTTTCTGNATATCAGCCCCTAATAGGACAATTCTATTTGTTGACCAT 1270

Qy       1260 TTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1319
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RESULT 14
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LOCUS       BD270445                 862 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Genes associated with diseases of the kidney.
ACCESSION   BD270445
VERSION     BD270445.1  GI:33080213
KEYWORDS    JP 2002541787-A/6.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 862)
  AUTHORS   Walker,M.G., Volkmuth,W., Klingler,T.M., Azimzai,Y. and Yue,H.
  TITLE     Genes associated with diseases of the kidney
  JOURNAL   Patent: JP 2002541787-A 6 10-DEC-2002;
            INCYTE PHARMACEUTICALS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002541787-A/6
            PD   10-DEC-2002
            PF   28-MAR-2000 JP 2000611563
            PR   09-APR-1999 US    09/289349
            PI   MICHAEL G WALKER,WAYNE VOLKMUTH,TOD M KLINGLER,YALDA AZIMZAI,
            PI   HENRY YUE
            PC   C12N15/09,A61K31/7115,A61K31/7125,A61K35/76,A61K38/00,A61K39/
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Qy       592 ATCCCCTCTGATCCCCTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGACAGAG 650
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Qy       651 GATGAGAGGCTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACAT 710
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Qy       771 CACCATTCTTCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTAT 830
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Qy       831 ACCCACCAACACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTT 890
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Qy       951 TTTAGAAATAAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAAT 1010
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Db       661 TGTAAATGGATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTAT 720

Qy      1191 CACACCAACAGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTT 1250
Db       721 CACACCAACAGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTT 780

Qy      1251 GTTGACCATTTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATC 1310
Db       781 GTTGACCATTTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATC 840

Qy      1311 ATCTCTTTTTAAAAAAAAAAAA 1332
Db       841 ATCTCTTAAAAAAAAAAAAAA 862


RESULT 15
AR177334
LOCUS       AR177334                848 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 27 from patent US 6312922.
ACCESSION   AR177334
VERSION     AR177334.1  GI:17919689
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 848)
  AUTHORS   Edwards,J.-B.Dumas.Milne., Duclert,A. and Bougueleret,L.
  TITLE     Complementary DNAs
  JOURNAL   Patent: US 6312922-A 27 06-NOV-2001;
FEATURES             Location/Qualifiers
     source          1. .848
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match           59.4%;  Score 799.4;  DB 6;  Length 848;
  Best Local Similarity   98.8%;  Pred. No. 1e-153;
  Matches  809;  Conservative    6;  Mismatches    3;  Indels    1;  Gaps    1;

Qy         1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60
Db        26 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 85

Qy        61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
Db        86 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 145

Qy       121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
Db       146 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 205

Qy       181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
Db       206 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 265

Qy       241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300
Db       266 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 325

Qy       301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360
Db       326 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 385

Qy       361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
Db       386 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 445

Qy       421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
Db       446 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 505

Qy       481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540
Db       506 GCACTACTGATTTTATCAGGGATCTGGCAACGTADAARAAAGAACAAAGAACCATCTGAA 565

Qy       541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 600
Db       566 GTGGATGACGCTGAARATAAKTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 625

Qy       601 GATCCCCTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 659
Db       626 GATCCCCTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 685

Qy       660 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 719
Db       686 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAARAAATTAAACATTTGTTTCTG 745

Qy       720 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 779
Db       746 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATWTTTTGTTTCACCATTCT 805

Qy       780 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAA 818
Db       806 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAAAAAAAA 844


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Job time : 5953.34 secs
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10941.049 Million cell updates/sec
Title: US-09-989-724-386
Perfect score: 1346
Sequence: 1 gaaagaatgttgtggctgct.....aaaaaaaaaaaaaaaaaaa 1346
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 4390206 seqs, 2959870667 residues
Total number of hits satisfying chosen parameters: 8780412
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries
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2: geneseqn1990s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description

RESULT 1
ID AAZ65097 standard; cDNA; 1346 BP.
DE Membrane-bound protein PRO1312 encoding cDNA.
PN WO9963088-A2.
PD 09-DEC-1999.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 3; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 2
ID AAC58612 standard; cDNA; 1346 BP.
DE Human PRO1312 protein UNQ678 encoding cDNA SEQ ID NO:160.
PN WO200053758-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 3; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 3
ID AAA77680 standard; cDNA; 1346 BP.
DE Human PRO1312 cDNA sequence SEQ ID NO:213.
PN WO200032221-A2.
PD 08-JUN-2000.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 3; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 4
ID AAS21484 standard; cDNA; 1346 BP.
DE Human cDNA sequence encoding for PRO1312 polypeptide.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 4; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 5
ID AAF44243 standard; cDNA; 1346 BP.
DE Human PRO1312 (UNQ678) nucleotide sequence SEQ ID NO:386.
PN WO200073454-A1.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 5; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 6
ID ACA64416 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 8; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 7
ID ACA03843 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 8; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 8
ID ABX89381 standard; cDNA; 1346 BP.
DE DNA encoding novel secreted and transmembrane protein PRO1312.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 8; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 9
ID ABX80875 standard; cDNA; 1346 BP.
DE Human secreted/transmembrane protein cDNA, #157.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1346; DB 8; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 10
ID ACD44384 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO1312 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 8; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 11
ID ACD42035 standard; cDNA; 1346 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #241.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 8; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 12
ID ABX79555 standard; cDNA; 1346 BP.
DE Human sectreted/transmembrane protein cDNA, #157.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 8; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 13
ID ACA93576 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1346; DB 8; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 14
ID ABX81258 standard; DNA; 1346 BP.
DE Novel human secreted or transmembrane protein PRO1192 DNA.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1346; DB 8; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 15
ID ACA04264 standard; cDNA; 1346 BP.

DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 481.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 8; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 16
ID ACA93074 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1346; DB 8; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 17
ID ABX17158 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 8; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 18
ID ACA68013 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 19
ID ACA88462 standard; cDNA; 1346 BP.
DE Human secreted and transmembrane polypeptide PRO1312 cDNA.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 20
ID ACD81969 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO1312 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 21
ID ADA46000 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 22
ID ADA76431 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 23
ID ADA19081 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 24
ID ADA61704 standard; cDNA; 1346 BP.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 25
ID ADB19489 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 26
ID ADB28030 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 27
ID ADA86509 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 28
ID ADB16073 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 29
ID ADA37897 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1312.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 30
ID ADA47859 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 31
ID ADA21583 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO1312.
PN US2003054404-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 32
ID ADA10370 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1312.
PN US2003059831-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 33
ID ADA67654 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;

RESULT 34
ID ADB30661 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 35
ID ADA85957 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 36
ID ADA17914 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO1312 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 37
ID ADA97169 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 38
ID ADA79473 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 39
ID ADA87612 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 40
ID ADB16814 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 41
ID ADA28022 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1312.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 42
ID ADA91906 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 43
ID ADB14969 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 44
ID ADB18930 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 45
ID ADA94145 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 46
ID ADB20041 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 47
ID ADB13353 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 48
ID ACD98664 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 49
ID ADA94602 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1312.
PN US2003059832-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 50
ID ADA74607 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 51
ID ADB24840 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide SEQ ID NO 481.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 52
ID ADA82364 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003082701-A1.
PD 01-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 53
ID ADA75327 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 54
ID ADA85405 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 55
ID ADA84853 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 56
ID ADB30109 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 57
ID ADA80637 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 58
ID ADA75879 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 59
ID ADA38827 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1312.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 60
ID ADA47104 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 61
ID ADB25400 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide SEQ ID NO 481.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 62
ID ADA93576 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 63
ID ADB26926 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 64
ID ADB31213 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 65
ID ADA92948 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1312.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 66
ID ADA61141 standard; cDNA; 1346 BP.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 67
ID ADB24288 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide SEQ ID NO 481.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 68
ID ADA96617 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 69
ID ADA81189 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 70
ID ADA96065 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 71

ID ADB26374 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 72
ID ADB21859 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 73
ID ADA77638 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 74
ID ADB18378 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 75
ID ADA87061 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 76
ID ADA88164 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 77
ID ADA46552 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 78
ID ADB28582 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 79
ID ADB29134 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 80
ID ACH65530 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1312.
PN US2003044806-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 81
ID ADA77086 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 82
ID ADA22509 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO1312.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 83
ID ADA88716 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 84
ID ADA97721 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 85
ID ADB27478 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003022239-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 86
ID ADB22411 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087344-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 87
ID ACD39520 standard; cDNA; 1346 BP.
DE Human cDNA encoding PRO1192.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 88
ID ADA06675 standard; cDNA; 1346 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #121.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 89
ID ADA39368 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1312.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 90
ID ADA67102 standard; cDNA; 1346 BP.

DE Human PRO polynucleotide #241.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 91
ID ADB22963 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 92
ID ADB23736 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide SEQ ID NO 481.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 93
ID ADA92458 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 94
ID ADB15521 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 95
ID ADB38773 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 96
ID ADB96394 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2003054403-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 97
ID ADB38221 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 98
ID ADB66693 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 99
ID ADB89773 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 100
ID ADB90505 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 101
ID ADB39606 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 102
ID ADB47229 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 103
ID ADB86836 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 104
ID ADB77441 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 105
ID ADB34598 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide SEQ ID NO 481.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 106
ID ADB35702 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide SEQ ID NO 481.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 107
ID ADB34046 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide SEQ ID NO 481.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 108
ID ADB35150 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide SEQ ID NO 481.
PN US2003077718-A1.
PD 24-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 109
ID ADB36254 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide SEQ ID NO 481.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 110
ID ADB46649 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 111
ID ADC57866 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2003027754-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 112
ID ADC55230 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2003045463-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 113
ID ADC12097 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1312.
PN US2003049681-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 114
ID ADC56519 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2003064375-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 115
ID ADC07574 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1312.
PN US2003068647-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 116
ID ADC11564 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1312.
PN US2003069403-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 117
ID ADC50522 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 118
ID ADC72069 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 119
ID ADC60048 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 120
ID ADC53055 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID481.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 121
ID ADC57409 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID481.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 122
ID ADC60600 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 123
ID ADC51075 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 124
ID ADC65602 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 125
ID ADC54700 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID481.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 126
ID ADC53661 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID481.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 127
ID ADC59184 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID481.
PN US2003087359-A1.
PD 08-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 128
ID ADC56062 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID481.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 129
ID ADC58632 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID481.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 130
ID ADC14686 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 131
ID ADD08218 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 132
ID ADD03306 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 133
ID ADC90298 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 134
ID ADC82043 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 135
ID ADC69717 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 136
ID ADC48606 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 137
ID ADD10135 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 138
ID ADD07685 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 139
ID ADD04710 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 140
ID ADC82576 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 141
ID ADC80666 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 142
ID ADD11173 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 143
ID ADC48054 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 144
ID ADD08756 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 145
ID ADC80114 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 146
ID ADD07005 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2002193300-A1.

PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 147
ID ADD09583 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 148
ID ADC83252 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 149
ID ADD41296 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 150
ID ADD52435 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 151
ID ADD53175 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 152
ID ADD53727 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 153
ID ADD55359 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 154
ID ADD56317 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 155
ID ADD51883 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 156
ID ADD02682 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 157
ID ADD02116 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 158
ID ADD54298 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 159
ID ADD54755 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 160
ID ADD92615 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 161
ID ADD91511 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 162
ID ADE04125 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 163
ID ADE26909 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087304-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 164
ID ADE32422 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 165
ID ADE22354 standard; cDNA; 1346 BP.

DE cDNA encoding human PRO polypeptide #241.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 166
ID ADD79578 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 167
ID ADE42114 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 168
ID ADE17931 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 169
ID ADD92063 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 170
ID ADE33526 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 171
ID ADE34078 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 172
ID ADD80130 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 173
ID ADD93167 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 174
ID ADE19587 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 175
ID ADE19035 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 176
ID ADE43231 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 177
ID ADD96020 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 178
ID ADE22906 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 179
ID ADD79024 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 180
ID ADE26376 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 181
ID ADE32974 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 182
ID ADE42666 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 183
ID ADD80682 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003207418-A1.
PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 184
ID ADD89710 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 185
ID ADE40994 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 186
ID ADE04793 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 187
ID ADE92922 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 188
ID ADF67313 standard; cDNA; 1346 BP.
DE Human PRO1312 nucleotide sequence SEQ ID NO:386.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 189
ID ADG21631 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 190
ID ADG23272 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 191
ID ADF97607 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 192
ID ADG80671 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 193
ID ADG80119 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 194
ID ADH55411 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 195
ID ADH55963 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 196
ID ADI35567 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2003050457-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 197
ID ADI64182 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 198
ID ADI65131 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 199
ID ADI63630 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 200
ID ADH82044 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 201
ID ADI00060 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 202

ID ADH81492 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 203
ID ABX77959 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2003027163-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 204
ID ABX80371 standard; DNA; 1346 BP.
DE Novel human secreted or transmembrane protein PRO1192 DNA.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 205
ID ACA69277 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1312.
PN US2003032023-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 206
ID ACD24093 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 207
ID ABX90348 standard; cDNA; 1346 BP.
DE Human secreted/transmembrane protein cDNA, #157.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 208
ID ABX64194 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO1312 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 209
ID ACA67234 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 210
ID ADM82661 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 11; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 211
ID ADN16060 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 11; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 212
ID ADN16689 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 11; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 213
ID ADN15508 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 11; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 214
ID ADN14956 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 11; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 215
ID ADC81218 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 216
ID ADD76666 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 217
ID ADD88030 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 218
ID ADD86434 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 219
ID ADE75882 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 220
ID ADE23458 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003092108-A1.
PD 15-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 221
ID ADE24010 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 222
ID ADE24653 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 223
ID ADD87478 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 224
ID ADE89344 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 225
ID ADE18483 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 226
ID ADE88792 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 227
ID ADE94812 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 228
ID ADE91223 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 229
ID ADF35512 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO1312 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 230
ID ADE95364 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 231
ID ADE93474 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 232
ID ADF35055 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 233
ID ADE92370 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 234
ID ADE90671 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 235
ID ADE91818 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 236
ID ADG11762 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO1312 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 237
ID ADG02397 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 238
ID ADG22183 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;

RESULT 239
ID ADG20253 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 240
ID ADF98159 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 241
ID ADG24376 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 242
ID ADF98730 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 243
ID ADG03561 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 244
ID ADF99282 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 245
ID ADG16867 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 246
ID ADG05326 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 247
ID ADG19593 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 248
ID ADG13430 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 249
ID ADG08487 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 250
ID ADG15657 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 251
ID ADF97055 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 252
ID ADG06240 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 253
ID ADG23824 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 254
ID ADG04113 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 255
ID ADG25014 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 256
ID ADG07311 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 257
ID ADG07863 standard; cDNA; 1346 BP.

DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 258
ID ADG55358 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 259
ID ADG61022 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 260
ID ADG62126 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 261
ID ADG82327 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 262
ID ADG57566 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 263
ID ADG57014 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 264
ID ADG55910 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 265
ID ADG58670 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 266
ID ADG71036 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 267
ID ADG58118 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 268
ID ADG53702 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 269
ID ADG71588 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 270
ID ADG81775 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003207805-A1.
PD 06-NOV-2003.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 271
ID ADH19632 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1312.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 272
ID ADH30737 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 273
ID ADH12104 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 274
ID ADG52526 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 275
ID ADG54254 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207416-A1.
PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 276
ID ADG81223 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 277
ID ADG56462 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 278
ID ADH12728 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 279
ID ADH21125 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1312.
PN US2003224358-A1.
PD 04-DEC-2003.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 280
ID ADG61574 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 281
ID ADH20165 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1312.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 282
ID ADH28661 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 283
ID ADG54806 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 284
ID ADG59846 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 285
ID ADI81270 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 286
ID ADG10013 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 287
ID ADI15484 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 288
ID ADG09361 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 289
ID ADI14816 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 290
ID ADI18411 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 291
ID ADJ63692 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 292
ID ADJ77587 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 293
ID ADJ65709 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;

RESULT 294
ID ADM27845 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 295
ID ADM42569 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 296
ID ADM28431 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 297
ID ADI95913 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 13; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 298
ID ADI96465 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 13; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 299
ID ADT94383 standard; cDNA; 1346 BP.
DE Human PRO1312 cDNA sequence.
PN AU2003259607-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 13; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 300
ID ADA39900 standard; cDNA; 1432 BP.
DE Human secreted protein encoding cDNA.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 98.5%; Score 1325.4; DB 8; Length 1432;
Best Local Similarity 99.5%; Pred. No. 3.3e-258;
RESULT 301
ID ADA11489 standard; DNA; 1432 BP.
DE Human cDNA encoding a novel secreted protein, SEQ ID NO 17.
PN US2003055236-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 98.5%; Score 1325.4; DB 9; Length 1432;
Best Local Similarity 99.5%; Pred. No. 3.3e-258;
RESULT 302
ID ADD37613 standard; cDNA; 1432 BP.
DE Human secreted protein encoding sequence #95.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 98.5%; Score 1325.4; DB 10; Length 1432;
Best Local Similarity 99.5%; Pred. No. 3.3e-258;
RESULT 303
ID ADA56090 standard; DNA; 1432 BP.
DE Gene encoding human secreted protein #269.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 98.5%; Score 1325.4; DB 10; Length 1432;
Best Local Similarity 99.5%; Pred. No. 3.3e-258;
RESULT 304
ID AAZ65261 standard; DNA; 1447 BP.
DE Human secreted protein gene 12.
PN WO9958660-A1.
PD 18-NOV-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 98.4%; Score 1324.6; DB 3; Length 1447;
Best Local Similarity 99.3%; Pred. No. 4.8e-258;
RESULT 305
ID ADE11650 standard; cDNA; 1447 BP.
DE Human secreted polypeptide cDNA #12.
PN US2003100051-A1.
PD 29-MAY-2003.
PA (RUBE/) RUBEN S M.
PA (FLOR/) FLORENCE K A.
PA (NIJJ/) NI J.
PA (ROSE/) ROSEN C A.
PA (CART/) CARTER K C.
PA (MOOR/) MOORE P A.
PA (OLSE/) OLSEN H S.
PA (SHIY/) SHI Y.
PA (YOUN/) YOUNG P E.
PA (WEIY/) WEI Y.
PA (BREW/) BREWER L A.
PA (SOPP/) SOPPET D R.
PA (LAFL/) LAFLEUR D W.
PA (ENDR/) ENDRESS G A.
PA (EBNE/) EBNER R.
PA (BIRS/) BIRSE C E.
Query Match 98.4%; Score 1324.6; DB 10; Length 1447;
Best Local Similarity 99.3%; Pred. No. 4.8e-258;
RESULT 306
ID AAV40540 standard; cDNA; 1401 BP.
DE Homo sapiens secreted protein clone AM42_3.
PN WO9832853-A2.
PD 30-JUL-1998.
PA (GEMY) GENETICS INST INC.
Query Match 98.2%; Score 1321.8; DB 2; Length 1401;
Best Local Similarity 99.8%; Pred. No. 1.8e-257;
RESULT 307
ID AAF94470 standard; cDNA; 1347 BP.
DE Human hydrophobic domain containing protein clone HP10720 cDNA #84.
PN WO200112660-A2.
PD 22-FEB-2001.
PA (SAGA) SAGAMI CHEM RES CENT.
PA (PROT-) PROTEGENE INC.
Query Match 97.3%; Score 1309.4; DB 4; Length 1347;
Best Local Similarity 99.8%; Pred. No. 5.6e-255;
RESULT 308
ID ABZ78127 standard; cDNA; 1345 BP.
DE Human cancer-related coding sequence, 156P1D4.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 97.2%; Score 1307.8; DB 8; Length 1345;
Best Local Similarity 99.8%; Pred. No. 1.2e-254;
RESULT 309
ID AAH98224 standard; cDNA; 1365 BP.
DE Human EST-derived coding sequence SEQ ID NO: 81.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 97.1%; Score 1307.4; DB 4; Length 1365;
Best Local Similarity 99.4%; Pred. No. 1.4e-254;
RESULT 310
ID AAX97957 standard; DNA; 1356 BP.

DE Human secreted protein gene 42.
PN WO9931117-A1.
PD 24-JUN-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 97.0%; Score 1305; DB 2; Length 1356;
Best Local Similarity 99.0%; Pred. No. 4.4e-254;
RESULT 311
ID ADA40381 standard; cDNA; 1356 BP.
DE Human secreted protein encoding cDNA.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 97.0%; Score 1305; DB 8; Length 1356;
Best Local Similarity 99.0%; Pred. No. 4.4e-254;
RESULT 312
ID ADA11594 standard; DNA; 1356 BP.
DE Human cDNA encoding a novel secreted protein, SEQ ID NO 122.
PN US2003055236-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 97.0%; Score 1305; DB 9; Length 1356;
Best Local Similarity 99.0%; Pred. No. 4.4e-254;
RESULT 313
ID ADD37752 standard; cDNA; 1356 BP.
DE Human secreted protein encoding sequence #234.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 97.0%; Score 1305; DB 10; Length 1356;
Best Local Similarity 99.0%; Pred. No. 4.4e-254;
RESULT 314
ID ADA56545 standard; DNA; 1356 BP.
DE Gene encoding human secreted protein #269.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 97.0%; Score 1305; DB 10; Length 1356;
Best Local Similarity 99.0%; Pred. No. 4.4e-254;
RESULT 315
ID ADI02664 standard; cDNA; 1312 BP.
DE Human cDNA differentially expressed in the vascular endothelium #205.
PN US2003166903-A1.
PD 04-SEP-2003.
PA (ASTR/) ASTROMOFF A.
PA (BAND/) BANDMAN O.
PA (COCK/) COCKS B G.
Query Match 96.4%; Score 1297; DB 10; Length 1312;
Best Local Similarity 99.9%; Pred. No. 1.8e-252;
RESULT 316
ID AAC66136 standard; DNA; 862 BP.
DE Human kidney disease associated gene SEQ ID 6.
PN WO200061622-A2.
PD 19-OCT-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 62.8%; Score 845.2; DB 3; Length 862;
Best Local Similarity 99.5%; Pred. No. 3.3e-161;
RESULT 317
ID AAX19983 standard; cDNA; 848 BP.
DE Human secreted protein 5' EST SEQ ID NO:27.
PN WO9906439-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 59.4%; Score 799.4; DB 2; Length 848;
Best Local Similarity 98.8%; Pred. No. 5.9e-152;
RESULT 318
ID AAX39430 standard; DNA; 848 BP.
DE Human secreted protein 5' EST SEQ ID NO: 27.
PN WO9906551-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 59.4%; Score 799.4; DB 2; Length 848;
Best Local Similarity 98.8%; Pred. No. 5.9e-152;
RESULT 319
ID AAX41369 standard; cDNA; 848 BP.
DE Extended cDNA obtained from 5' EST, SEQ ID NO: 27 from WO 9906553.
PN WO9906553-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 59.4%; Score 799.4; DB 2; Length 848;
Best Local Similarity 98.8%; Pred. No. 5.9e-152;
RESULT 320
ID AAX97564 standard; DNA; 848 BP.
DE Extended human secreted protein coding sequence, SEQ ID NO. 27.
PN WO9931236-A2.
PD 24-JUN-1999.
PA (GEST) GENSET.
Query Match 59.4%; Score 799.4; DB 2; Length 848;
Best Local Similarity 98.8%; Pred. No. 5.9e-152;
RESULT 321
ID AAZ40770 standard; DNA; 848 BP.
DE Secreted protein extended EST coding sequence #6.
PN WO9940189-A2.
PD 12-AUG-1999.
PA (GEST) GENSET.
Query Match 59.4%; Score 799.4; DB 2; Length 848;
Best Local Similarity 98.8%; Pred. No. 5.9e-152;
RESULT 322
ID AAX26672 standard; RNA; 848 BP.
DE Extended cDNA derived from a 5' EST encoding a secreted protien.
PN WO9906554-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 59.4%; Score 799.4; DB 2; Length 848;
Best Local Similarity 98.8%; Pred. No. 5.9e-152;
RESULT 323
ID AAX51777 standard; cDNA; 848 BP.
DE Human secreted protein 5' EST clone 58-35-2-F10-FL2.
PN WO9906552-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 59.4%; Score 799.4; DB 2; Length 848;
Best Local Similarity 98.8%; Pred. No. 5.9e-152;
RESULT 324
ID AAX51449 standard; DNA; 848 BP.
DE Human secreted protein 5' EST SEQ ID NO. 27.
PN WO9906549-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 59.4%; Score 799.4; DB 2; Length 848;
Best Local Similarity 98.8%; Pred. No. 5.9e-152;
RESULT 325
ID AAX40428 standard; cDNA; 848 BP.
DE Extended cDNA derived from 5' EST.
PN WO9906550-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 59.4%; Score 799.4; DB 2; Length 848;
Best Local Similarity 98.8%; Pred. No. 5.9e-152;
RESULT 326
ID AAZ42251 standard; cDNA; 848 BP.
DE Human full length cDNA 58-35-2-F10-FL2.
PN WO9953051-A2.
PD 21-OCT-1999.
PA (GEST) GENSET.
Query Match 59.4%; Score 799.4; DB 3; Length 848;
Best Local Similarity 98.8%; Pred. No. 5.9e-152;
RESULT 327
ID AAC00012 standard; cDNA; 848 BP.
DE Human secreted protein cDNA sequence #3.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 59.4%; Score 799.4; DB 3; Length 848;
Best Local Similarity 98.8%; Pred. No. 5.9e-152;
RESULT 328
ID ADJ45874 standard; cDNA; 848 BP.

DE Novel human secreted protein-related cDNA sequence SeqID27.
PN US2003144490-A1.
PD 31-JUL-2003.
PA (EDWA/) EDWARDS J D M.
PA (DUCL/) DUCLERT A.
PA (BOUG/) BOUGUELERET L.
Query Match 59.4%; Score 799.4; DB 10; Length 848;
Best Local Similarity 98.8%; Pred. No. 5.9e-152;
RESULT 329
ID ADM77746 standard; cDNA; 848 BP.
DE EST encoding signal sequence #6.
PN US2003162176-A1.
PD 28-AUG-2003.
PA (EDWA/) EDWARDS J D M.
PA (DUCL/) DUCLERT A.
PA (BOUG/) BOUGUELERET L.
Query Match 59.4%; Score 799.4; DB 11; Length 848;
Best Local Similarity 98.8%; Pred. No. 5.9e-152;
RESULT 330
ID AAX88191 standard; cDNA; 848 BP.
DE Human secreted protein 6 extended cDNA.
PN WO9925825-A2.
PD 27-MAY-1999.
PA (GEST) GENSET.
Query Match 59.3%; Score 798.8; DB 2; Length 848;
Best Local Similarity 98.8%; Pred. No. 7.7e-152;
RESULT 331
ID AAX30083 standard; cDNA; 847 BP.
DE Human secreted protein 5' EST SEQ ID NO:27.
PN WO9906548-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 59.3%; Score 797.8; DB 2; Length 847;
Best Local Similarity 98.7%; Pred. No. 1.2e-151;
RESULT 332
ID AAF94460 standard; cDNA; 666 BP.
DE Human hydrophobic domain containing protein clone HP10720 cDNA #74.
PN WO200112660-A2.
PD 22-FEB-2001.
PA (SAGA) SAGAMI CHEM RES CENT.
PA (PROT-) PROTEGENE INC.
Query Match 48.6%; Score 654; DB 4; Length 666;
Best Local Similarity 99.8%; Pred. No. 1.3e-122;
RESULT 333
ID ADO07092 standard; cDNA; 774 BP.
DE Human protein modification and maintenance molecule 26 (PMMM-26) cDNA.
PN WO2004033636-A2.
PD 22-APR-2004.
PA (INCY-) INCYTE CORP.
Query Match 42.9%; Score 578; DB 12; Length 774;
Best Local Similarity 88.7%; Pred. No. 3.1e-107;
RESULT 334
ID ABT42042 standard; DNA; 1181 BP.
DE Toxicity modelling related rat gene SEQ ID No 1744.
PN WO200295000-A2.
PD 28-NOV-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 40.1%; Score 539.6; DB 10; Length 1181;
Best Local Similarity 71.5%; Pred. No. 1.9e-99;
RESULT 335
ID AAX40832 standard; cDNA; 439 BP.
DE Human secreted protein 5' EST SEQ ID NO: 44.
PN WO9906554-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 30.4%; Score 409.4; DB 2; Length 439;
Best Local Similarity 99.8%; Pred. No. 3.4e-73;
RESULT 336
ID AAV86301 standard; cDNA; 462 BP.
DE EST clone AM42.
PN WO9845435-A2.
PD 15-OCT-1998.
PA (GEMY) GENETICS INST INC.
Query Match 30.1%; Score 405; DB 2; Length 462;
Best Local Similarity 98.1%; Pred. No. 2.6e-72;
RESULT 337
ID ABS69507 standard; DNA; 532 BP.
DE Novel murine polynucleotide isolated using gene trap technology #570.
PN US2002102543-A1.
PD 01-AUG-2002.
PA (FRIE/) FRIEDRICH G.
PA (ZAMB/) ZAMBROWICZ B.
PA (SAND/) SANDS A T.
Query Match 23.5%; Score 316.6; DB 6; Length 532;
Best Local Similarity 84.9%; Pred. No. 1.9e-54;
RESULT 338
ID ADQ50701 standard; DNA; 609 BP.
DE Novel canine microarray-related DNA sequence SeqID2003.
PN WO2004063324-A2.
PD 29-JUL-2004.
PA (GENE-) GENE LOGIC INC.
PA (PFIZ) PFIZER PROD INC.
Query Match 19.3%; Score 260.4; DB 13; Length 609;
Best Local Similarity 72.2%; Pred. No. 4.5e-43;
RESULT 339
ID ABL78658 standard; cDNA; 355 BP.
DE Human ovarian cancer related cDNA clone SEQ ID NO:1636.
PN WO200192581-A2.
PD 06-DEC-2001.
PA (CORI-) CORIXA CORP.
Query Match 17.3%; Score 232.6; DB 6; Length 355;
Best Local Similarity 83.9%; Pred. No. 1.7e-37;
RESULT 340
ID ABZ78108 standard; cDNA; 212 BP.
DE Human Suppression subtractive hybridisation cDNA fragment #7.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 15.8%; Score 212; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 2.3e-33;
RESULT 341
ID ADN43035 standard; cDNA; 379 BP.
DE Human secreted protein SECP-21 cDNA.
PN WO2004037987-A2.
PD 06-MAY-2004.
PA (INCY-) INCYTE CORP.
Query Match 15.2%; Score 204.4; DB 12; Length 379;
Best Local Similarity 99.5%; Pred. No. 8.7e-32;
RESULT 342
ID ABA71751 standard; DNA; 213 BP.
DE Human foetal liver single exon nucleic acid probe #20056.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 14.7%; Score 197.4; DB 4; Length 213;
Best Local Similarity 99.5%; Pred. No. 2.1e-30;
RESULT 343
ID AAI52077 standard; DNA; 213 BP.
DE Probe #20763 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 14.7%; Score 197.4; DB 4; Length 213;
Best Local Similarity 99.5%; Pred. No. 2.1e-30;
RESULT 344
ID ABA37840 standard; DNA; 213 BP.
DE Probe #16306 for gene expression analysis in human heart cell sample.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 14.7%; Score 197.4; DB 4; Length 213;
Best Local Similarity 99.5%; Pred. No. 2.1e-30;
RESULT 345
ID AAK46169 standard; DNA; 213 BP.
DE Human bone marrow expressed single exon probe SEQ ID NO: 20726.
PN WO200157276-A2.

PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 14.7%; Score 197.4; DB 4; Length 213;
Best Local Similarity 99.5%; Pred. No. 2.1e-30;
RESULT 346
ID AAK20115 standard; DNA; 213 BP.
DE Human brain expressed single exon probe SEQ ID NO: 20106.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 14.7%; Score 197.4; DB 4; Length 213;
Best Local Similarity 99.5%; Pred. No. 2.1e-30;
RESULT 347
ID ABS45886 standard; DNA; 213 BP.
DE Human liver single exon probe, SEQ ID No 20876.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 14.7%; Score 197.4; DB 4; Length 213;
Best Local Similarity 99.5%; Pred. No. 2.1e-30;
RESULT 348
ID ABS20478 standard; DNA; 213 BP.
DE Human genome-derived single exon probe ORF from lung SEQ ID No 20469.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 14.7%; Score 197.4; DB 6; Length 213;
Best Local Similarity 99.5%; Pred. No. 2.1e-30;
RESULT 349
ID ABA59231 standard; DNA; 464 BP.
DE Human foetal liver single exon nucleic acid probe #7536.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 14.0%; Score 188.2; DB 4; Length 464;
Best Local Similarity 96.0%; Pred. No. 1.7e-28;
RESULT 350
ID AAI39012 standard; DNA; 464 BP.
DE Probe #7698 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 14.0%; Score 188.2; DB 4; Length 464;
Best Local Similarity 96.0%; Pred. No. 1.7e-28;
RESULT 351
ID ABA27979 standard; DNA; 464 BP.
DE Probe #6445 for gene expression analysis in human heart cell sample.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 14.0%; Score 188.2; DB 4; Length 464;
Best Local Similarity 96.0%; Pred. No. 1.7e-28;
RESULT 352
ID AAK33216 standard; DNA; 464 BP.
DE Human bone marrow expressed single exon probe SEQ ID NO: 7773.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 14.0%; Score 188.2; DB 4; Length 464;
Best Local Similarity 96.0%; Pred. No. 1.7e-28;
RESULT 353
ID AAK07438 standard; DNA; 464 BP.
DE Human brain expressed single exon probe SEQ ID NO: 7429.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 14.0%; Score 188.2; DB 4; Length 464;
Best Local Similarity 96.0%; Pred. No. 1.7e-28;
RESULT 354
ID ABS32964 standard; DNA; 464 BP.
DE Human liver single exon probe, SEQ ID No 7954.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 14.0%; Score 188.2; DB 4; Length 464;
Best Local Similarity 96.0%; Pred. No. 1.7e-28;
RESULT 355
ID ABS08046 standard; DNA; 464 BP.
DE Human genome-derived single exon probe from lung SEQ ID No 8037.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 14.0%; Score 188.2; DB 6; Length 464;
Best Local Similarity 96.0%; Pred. No. 1.7e-28;
RESULT 356
ID AAC84367 standard; DNA; 2415 BP.
DE Human Zace2 protein encoding degenerate sequence.
PN WO200070032-A1.
PD 23-NOV-2000.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 10.7%; Score 144.2; DB 4; Length 2415;
Best Local Similarity 39.1%; Pred. No. 1.7e-19;
RESULT 357
ID ABX93334 standard; DNA; 2415 BP.
DE Degenerate DNA sequence encoding human zinc metallopeptidase Zace2.
PN US2002177211-A1.
PD 28-NOV-2002.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 10.7%; Score 144.2; DB 10; Length 2415;
Best Local Similarity 39.1%; Pred. No. 1.7e-19;
RESULT 358
ID AAC84369 standard; DNA; 2415 BP.
DE Mouse Zace2-5 protein encoding degenerate sequence.
PN WO200070032-A1.
PD 23-NOV-2000.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 9.3%; Score 125.6; DB 4; Length 2415;
Best Local Similarity 38.6%; Pred. No. 9.6e-16;
RESULT 359
ID ABX93336 standard; DNA; 2415 BP.
DE Degenerate DNA sequence encoding mouse zinc metallopeptidase mZace-5.
PN US2002177211-A1.
PD 28-NOV-2002.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 9.3%; Score 125.6; DB 10; Length 2415;
Best Local Similarity 38.6%; Pred. No. 9.6e-16;
RESULT 360
ID ADL95396 standard; cDNA; 2415 BP.
DE Angiotensin converting enzyme-2 (ACE-2) coding sequence.
PN US6610497-B1.
PD 26-AUG-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 9.3%; Score 125; DB 11; Length 2415;
Best Local Similarity 57.3%; Pred. No. 1.3e-15;
RESULT 361
ID AAZ59465 standard; DNA; 2418 BP.
DE Human MPROT15 coding sequence #1.
PN JP11318472-A.
PD 24-NOV-1999.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 9.3%; Score 125; DB 3; Length 2418;
Best Local Similarity 57.3%; Pred. No. 1.3e-15;
RESULT 362
ID ACN43792 standard; cDNA; 3064 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2667.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 9.3%; Score 125; DB 13; Length 3064;
Best Local Similarity 57.3%; Pred. No. 1.3e-15;
RESULT 363
ID ACH03967 standard; cDNA; 3324 BP.
DE Human cDNA differentially expressed in lung cancer #172.
PN US2003065157-A1.
PD 03-APR-2003.
PA (LASE/) LASEK A W.

Query Match 9.3%; Score 125; DB 9; Length 3324;
Best Local Similarity 57.3%; Pred. No. 1.3e-15;
RESULT 364
ID ADC38727 standard; cDNA; 3325 BP.
DE Human cDNA encoding a secreted protein #41.
PN US2002193567-A1.
PD 19-DEC-2002.
PA (GEMY) GENETICS INST INC.
Query Match 9.3%; Score 125; DB 10; Length 3325;
Best Local Similarity 57.3%; Pred. No. 1.3e-15;
RESULT 365
ID AAC84366 standard; cDNA; 3334 BP.
DE Human Zace2 protein encoding cDNA.
PN WO200070032-A1.
PD 23-NOV-2000.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 9.3%; Score 125; DB 4; Length 3334;
Best Local Similarity 57.3%; Pred. No. 1.3e-15;
RESULT 366
ID ABX93333 standard; cDNA; 3334 BP.
DE cDNA encoding human zinc metallopeptidase Zace2.
PN US2002177211-A1.
PD 28-NOV-2002.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 9.3%; Score 125; DB 10; Length 3334;
Best Local Similarity 57.3%; Pred. No. 1.3e-15;
RESULT 367
ID AAA12764 standard; cDNA; 3396 BP.
DE cDNA encoding a human angiotensin converting enzyme-2 (ACE-2).
PN WO200018899-A2.
PD 06-APR-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 9.3%; Score 125; DB 3; Length 3396;
Best Local Similarity 57.3%; Pred. No. 1.3e-15;
RESULT 368
ID AAD02758 standard; cDNA; 3396 BP.
DE Human angiotensin converting enzyme-2 (ACE-2) cDNA.
PN US6194556-B1.
PD 27-FEB-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 9.3%; Score 125; DB 4; Length 3396;
Best Local Similarity 57.3%; Pred. No. 1.3e-15;
RESULT 369
ID AAD32586 standard; cDNA; 3396 BP.
DE Human ACE-2 full-length cDNA.
PN WO200212471-A2.
PD 14-FEB-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 9.3%; Score 125; DB 6; Length 3396;
Best Local Similarity 57.3%; Pred. No. 1.3e-15;
RESULT 370
ID ABK87623 standard; cDNA; 3396 BP.
DE cDNA encoding human angiotensin converting enzyme-2 (ACE-2) protein.
PN WO200239997-A2.
PD 23-MAY-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 9.3%; Score 125; DB 6; Length 3396;
Best Local Similarity 57.3%; Pred. No. 1.3e-15;
RESULT 371
ID ADA03343 standard; DNA; 3396 BP.
DE Human angiotensin converting enzyme 2-like protein gene.
PN WO200298448-A1.
PD 12-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.3%; Score 125; DB 8; Length 3396;
Best Local Similarity 57.3%; Pred. No. 1.3e-15;
RESULT 372
ID ACC79022 standard; cDNA; 3396 BP.
DE Human ACE-2 protein encoding cDNA SEQ ID NO:141.
PN WO200298906-A1.
PD 12-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.3%; Score 125; DB 8; Length 3396;
Best Local Similarity 57.3%; Pred. No. 1.3e-15;
RESULT 373
ID ADL95394 standard; cDNA; 3396 BP.
DE Human angiotensin converting enzyme-2 (ACE-2) cDNA.
PN US6610497-B1.
PD 26-AUG-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 9.3%; Score 125; DB 11; Length 3396;
Best Local Similarity 57.3%; Pred. No. 1.3e-15;
RESULT 374
ID ADH51356 standard; DNA; 3404 BP.
DE Human angiotensin-converting enzyme homologue ACE2 DNA.
PN WO2004000367-A1.
PD 31-DEC-2003.
PA (UYHE-) UNIV HEALTH NETWORK.
Query Match 9.3%; Score 125; DB 12; Length 3404;
Best Local Similarity 57.3%; Pred. No. 1.3e-15;
RESULT 375
ID ABS60632 standard; cDNA; 3405 BP.
DE Human cDNA encoding angiotensin converting enzyme 2 variant #1.
PN WO200261131-A2.
PD 08-AUG-2002.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
PA (TSUC/) TSUCHIHASHI Z.
PA (HUIL/) HUI L.
Query Match 9.3%; Score 125; DB 6; Length 3405;
Best Local Similarity 57.3%; Pred. No. 1.3e-15;
RESULT 376
ID ABS60371 standard; cDNA; 3405 BP.
DE Human cDNA encoding angiotensin converting enzyme 2.
PN WO200261131-A2.
PD 08-AUG-2002.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
PA (TSUC/) TSUCHIHASHI Z.
PA (HUIL/) HUI L.
Query Match 9.3%; Score 125; DB 6; Length 3405;
Best Local Similarity 57.3%; Pred. No. 1.3e-15;
RESULT 377
ID AAS21279 standard; cDNA; 3732 BP.
DE Human cDNA sequence encoding for PRO1885 polypeptide.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 4; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 378
ID ACA03638 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 8; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 379
ID ABX89176 standard; cDNA; 3732 BP.
DE DNA encoding novel secreted and transmembrane protein PRO1885.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 8; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 380
ID ACD41830 standard; cDNA; 3732 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #36.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 8; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 381
ID ACA04059 standard; cDNA; 3732 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 71.
PN US2003032155-A1.

PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 8; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 382
ID ADA45590 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 383
ID ADA76021 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 384
ID ADA18671 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 385
ID ADA61294 standard; cDNA; 3732 BP.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 386
ID ADB19079 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 387
ID ADB27620 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 388
ID ADA86099 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 389
ID ADB15663 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 390
ID ADA47449 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 391
ID ADA67244 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 392
ID ADB30251 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 393
ID ADA85547 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 394
ID ADA96759 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 395
ID ADA79063 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 396
ID ADA87202 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 397
ID ADB16404 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 398
ID ADA91496 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 399
ID ADB14559 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 400
ID ADB18520 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 401
ID ADA93735 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 402
ID ADB19631 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 403
ID ADB12943 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 404
ID ACD98459 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 405
ID ADA74197 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 406
ID ADB24430 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide SEQ ID NO 71.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 407
ID ADA81954 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 408
ID ADA74917 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 409
ID ADA84995 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 410
ID ADA84443 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 411
ID ADB29699 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 412
ID ADA80227 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 413
ID ADA75469 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 414
ID ADA46694 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 415
ID ADB24990 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide SEQ ID NO 71.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 416
ID ADA93166 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 417
ID ADB26516 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;

RESULT 418
ID ADB30803 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 419
ID ADA60731 standard; cDNA; 3732 BP.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 420
ID ADB23878 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide SEQ ID NO 71.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 421
ID ADA96207 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 422
ID ADA80779 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 423
ID ADA95655 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 424
ID ADB25964 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 425
ID ADB21449 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 426
ID ADA77228 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 427
ID ADB17968 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 428
ID ADA86651 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 429
ID ADA87754 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 430
ID ADA46142 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 431
ID ADB28172 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 432
ID ADB28724 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 433
ID ADA76676 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 434
ID ADA88306 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 435
ID ADA97311 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 436
ID ADB27068 standard; cDNA; 3732 BP.

DE cDNA encoding human PRO polypeptide #36.
PN US2003022239-A1.
PD 30-JAN-2003.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 437
ID ADB22001 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003087344-A1.
PD 08-MAY-2003.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 438
ID ADA66692 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 439
ID ADB22553 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 440
ID ADB23326 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide SEQ ID NO 71.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 441
ID ADA92048 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 442
ID ADB15111 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 443
ID ADB38363 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 444
ID ADB37811 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 445
ID ADB66283 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 9; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 446
ID ADB89363 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 447
ID ADB90095 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 448
ID ADB39196 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 449
ID ADB46819 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 450
ID ADB86426 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 451
ID ADB77031 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 452
ID ADB34188 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide SEQ ID NO 71.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 453
ID ADB35292 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide SEQ ID NO 71.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 454
ID ADB33636 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide SEQ ID NO 71.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 455
ID ADB34740 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide SEQ ID NO 71.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 456
ID ADB35844 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide SEQ ID NO 71.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 457
ID ADB46239 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 458
ID ADC50112 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 459
ID ADC71659 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 460
ID ADC59638 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 461
ID ADC52645 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID71.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 462
ID ADC56999 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID71.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 463
ID ADC60190 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 464
ID ADC50665 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 465
ID ADC65192 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 466
ID ADC54290 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID71.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 467
ID ADC53251 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID71.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 468
ID ADC58774 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID71.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 469
ID ADC55652 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID71.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 470
ID ADC58222 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID71.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 471
ID ADD02896 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 472
ID ADC89888 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;

RESULT 473
ID ADC69307 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 474
ID ADC48196 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 475
ID ADD09725 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 476
ID ADD04300 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 477
ID ADC80256 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 478
ID ADD10763 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 479
ID ADC47644 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 480
ID ADC79704 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 481
ID ADD09173 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 482
ID ADD40886 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 483
ID ADD52025 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 484
ID ADD52765 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 485
ID ADD53317 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 486
ID ADD51473 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 487
ID ADD02272 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 488
ID ADD01706 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 489
ID ADD53888 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 490
ID ADD92205 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 491
ID ADD91101 standard; cDNA; 3732 BP.

DE Human PRO polynucleotide #36.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 492
ID ADE03715 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 493
ID ADE32012 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 494
ID ADE21944 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 495
ID ADD79168 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 496
ID ADE41704 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 497
ID ADE17521 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 498
ID ADD91653 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 499
ID ADE33116 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 500
ID ADE33668 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 501
ID ADD79720 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 502
ID ADD92757 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 503
ID ADE19177 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 504
ID ADE18625 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 505
ID ADE42821 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 506
ID ADD95610 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 507
ID ADE22496 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 508
ID ADD78614 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 509
ID ADE32564 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003194766-A1.

PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 510
ID ADE42256 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 511
ID ADD80272 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 512
ID ADD89300 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 513
ID ADE40584 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 514
ID ADE04383 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 515
ID ADE92512 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 516
ID ADG21221 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 517
ID ADG22862 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 518
ID ADF97197 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 519
ID ADG80261 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 520
ID ADG79709 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 521
ID ADH55001 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 522
ID ADH55553 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 523
ID ADI64721 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 524
ID ADH81634 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 525
ID ADH81082 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 526
ID ACD23888 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 527
ID ACA67029 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.

Query Match 8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 528
ID ADM82251 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 11; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 529
ID ADN15650 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 11; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 530
ID ADN16279 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 11; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 531
ID ADN15098 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 11; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 532
ID ADN14546 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 11; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 533
ID ADI63772 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 11; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 534
ID ADI63220 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 11; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 535
ID ADC80808 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 536
ID ADD76256 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 537
ID ADD87620 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 538
ID ADD86024 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 539
ID ADE75472 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 540
ID ADE23048 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 541
ID ADE23600 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 542
ID ADE24243 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 543
ID ADD87068 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 544
ID ADE88934 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 545
ID ADE18073 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;

RESULT 546
ID ADE88382 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 547
ID ADE94402 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 548
ID ADE90813 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 549
ID ADE94954 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 550
ID ADE93064 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 551
ID ADF34645 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 552
ID ADE91960 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 553
ID ADE90261 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 554
ID ADE91408 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 555
ID ADG01987 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 556
ID ADG21773 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 557
ID ADG19843 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 558
ID ADF97749 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 559
ID ADG23966 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 560
ID ADF98320 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 561
ID ADG03151 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 562
ID ADF98872 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 563
ID ADG16457 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 564
ID ADG04916 standard; cDNA; 3732 BP.

DE Human PRO polynucleotide #36.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 565
ID ADG19183 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 566
ID ADG13020 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 567
ID ADG08077 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 568
ID ADG15247 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 569
ID ADF96645 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 570
ID ADG05830 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 571
ID ADG23414 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 572
ID ADG03703 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 573
ID ADG24604 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 574
ID ADG06901 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 575
ID ADG07453 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 576
ID ADG54948 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 577
ID ADG60612 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 578
ID ADG61716 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 579
ID ADG81917 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 580
ID ADG57156 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 581
ID ADG56604 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 582
ID ADG55500 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207365-A1.

PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 583
ID ADG58260 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 584
ID ADG70626 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 585
ID ADG57708 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 586
ID ADG53292 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 587
ID ADG71178 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 588
ID ADG81365 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003207805-A1.
PD 06-NOV-2003.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 589
ID ADH30327 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 590
ID ADH11694 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 591
ID ADG52116 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 592
ID ADG53844 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 593
ID ADG80813 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 594
ID ADG56052 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 595
ID ADH12318 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 596
ID ADG61164 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 597
ID ADH28251 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 598
ID ADG54396 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 599
ID ADG59436 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 600
ID ADI80860 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;

Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 601
ID ADG09603 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 602
ID ADI15074 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 603
ID ADG08951 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 604
ID ADI14406 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 605
ID ADI18001 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 606
ID ADJ63282 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 607
ID ADJ77177 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 608
ID ADJ65299 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 609
ID ADM27435 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 610
ID ADM42159 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 611
ID ADM28021 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 612
ID ADI95503 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 13; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 613
ID ADI96055 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.9%; Score 119.8; DB 13; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 614
ID AAS14890 standard; cDNA; 2911 BP.
DE Human cDNA encoding novel human protein NHP #11.
PN WO200174896-A1.
PD 11-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.7%; Score 117; DB 4; Length 2911;
Best Local Similarity 57.6%; Pred. No. 5.4e-14;
RESULT 615
ID AAS14880 standard; cDNA; 2920 BP.
DE Human cDNA encoding novel human protein NHP #1.
PN WO200174896-A1.
PD 11-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.7%; Score 117; DB 4; Length 2920;
Best Local Similarity 57.6%; Pred. No. 5.4e-14;
RESULT 616
ID ADA03339 standard; DNA; 2920 BP.
DE Human angiotensin converting enzyme 2 gene.
PN WO200298448-A1.
PD 12-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.7%; Score 117; DB 8; Length 2920;
Best Local Similarity 57.6%; Pred. No. 5.4e-14;
RESULT 617
ID ACC79021 standard; cDNA; 2920 BP.
DE Human ACE-2 protein encoding cDNA SEQ ID NO:137.
PN WO200298906-A1.
PD 12-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.7%; Score 117; DB 8; Length 2920;
Best Local Similarity 57.6%; Pred. No. 5.4e-14;
RESULT 618
ID ABL78659 standard; cDNA; 435 BP.
DE Human ovarian cancer related cDNA clone SEQ ID NO:1637.
PN WO200192581-A2.
PD 06-DEC-2001.
PA (CORI-) CORIXA CORP.
Query Match 8.3%; Score 111.4; DB 6; Length 435;
Best Local Similarity 63.3%; Pred. No. 5.5e-13;
RESULT 619

ID AAC84368 standard; cDNA; 2638 BP.
DE Mouse Zace2-5 protein encoding cDNA.
PN WO200070032-A1.
PD 23-NOV-2000.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 8.3%; Score 111.4; DB 4; Length 2638;
Best Local Similarity 56.9%; Pred. No. 7.2e-13;
RESULT 620
ID ABX93335 standard; cDNA; 2638 BP.
DE cDNA encoding mouse zinc metallopeptidase mZace-5.
PN US2002177211-A1.
PD 28-NOV-2002.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 8.3%; Score 111.4; DB 10; Length 2638;
Best Local Similarity 56.9%; Pred. No. 7.2e-13;
RESULT 621
ID AAC84370 standard; cDNA; 2638 BP.
DE Mouse Zace2-10 protein encoding cDNA.
PN WO200070032-A1.
PD 23-NOV-2000.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 8.0%; Score 108.2; DB 4; Length 2638;
Best Local Similarity 56.5%; Pred. No. 3.2e-12;
RESULT 622
ID ABX93337 standard; cDNA; 2638 BP.
DE cDNA encoding mouse zinc metallopeptidase mZace-10.
PN US2002177211-A1.
PD 28-NOV-2002.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 8.0%; Score 108.2; DB 10; Length 2638;
Best Local Similarity 56.5%; Pred. No. 3.2e-12;
RESULT 623
ID ADH51358 standard; DNA; 2739 BP.
DE Mouse angiotensin-converting enzyme homologue ACE2 DNA.
PN WO2004000367-A1.
PD 31-DEC-2003.
PA (UYHE-) UNIV HEALTH NETWORK.
Query Match 8.0%; Score 108.2; DB 12; Length 2739;
Best Local Similarity 56.5%; Pred. No. 3.2e-12;
RESULT 624
ID ABQ57861 standard; cDNA; 561 BP.
DE Human colon cancer related nucleotide sequence SEQ ID NO:1556.
PN WO200229086-A2.
PD 11-APR-2002.
PA (FARB) BAYER CORP.
Query Match 7.2%; Score 96.8; DB 6; Length 561;
Best Local Similarity 57.8%; Pred. No. 5.1e-10;
RESULT 625
ID AAZ59466 standard; DNA; 2262 BP.
DE Human MPROT15 coding sequence #2.
PN JP11318472-A.
PD 24-NOV-1999.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 7.2%; Score 96.8; DB 3; Length 2262;
Best Local Similarity 57.8%; Pred. No. 6.2e-10;
RESULT 626
ID ACN43791 standard; cDNA; 3072 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2666.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 7.2%; Score 96.8; DB 13; Length 3072;
Best Local Similarity 57.8%; Pred. No. 6.5e-10;
RESULT 627
ID ABK30270 standard; cDNA; 2350 BP.
DE Human G-protein-coupled protease #40.
PN US6331427-B1.
PD 18-DEC-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 5.2%; Score 69.4; DB 6; Length 2350;
Best Local Similarity 55.1%; Pred. No. 0.00022;
RESULT 628
ID ABZ10246 standard; DNA; 8056 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #386.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 5.0%; Score 67; DB 8; Length 8056;
Best Local Similarity 48.3%; Pred. No. 0.00079;
RESULT 629
ID AAS42515 standard; cDNA; 3474 BP.
DE Human cDNA encoding an mddt protein, clone LI:347572.1:2000MAY01.
PN WO200162922-A2.
PD 30-AUG-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 4.7%; Score 63; DB 5; Length 3474;
Best Local Similarity 55.8%; Pred. No. 0.0045;
RESULT 630
ID ADS89278 standard; DNA; 5286 BP.
DE Oligonucleotide of the invention SEQ ID NO:294.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 62.8; DB 13; Length 5286;
Best Local Similarity 48.0%; Pred. No. 0.0053;
RESULT 631
ID ADS89552 standard; DNA; 5286 BP.
DE Oligonucleotide of the invention SEQ ID NO:568.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.7%; Score 62.8; DB 13; Length 5286;
Best Local Similarity 48.0%; Pred. No. 0.0053;
RESULT 632
ID AAS46694 standard; DNA; 5413 BP.
DE Tumour suppressor gene derived chemically modified sequence #417.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.6%; Score 62.4; DB 4; Length 5413;
Best Local Similarity 45.6%; Pred. No. 0.0064;
RESULT 633
ID ABL32426 standard; DNA; 9810 BP.
DE Human immune system associated gene SEQ ID NO: 399.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.6%; Score 62.4; DB 6; Length 9810;
Best Local Similarity 45.6%; Pred. No. 0.0069;
RESULT 634
ID ABZ10100 standard; DNA; 8056 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #240.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.6%; Score 62.2; DB 8; Length 8056;
Best Local Similarity 47.8%; Pred. No. 0.0074;
RESULT 635
ID ADL17884 standard; cDNA; 158001 BP.
DE Human phosphotyrosyl phosphatase activator, PTPA, gene.
PN US2004023906-A1.
PD 05-FEB-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 4.6%; Score 61.8; DB 12; Length 158001;
Best Local Similarity 46.1%; Pred. No. 0.014;
RESULT 636
ID ABQ67093 standard; DNA; 83391 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 123.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.5%; Score 60.6; DB 6; Length 83391;
Best Local Similarity 44.8%; Pred. No. 0.022;
RESULT 637
ID ABN36017 standard; DNA; 60 BP.
DE Human spliced transcript detection oligonucleotide SEQ ID NO:8765.

PN WO200210449-A2.
PD 07-FEB-2002.
PA (COMP-) COMPUGEN INC.
Query Match 4.5%; Score 60; DB 6; Length 60;
Best Local Similarity 100.0%; Pred. No. 0.0099;
RESULT 638
ID AAQ53480 standard; cDNA; 2503 BP.
DE pNPX30 xylanase cDNA.
PN WO9325671-A1.
PD 23-DEC-1993.
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
Query Match 4.4%; Score 58.8; DB 2; Length 2503;
Best Local Similarity 45.6%; Pred. No. 0.03;
RESULT 639
ID ABL32369 standard; DNA; 9997 BP.
DE Human immune system associated gene SEQ ID NO: 342.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.4%; Score 58.8; DB 6; Length 9997;
Best Local Similarity 47.1%; Pred. No. 0.037;
RESULT 640
ID ABL34485 standard; DNA; 9997 BP.
DE Human metastasis associated gene SEQ ID NO: 38.
PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.4%; Score 58.8; DB 6; Length 9997;
Best Local Similarity 47.1%; Pred. No. 0.037;
RESULT 641
ID ADS99746 standard; DNA; 9997 BP.
DE Complement of bisulphite treated metastasis-associated human gene #19.
PN US2003148327-A1.
PD 07-AUG-2003.
PA (OLEK/) OLEK A.
PA (PIEP/) PIEPENBROCK C.
PA (BERL/) BERLIN K.
Query Match 4.4%; Score 58.8; DB 7; Length 9997;
Best Local Similarity 47.1%; Pred. No. 0.037;
RESULT 642
ID ADB37663 standard; DNA; 29993 BP.
DE Human chemically pretreated EYA4 gene SEQ ID NO:5.
PN WO2003072812-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.4%; Score 58.8; DB 10; Length 29993;
Best Local Similarity 43.4%; Pred. No. 0.044;
RESULT 643
ID ADB37661 standard; DNA; 29993 BP.
DE Human chemically pretreated EYA4 gene SEQ ID NO:3.
PN WO2003072812-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.4%; Score 58.8; DB 10; Length 29993;
Best Local Similarity 43.4%; Pred. No. 0.044;
RESULT 644
ID AAS46746 standard; DNA; 38342 BP.
DE Tumour suppressor gene derived chemically modified sequence #470.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.4%; Score 58.8; DB 4; Length 38342;
Best Local Similarity 43.4%; Pred. No. 0.046;
RESULT 645
ID ABK31507 standard; DNA; 38342 BP.
DE Signal transduction associated gene modified complementary DNA #175.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.4%; Score 58.8; DB 6; Length 38342;
Best Local Similarity 43.4%; Pred. No. 0.046;
RESULT 646
ID ABL32427 standard; DNA; 9810 BP.
DE Human immune system associated gene SEQ ID NO: 400.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.4%; Score 58.6; DB 6; Length 9810;
Best Local Similarity 44.8%; Pred. No. 0.041;
RESULT 647
ID ABL34174 standard; DNA; 113515 BP.
DE Human immune system associated gene SEQ ID NO: 2147.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.4%; Score 58.6; DB 6; Length 113515;
Best Local Similarity 45.7%; Pred. No. 0.059;
RESULT 648
ID ABZ10246 standard; DNA; 8056 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #386.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.2%; Score 57.2; DB 8; Length 8056;
Best Local Similarity 48.8%; Pred. No. 0.076;
RESULT 649
ID ADH10017 standard; DNA; 365186 BP.
DE Human chromosome 2p21-22 fragment containing the DRIP gene.
PN WO2003093310-A1.
PD 13-NOV-2003.
PA (UYBR-) UNIV BREMEN.
Query Match 4.2%; Score 57.2; DB 10; Length 110000;
Best Local Similarity 44.6%; Pred. No. 0.11;
RESULT 650
ID ADQ97960 standard; DNA; 390183 BP.
DE Human cancer associated sequence HD11-029, SEQ ID 937.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 4.2%; Score 56.8; DB 12; Length 110000;
Best Local Similarity 45.1%; Pred. No. 0.14;
RESULT 651
ID ADS89008 standard; DNA; 5286 BP.
DE Human GGT1 gene SEQ ID NO:24.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.2%; Score 56.4; DB 13; Length 5286;
Best Local Similarity 47.2%; Pred. No. 0.1;
RESULT 652
ID ADS89278 standard; DNA; 5286 BP.
DE Oligonucleotide of the invention SEQ ID NO:294.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 55.4; DB 13; Length 5286;
Best Local Similarity 44.4%; Pred. No. 0.16;
RESULT 653
ID ADS89552 standard; DNA; 5286 BP.
DE Oligonucleotide of the invention SEQ ID NO:568.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 55.4; DB 13; Length 5286;
Best Local Similarity 44.4%; Pred. No. 0.16;
RESULT 654
ID ABL33544 standard; DNA; 10328 BP.
DE Human immune system associated gene SEQ ID NO: 1517.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 55.4; DB 6; Length 10328;
Best Local Similarity 47.3%; Pred. No. 0.18;
RESULT 655
ID AAK73165 standard; DNA; 20420 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27977.

PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 55.2; DB 4; Length 20420;
Best Local Similarity 48.0%; Pred. No. 0.22;
RESULT 656
ID ABK69933 standard; DNA; 20420 BP.
DE Human secreted protein gene 68 genomic DNA fragment #21.
PN WO200226931-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 55.2; DB 6; Length 20420;
Best Local Similarity 48.0%; Pred. No. 0.22;
RESULT 657
ID ADA71938 standard; DNA; 2000 BP.
DE Rice gene, SEQ ID 5263.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 4.1%; Score 55; DB 8; Length 2000;
Best Local Similarity 9.3%; Pred. No. 0.17;
RESULT 658
ID ADS89551 standard; DNA; 5286 BP.
DE Oligonucleotide of the invention SEQ ID NO:567.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 55; DB 13; Length 5286;
Best Local Similarity 47.0%; Pred. No. 0.2;
RESULT 659
ID ADS89277 standard; DNA; 5286 BP.
DE Oligonucleotide of the invention SEQ ID NO:293.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 55; DB 13; Length 5286;
Best Local Similarity 47.0%; Pred. No. 0.2;
RESULT 660
ID ABK31366 standard; DNA; 6181 BP.
DE Signal transduction associated gene modified DNA #105.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 55; DB 6; Length 6181;
Best Local Similarity 46.1%; Pred. No. 0.2;
RESULT 661
ID ABL70323 standard; DNA; 6181 BP.
DE Chemically treated cell signalling DNA sequence#107.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 55; DB 6; Length 6181;
Best Local Similarity 46.1%; Pred. No. 0.2;
RESULT 662
ID AAS61270 standard; DNA; 6181 BP.
DE Human gene regulation-associated gene oligonucleotide #225.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 55; DB 6; Length 6181;
Best Local Similarity 46.1%; Pred. No. 0.2;
RESULT 663
ID ABL32625 standard; DNA; 16217 BP.
DE Human immune system associated gene SEQ ID NO: 598.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 55; DB 6; Length 16217;
Best Local Similarity 46.3%; Pred. No. 0.23;
RESULT 664
ID ADL13897 standard; DNA; 11631 BP.
DE Osteoarthritis-associated polymorphic nucleotide #429.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 4.1%; Score 54.8; DB 10; Length 11631;
Best Local Similarity 46.3%; Pred. No. 0.24;
RESULT 665
ID ADI73089 standard; DNA; 500 BP.
DE Human ovarian cancer DNA marker #5831.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 54.4; DB 5; Length 500;
Best Local Similarity 39.1%; Pred. No. 0.18;
RESULT 666
ID ADL38222 standard; DNA; 500 BP.
DE Human ovarian cancer DNA marker #12112.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 54.4; DB 5; Length 500;
Best Local Similarity 39.1%; Pred. No. 0.18;
RESULT 667
ID AAH93026 standard; DNA; 700 BP.
DE Human inflammatory bowel disease related gene fragment IGR3319a.
PN WO200142511-A2.
PD 14-JUN-2001.
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
PA (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.
Query Match 4.0%; Score 54.4; DB 4; Length 700;
Best Local Similarity 46.2%; Pred. No. 0.19;
RESULT 668
ID ABL33730 standard; DNA; 6109 BP.
DE Human immune system associated gene SEQ ID NO: 1703.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 54.4; DB 6; Length 6109;
Best Local Similarity 47.5%; Pred. No. 0.27;
RESULT 669
ID ABK28339 standard; DNA; 6631 BP.
DE DNA transcription associated genomic DNA #107.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 54.4; DB 6; Length 6631;
Best Local Similarity 49.5%; Pred. No. 0.27;
RESULT 670
ID ABL32283 standard; DNA; 7490 BP.
DE Human immune system associated gene SEQ ID NO: 256.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 54.4; DB 6; Length 7490;
Best Local Similarity 48.2%; Pred. No. 0.28;
RESULT 671
ID ABL33964 standard; DNA; 9180 BP.
DE Human immune system associated gene SEQ ID NO: 1937.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 54.2; DB 6; Length 9180;
Best Local Similarity 46.7%; Pred. No. 0.31;
RESULT 672
Query Match 4.0%; Score 54.2; DB 13; Length 110000;
Best Local Similarity 43.5%; Pred. No. 0.45;
RESULT 673
ID AAS46430 standard; DNA; 6106 BP.
DE Tumour suppressor gene derived chemically modified sequence #152.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 54; DB 4; Length 6106;
Best Local Similarity 46.7%; Pred. No. 0.32;
RESULT 674

ID ABK40032 standard; DNA; 6106 BP.
DE Human chemically pretreated gene sequence #57 strand 2.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 54; DB 6; Length 6106;
Best Local Similarity 46.7%; Pred. No. 0.32;
RESULT 675
ID ABL33473 standard; DNA; 6106 BP.
DE Human immune system associated gene SEQ ID NO: 1446.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 54; DB 6; Length 6106;
Best Local Similarity 46.7%; Pred. No. 0.32;
RESULT 676
ID AAQ90512 standard; DNA; 11288 BP.
DE CEA clone HindIII-Sau3A fragment.
PN WO9514100-A2.
PD 26-MAY-1995.
PA (WELL) WELLCOME FOUND LTD.
Query Match 4.0%; Score 54; DB 2; Length 11288;
Best Local Similarity 62.1%; Pred. No. 0.35;
RESULT 677
ID AAS14778 standard; DNA; 11288 BP.
DE Human carcinoembryonic antigen (CEA) genomic DNA.
PN WO200174861-A2.
PD 11-OCT-2001.
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
Query Match 4.0%; Score 54; DB 5; Length 11288;
Best Local Similarity 62.1%; Pred. No. 0.35;
RESULT 678
ID AAV52967 standard; DNA; 15056 BP.
DE Carcinoembryonic antigen gene 5' flanking region.
PN WO9839467-A2.
PD 11-SEP-1998.
PA (CALY-) CALYDON INC.
Query Match 4.0%; Score 54; DB 2; Length 15056;
Best Local Similarity 62.1%; Pred. No. 0.37;
RESULT 679
ID AAZ99933 standard; DNA; 15056 BP.
DE DNA sequence of comprising a carcinoembryonic antigen TRE.
PN WO200015820-A1.
PD 23-MAR-2000.
PA (CALY-) CALYDON INC.
Query Match 4.0%; Score 54; DB 3; Length 15056;
Best Local Similarity 62.1%; Pred. No. 0.37;
RESULT 680
ID AAA46851 standard; DNA; 15056 BP.
DE Nucleotide sequence of a CEA-TRE.
PN WO200039319-A2.
PD 06-JUL-2000.
PA (CALY-) CALYDON INC.
Query Match 4.0%; Score 54; DB 3; Length 15056;
Best Local Similarity 62.1%; Pred. No. 0.37;
RESULT 681
ID AAH43620 standard; cDNA; 15056 BP.
DE CEA-TRE.
PN WO200173093-A2.
PD 04-OCT-2001.
PA (CALY-) CALYDON INC.
Query Match 4.0%; Score 54; DB 5; Length 15056;
Best Local Similarity 62.1%; Pred. No. 0.37;
RESULT 682
ID AAF87238 standard; DNA; 15056 BP.
DE CEA-TRE fusion protein coding sequence.
PN WO200172341-A2.
PD 04-OCT-2001.
PA (CALY-) CALYDON INC.
Query Match 4.0%; Score 54; DB 5; Length 15056;
Best Local Similarity 62.1%; Pred. No. 0.37;
RESULT 683
ID ABK99582 standard; DNA; 15056 BP.
DE Prostate-specific antigen transcriptional regulatory elelment (TRE).
PN US2002068049-A1.
PD 06-JUN-2002.
PA (HEND/) HENDERSON D R.
PA (SCHU/) SCHUUR E R.
Query Match 4.0%; Score 54; DB 6; Length 15056;
Best Local Similarity 62.1%; Pred. No. 0.37;
RESULT 684
ID ACD07309 standard; DNA; 15056 BP.
DE Human carcinoembryonic antigen (CEA) TRE.
PN US2003044383-A1.
PD 06-MAR-2003.
PA (HEND/) HENDERSON D R.
PA (SCHU/) SCHUUR E R.
Query Match 4.0%; Score 54; DB 8; Length 15056;
Best Local Similarity 62.1%; Pred. No. 0.37;
RESULT 685
ID ABL32315 standard; DNA; 6641 BP.
DE Human immune system associated gene SEQ ID NO: 288.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 53.4; DB 6; Length 6641;
Best Local Similarity 44.3%; Pred. No. 0.43;
RESULT 686
ID ABL54336 standard; DNA; 6641 BP.
DE Chemically treated apoptosis gene complementary to gene #18.
PN WO200177164-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 53.4; DB 6; Length 6641;
Best Local Similarity 44.3%; Pred. No. 0.43;
RESULT 687
ID ABL32356 standard; DNA; 9642 BP.
DE Human immune system associated gene SEQ ID NO: 329.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 53.4; DB 6; Length 9642;
Best Local Similarity 44.9%; Pred. No. 0.46;
RESULT 688
ID AAK73166 standard; DNA; 19965 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27978.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 53.4; DB 4; Length 19965;
Best Local Similarity 47.2%; Pred. No. 0.51;
RESULT 689
ID ABK69932 standard; DNA; 19965 BP.
DE Human secreted protein gene 68 genomic DNA fragment #20.
PN WO200226931-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 53.4; DB 6; Length 19965;
Best Local Similarity 47.2%; Pred. No. 0.51;
RESULT 690
ID ABD32659 standard; DNA; 163382 BP.
DE Human cancer-associated genomic DNA HD13-065.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 4.0%; Score 53.4; DB 13; Length 163382;
Best Local Similarity 46.9%; Pred. No. 0.7;
RESULT 691
ID ADI72552 standard; DNA; 530 BP.
DE Human ovarian cancer DNA marker #5294.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.9%; Score 53; DB 5; Length 530;
Best Local Similarity 46.1%; Pred. No. 0.36;
RESULT 692

ID ADL37691 standard; DNA; 530 BP.
DE Human ovarian cancer DNA marker #11581.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.9%; Score 53; DB 5; Length 530;
Best Local Similarity 46.1%; Pred. No. 0.36;
RESULT 693
ID ABL34495 standard; DNA; 18817 BP.
DE Human metastasis associated gene SEQ ID NO: 48.
PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.9%; Score 53; DB 6; Length 18817;
Best Local Similarity 45.9%; Pred. No. 0.61;
RESULT 694
ID ABL70162 standard; DNA; 18817 BP.
DE Chemically treated cell signalling DNA sequence complementary to#26.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.9%; Score 53; DB 6; Length 18817;
Best Local Similarity 45.9%; Pred. No. 0.61;
RESULT 695
ID ADS99756 standard; DNA; 18817 BP.
DE Complement of bisulphite treated metastasis-associated human gene #24.
PN US2003148327-A1.
PD 07-AUG-2003.
PA (OLEK/) OLEK A.
PA (PIEP/) PIEPENBROCK C.
PA (BERL/) BERLIN K.
Query Match 3.9%; Score 53; DB 7; Length 18817;
Best Local Similarity 45.9%; Pred. No. 0.61;
RESULT 696
ID AAQ24134 standard; DNA; 1671 BP.
DE 50 kD subunit of SceI.
PN JP04104793-A.
PD 07-APR-1992.
PA (RIKA) RIKAGAKU KENKYUSHO.
Query Match 3.9%; Score 52.8; DB 2; Length 1671;
Best Local Similarity 44.7%; Pred. No. 0.46;
RESULT 697
ID AAK86271 standard; DNA; 9599 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41083.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 52.8; DB 4; Length 9599;
Best Local Similarity 47.3%; Pred. No. 0.6;
RESULT 698
ID AAD52172 standard; DNA; 26000 BP.
DE Human interferon gamma receptor 1 (IFNGR1) gene.
PN WO200288162-A1.
PD 07-NOV-2002.
PA (ISIS-) ISIS PHARM INC.
Query Match 3.9%; Score 52.8; DB 10; Length 26000;
Best Local Similarity 47.3%; Pred. No. 0.7;
RESULT 699
ID ABL34174 standard; DNA; 113515 BP.
DE Human immune system associated gene SEQ ID NO: 2147.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.9%; Score 52.6; DB 6; Length 113515;
Best Local Similarity 44.5%; Pred. No. 0.96;
RESULT 700
ID ABN80031 standard; DNA; 5942 BP.
DE Human chemically modified disease associated gene SEQ ID NO 48.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.9%; Score 52.4; DB 6; Length 5942;
Best Local Similarity 45.1%; Pred. No. 0.68;

RESULT 701
ID AAS45395 standard; DNA; 11836 BP.
DE Chemically pretreated complementary DNA associated with cell cycle #50.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.9%; Score 52.4; DB 4; Length 11836;
Best Local Similarity 47.3%; Pred. No. 0.75;
RESULT 702
ID ABK28240 standard; DNA; 11836 BP.
DE DNA transcription associated complementary genomic DNA #57.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.9%; Score 52.4; DB 6; Length 11836;
Best Local Similarity 47.3%; Pred. No. 0.75;
RESULT 703
ID AAS46520 standard; DNA; 15872 BP.
DE Tumour suppressor gene derived chemically modified sequence #242.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.9%; Score 52.2; DB 4; Length 15872;
Best Local Similarity 47.8%; Pred. No. 0.86;
RESULT 704
ID ABL33165 standard; DNA; 6134 BP.
DE Human immune system associated gene SEQ ID NO: 1138.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.9%; Score 52; DB 6; Length 6134;
Best Local Similarity 47.3%; Pred. No. 0.82;
RESULT 705
ID ABL33013 standard; DNA; 7597 BP.
DE Human immune system associated gene SEQ ID NO: 986.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.9%; Score 52; DB 6; Length 7597;
Best Local Similarity 45.2%; Pred. No. 0.84;
RESULT 706
ID ABL33307 standard; DNA; 6175 BP.
DE Human immune system associated gene SEQ ID NO: 1280.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.8%; Score 51.8; DB 6; Length 6175;
Best Local Similarity 47.1%; Pred. No. 0.9;
RESULT 707
ID ABZ10100 standard; DNA; 8056 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #240.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.8%; Score 51.8; DB 8; Length 8056;
Best Local Similarity 44.1%; Pred. No. 0.93;
RESULT 708
ID ABL32348 standard; DNA; 5145 BP.
DE Human immune system associated gene SEQ ID NO: 321.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.8%; Score 51.6; DB 6; Length 5145;
Best Local Similarity 44.5%; Pred. No. 0.96;
RESULT 709
ID ABL34464 standard; DNA; 5145 BP.
DE Human metastasis associated gene SEQ ID NO: 17.
PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.8%; Score 51.6; DB 6; Length 5145;
Best Local Similarity 44.5%; Pred. No. 0.96;
RESULT 710

ID ADS99725 standard; DNA; 5145 BP.
DE Bisulphite treated human gene associated with metastasis #9.
PN US2003148327-A1.
PD 07-AUG-2003.
PA (OLEK/) OLEK A.
PA (PIEP/) PIEPENBROCK C.
PA (BERL/) BERLIN K.
Query Match 3.8%; Score 51.6; DB 7; Length 5145;
Best Local Similarity 44.5%; Pred. No. 0.96;
RESULT 711
ID ABL32594 standard; DNA; 11976 BP.
DE Human immune system associated gene SEQ ID NO: 567.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.8%; Score 51.6; DB 6; Length 11976;
Best Local Similarity 45.2%; Pred. No. 1.1;
RESULT 712
ID ABL34469 standard; DNA; 16173 BP.
DE Human metastasis associated gene SEQ ID NO: 22.
PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.8%; Score 51.6; DB 6; Length 16173;
Best Local Similarity 46.0%; Pred. No. 1.1;
RESULT 713
ID ADS99730 standard; DNA; 16173 BP.
DE Complement of bisulphite treated metastasis-associated human gene #11.
PN US2003148327-A1.
PD 07-AUG-2003.
PA (OLEK/) OLEK A.
PA (PIEP/) PIEPENBROCK C.
PA (BERL/) BERLIN K.
Query Match 3.8%; Score 51.6; DB 7; Length 16173;
Best Local Similarity 46.0%; Pred. No. 1.1;
RESULT 714
ID AAH21613 standard; DNA; 168575 BP.
DE Human hypocretin receptor 2 (HCRTR2) gene SEQ ID NO:1.
PN WO200130991-A2.
PD 03-MAY-2001.
PA (DECO-) DECODE GENETICS EHF.
Query Match 3.8%; Score 51.6; DB 4; Length 168575;
Best Local Similarity 47.5%; Pred. No. 1.6;
RESULT 715
ID ABL33393 standard; DNA; 6494 BP.
DE Human immune system associated gene SEQ ID NO: 1366.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.8%; Score 51.4; DB 6; Length 6494;
Best Local Similarity 42.8%; Pred. No. 1.1;
RESULT 716
ID AAD28391 standard; DNA; 6494 BP.
DE Human chemically treated genomic DNA #32.
PN WO200202809-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.8%; Score 51.4; DB 6; Length 6494;
Best Local Similarity 42.8%; Pred. No. 1.1;
RESULT 717
ID ABL33568 standard; DNA; 8305 BP.
DE Human immune system associated gene SEQ ID NO: 1541.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.8%; Score 51.4; DB 6; Length 8305;
Best Local Similarity 46.4%; Pred. No. 1.1;
RESULT 718
ID ABK39937 standard; DNA; 11422 BP.
DE Human chemically pretreated gene sequence #9 strand 2.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.8%; Score 51.4; DB 6; Length 11422;
Best Local Similarity 46.9%; Pred. No. 1.2;
RESULT 719
ID ABL32219 standard; DNA; 11422 BP.
DE Human immune system associated gene SEQ ID NO: 192.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.8%; Score 51.4; DB 6; Length 11422;
Best Local Similarity 46.9%; Pred. No. 1.2;
RESULT 720
ID ABK31423 standard; DNA; 13123 BP.
DE Signal transduction associated gene modified complementary DNA #133.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.8%; Score 51.4; DB 6; Length 13123;
Best Local Similarity 42.9%; Pred. No. 1.2;
RESULT 721
ID ABL54364 standard; DNA; 13123 BP.
DE Chemically treated apoptosis gene complementary to gene #32.
PN WO200177164-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.8%; Score 51.4; DB 6; Length 13123;
Best Local Similarity 42.9%; Pred. No. 1.2;
RESULT 722
ID ABK28395 standard; DNA; 15743 BP.
DE DNA transcription associated genomic DNA #135.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.8%; Score 51.4; DB 6; Length 15743;
Best Local Similarity 49.1%; Pred. No. 1.2;
RESULT 723
ID ABL92249 standard; DNA; 13131 BP.
DE Chemically treated DNA repair gene fragment complementary to#29.
PN WO200181622-A2.
PD 01-NOV-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.8%; Score 51.2; DB 6; Length 13131;
Best Local Similarity 44.9%; Pred. No. 1.3;
RESULT 724
ID ABL70544 standard; DNA; 15649 BP.
DE Chemically treated cell signalling DNA sequence complementary to#217.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.8%; Score 51.2; DB 6; Length 15649;
Best Local Similarity 43.9%; Pred. No. 1.4;
RESULT 725
ID ABL33776 standard; DNA; 6239 BP.
DE Human immune system associated gene SEQ ID NO: 1749.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.8%; Score 51; DB 6; Length 6239;
Best Local Similarity 47.4%; Pred. No. 1.3;
RESULT 726
ID ABK28297 standard; DNA; 6239 BP.
DE DNA transcription associated genomic DNA #86.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.8%; Score 51; DB 6; Length 6239;
Best Local Similarity 47.4%; Pred. No. 1.3;
RESULT 727
ID AAS46541 standard; DNA; 10595 BP.
DE Tumour suppressor gene derived chemically modified sequence #263.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.8%; Score 51; DB 4; Length 10595;

Best Local Similarity 50.6%; Pred. No. 1.4;
RESULT 728
ID ABL33514 standard; DNA; 15399 BP.
DE Human immune system associated gene SEQ ID NO: 1487.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.8%; Score 51; DB 6; Length 15399;
Best Local Similarity 47.0%; Pred. No. 1.5;
RESULT 729
ID ABL34609 standard; DNA; 18585 BP.
DE Human metastasis associated gene SEQ ID NO: 162.
PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.8%; Score 51; DB 6; Length 18585;
Best Local Similarity 44.3%; Pred. No. 1.5;
RESULT 730
ID ADS99870 standard; DNA; 18585 BP.
DE Complement of bisulphite treated metastasis-associated human gene #81.
PN US2003148327-A1.
PD 07-AUG-2003.
PA (OLEK/) OLEK A.
PA (PIEP/) PIEPENBROCK C.
PA (BERL/) BERLIN K.
Query Match 3.8%; Score 51; DB 7; Length 18585;
Best Local Similarity 44.3%; Pred. No. 1.5;
RESULT 731
ID ABL32326 standard; DNA; 6109 BP.
DE Human immune system associated gene SEQ ID NO: 299.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.8%; Score 50.8; DB 6; Length 6109;
Best Local Similarity 44.8%; Pred. No. 1.4;
RESULT 732
ID AAS61077 standard; DNA; 6109 BP.
DE Human gene regulation-associated gene oligonucleotide #32.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.8%; Score 50.8; DB 6; Length 6109;
Best Local Similarity 44.8%; Pred. No. 1.4;
RESULT 733
ID ABK28340 standard; DNA; 6631 BP.
DE DNA transcription associated complementary genomic DNA #107.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.8%; Score 50.8; DB 6; Length 6631;
Best Local Similarity 47.0%; Pred. No. 1.4;
RESULT 734
ID ABL32983 standard; DNA; 7143 BP.
DE Human immune system associated gene SEQ ID NO: 956.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.8%; Score 50.8; DB 6; Length 7143;
Best Local Similarity 45.7%; Pred. No. 1.5;
RESULT 735
ID AAS46591 standard; DNA; 6286 BP.
DE Tumour suppressor gene derived chemically modified sequence #313.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.7%; Score 50.4; DB 4; Length 6286;
Best Local Similarity 45.0%; Pred. No. 1.7;
RESULT 736
ID ABD32715 standard; DNA; 337344 BP.
DE Human cancer-associated genomic DNA HD14-044.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.7%; Score 50.4; DB 13; Length 337344;
Best Local Similarity 48.0%; Pred. No. 3.1;
RESULT 737
ID ABZ10188 standard; DNA; 1501 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #328.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.7%; Score 50.2; DB 8; Length 1501;
Best Local Similarity 45.6%; Pred. No. 1.5;
RESULT 738
ID ADE84162 standard; DNA; 1501 BP.
DE Human lymphoid cell proliferative disorder gene derived DNA #98.
PN WO2003044226-A2.
PD 30-MAY-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.7%; Score 50.2; DB 10; Length 1501;
Best Local Similarity 45.6%; Pred. No. 1.5;
RESULT 739
ID ABK31511 standard; DNA; 47108 BP.
DE Signal transduction associated gene modified complementary DNA #177.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.7%; Score 50.2; DB 6; Length 47108;
Best Local Similarity 42.8%; Pred. No. 2.6;
RESULT 740
ID ABL56201 standard; DNA; 50000 BP.
DE AmEPV genome fragment#3.
PN WO200212526-A2.
PD 14-FEB-2002.
PA (UYFL) UNIV FLORIDA.
Query Match 3.7%; Score 50.2; DB 6; Length 50000;
Best Local Similarity 46.7%; Pred. No. 2.6;
RESULT 741
ID ABV08149 standard; cDNA; 391 BP.
DE Human prostate expression marker cDNA 8140.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.7%; Score 50; DB 5; Length 391;
Best Local Similarity 49.7%; Pred. No. 1.4;
RESULT 742
ID ACN47472 standard; cDNA; 560 BP.
DE Cotton primed seed EST Clone ID: LIB3825-011-Q1-N6-C9, SEQ:2253.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 3.7%; Score 50; DB 13; Length 560;
Best Local Similarity 55.9%; Pred. No. 1.4;
RESULT 743
ID AAA70201 standard; DNA; 2010 BP.
DE Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:334.
PN WO200025728-A2.
PD 11-MAY-2000.
PA (HOFF/) HOFFMAN S.
PA (CARU/) CARUCCI D.
PA (GARD/) GARDNER M.
PA (VENT/) VENTER J C.
Query Match 3.7%; Score 49.8; DB 3; Length 2010;
Best Local Similarity 45.8%; Pred. No. 1.9;
RESULT 744
ID ABL32853 standard; DNA; 5999 BP.
DE Human immune system associated gene SEQ ID NO: 826.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.7%; Score 49.8; DB 6; Length 5999;
Best Local Similarity 44.9%; Pred. No. 2.3;
RESULT 745

ID ABK28192 standard; DNA; 5999 BP.
DE DNA transcription associated complementary genomic DNA #33.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.7%; Score 49.8; DB 6; Length 5999;
Best Local Similarity 44.9%; Pred. No. 2.3;
RESULT 746
ID AAS46608 standard; DNA; 6767 BP.
DE Tumour suppressor gene derived chemically modified sequence #330.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.7%; Score 49.8; DB 4; Length 6767;
Best Local Similarity 44.8%; Pred. No. 2.3;
RESULT 747
ID ABL16590 standard; DNA; 8786 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 1243.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.7%; Score 49.8; DB 4; Length 8786;
Best Local Similarity 46.7%; Pred. No. 2.4;
RESULT 748
ID ABX46069 standard; cDNA; 419 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #11234.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 3.7%; Score 49.6; DB 8; Length 419;
Best Local Similarity 54.3%; Pred. No. 1.7;
RESULT 749
ID ACN85818 standard; DNA; 994 BP.
DE Breast cancer related marker, seq id 6968.
PN US2003099974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 3.7%; Score 49.6; DB 11; Length 994;
Best Local Similarity 27.9%; Pred. No. 1.9;
RESULT 750
ID AAZ37082 standard; DNA; 1431 BP.
DE DNA sequence encoding a yeast SceI endonuclease.
PN EP972836-A2.
PD 19-JAN-2000.
PA (RIKA) INST PHYSICAL & CHEM RES.
Query Match 3.7%; Score 49.6; DB 3; Length 1431;
Best Local Similarity 44.3%; Pred. No. 2;
RESULT 751
ID ABL32245 standard; DNA; 5388 BP.
DE Human immune system associated gene SEQ ID NO: 218.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.7%; Score 49.6; DB 6; Length 5388;
Best Local Similarity 45.3%; Pred. No. 2.4;
RESULT 752
ID AAS46283 standard; DNA; 6591 BP.
DE Tumour suppressor gene derived chemically modified sequence #5.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.7%; Score 49.6; DB 4; Length 6591;
Best Local Similarity 47.3%; Pred. No. 2.5;
RESULT 753
ID ABL32400 standard; DNA; 7167 BP.
DE Human immune system associated gene SEQ ID NO: 373.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.7%; Score 49.4; DB 6; Length 7167;
Best Local Similarity 45.0%; Pred. No. 2.8;
RESULT 754
ID ABL33748 standard; DNA; 11805 BP.
DE Human immune system associated gene SEQ ID NO: 1721.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.7%; Score 49.4; DB 6; Length 11805;
Best Local Similarity 44.2%; Pred. No. 3;
RESULT 755
ID ABL32185 standard; DNA; 15387 BP.
DE Human immune system associated gene SEQ ID NO: 158.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.7%; Score 49.4; DB 6; Length 15387;
Best Local Similarity 45.3%; Pred. No. 3.1;
RESULT 756
ID ABL32570 standard; DNA; 18997 BP.
DE Human immune system associated gene SEQ ID NO: 543.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.7%; Score 49.4; DB 6; Length 18997;
Best Local Similarity 43.7%; Pred. No. 3.2;
RESULT 757
ID ABK33948 standard; DNA; 18997 BP.
DE Human DNA for staging of Astrocytomas #16.
PN WO200202808-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.7%; Score 49.4; DB 6; Length 18997;
Best Local Similarity 43.7%; Pred. No. 3.2;
RESULT 758
ID ADA20352 standard; DNA; 18997 BP.
DE Prostate tumour related genomic DNA sample #9.
PN WO2002103042-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.7%; Score 49.4; DB 8; Length 18997;
Best Local Similarity 43.7%; Pred. No. 3.2;
RESULT 759
ID ADA84159 standard; DNA; 18997 BP.
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:17.
PN WO2002103041-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.7%; Score 49.4; DB 8; Length 18997;
Best Local Similarity 43.7%; Pred. No. 3.2;
RESULT 760
ID ADL37109 standard; DNA; 476 BP.
DE Human ovarian cancer DNA marker #10999.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.7%; Score 49.2; DB 5; Length 476;
Best Local Similarity 38.1%; Pred. No. 2;
RESULT 761
ID ADI71958 standard; DNA; 476 BP.
DE Human ovarian cancer DNA marker #4700.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.7%; Score 49.2; DB 5; Length 476;
Best Local Similarity 38.1%; Pred. No. 2;
RESULT 762
ID AAS46429 standard; DNA; 6106 BP.
DE Tumour suppressor gene derived chemically modified sequence #151.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.7%; Score 49.2; DB 4; Length 6106;
Best Local Similarity 45.5%; Pred. No. 3;

RESULT 763
ID ABK40031 standard; DNA; 6106 BP.
DE Human chemically pretreated gene sequence #57 strand 1.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.7%; Score 49.2; DB 6; Length 6106;
Best Local Similarity 45.5%; Pred. No. 3;
RESULT 764
ID ABL33472 standard; DNA; 6106 BP.
DE Human immune system associated gene SEQ ID NO: 1445.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.7%; Score 49.2; DB 6; Length 6106;
Best Local Similarity 45.5%; Pred. No. 3;
RESULT 765
ID AAS46617 standard; DNA; 6863 BP.
DE Tumour suppressor gene derived chemically modified sequence #339.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.7%; Score 49.2; DB 4; Length 6863;
Best Local Similarity 48.6%; Pred. No. 3.1;
RESULT 766
ID ABL34155 standard; DNA; 15548 BP.
DE Human immune system associated gene SEQ ID NO: 2128.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.7%; Score 49.2; DB 6; Length 15548;
Best Local Similarity 43.0%; Pred. No. 3.5;
RESULT 767
ID ABL32486 standard; DNA; 17183 BP.
DE Human immune system associated gene SEQ ID NO: 459.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.7%; Score 49.2; DB 6; Length 17183;
Best Local Similarity 46.8%; Pred. No. 3.5;
RESULT 768
ID ABL55643 standard; DNA; 50000 BP.
DE AmEPV genome fragment#1.
PN WO200212526-A2.
PD 14-FEB-2002.
PA (UYFL) UNIV FLORIDA.
Query Match 3.7%; Score 49.2; DB 6; Length 50000;
Best Local Similarity 43.7%; Pred. No. 4.1;
RESULT 769
ID ACN44010 standard; DNA; 198522 BP.
DE Human genomic sequence hCG1643869.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.7%; Score 49.2; DB 11; Length 198522;
Best Local Similarity 46.8%; Pred. No. 5.1;
RESULT 770
ID ABL32029 standard; DNA; 7351 BP.
DE Human immune system associated gene SEQ ID NO: 2.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 49; DB 6; Length 7351;
Best Local Similarity 45.4%; Pred. No. 3.4;
RESULT 771
ID ACN44010 standard; DNA; 198522 BP.
DE Human genomic sequence hCG1643869.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.6%; Score 49; DB 11; Length 198522;
Best Local Similarity 49.4%; Pred. No. 5.6;
RESULT 772
ID ACF05254 standard; cDNA; 3197 BP.
DE Plasmodium falciparum cGMP dependent protein kinase cDNA.
PN WO2003054157-A2.
PD 03-JUL-2003.
PA (MERI) MERCK & CO INC.
Query Match 3.6%; Score 48.8; DB 9; Length 3197;
Best Local Similarity 48.1%; Pred. No. 3.3;
RESULT 773
ID ABL32142 standard; DNA; 5398 BP.
DE Human immune system associated gene SEQ ID NO: 115.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 48.8; DB 6; Length 5398;
Best Local Similarity 45.5%; Pred. No. 3.6;
RESULT 774
ID ABQ67070 standard; DNA; 5611 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 100.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 48.8; DB 6; Length 5611;
Best Local Similarity 44.8%; Pred. No. 3.6;
RESULT 775
ID ABL32693 standard; DNA; 6222 BP.
DE Human immune system associated gene SEQ ID NO: 666.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 48.8; DB 6; Length 6222;
Best Local Similarity 44.5%; Pred. No. 3.6;
RESULT 776
ID ABL33761 standard; DNA; 7851 BP.
DE Human immune system associated gene SEQ ID NO: 1734.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 48.8; DB 6; Length 7851;
Best Local Similarity 48.5%; Pred. No. 3.8;
RESULT 777
ID ACF62816 standard; DNA; 8222 BP.
DE Colon cancer analysis related genomic DNA SEQ ID NO:65.
PN WO2003014388-A2.
PD 20-FEB-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 48.8; DB 8; Length 8222;
Best Local Similarity 43.2%; Pred. No. 3.8;
RESULT 778
ID ACF62794 standard; DNA; 8222 BP.
DE Colon cancer analysis related genomic DNA SEQ ID NO:43.
PN WO2003014388-A2.
PD 20-FEB-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 48.8; DB 8; Length 8222;
Best Local Similarity 43.2%; Pred. No. 3.8;
RESULT 779
ID ABL33569 standard; DNA; 8305 BP.
DE Human immune system associated gene SEQ ID NO: 1542.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 48.8; DB 6; Length 8305;
Best Local Similarity 49.2%; Pred. No. 3.8;
RESULT 780
ID ABL33591 standard; DNA; 10279 BP.
DE Human immune system associated gene SEQ ID NO: 1564.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 48.8; DB 6; Length 10279;
Best Local Similarity 47.2%; Pred. No. 3.9;
RESULT 781
ID ABL92277 standard; DNA; 10279 BP.

DE Chemically treated DNA repair gene fragment complementary to#43.
PN WO200181622-A2.
PD 01-NOV-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 48.8; DB 6; Length 10279;
Best Local Similarity 47.2%; Pred. No. 3.9;
RESULT 782
ID AAD22328 standard; DNA; 10279 BP.
DE Chemically treated human genomic DNA #18 associated with DNA adducts.
PN WO200177378-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 48.8; DB 6; Length 10279;
Best Local Similarity 47.2%; Pred. No. 3.9;
RESULT 783
ID ADB54190 standard; DNA; 11222 BP.
DE Pretreated genomic DNA region 114.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 48.8; DB 10; Length 11222;
Best Local Similarity 43.2%; Pred. No. 4;
RESULT 784
ID ADB54318 standard; DNA; 11222 BP.
DE Pretreated genomic DNA region 242.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 48.8; DB 10; Length 11222;
Best Local Similarity 43.2%; Pred. No. 4;
RESULT 785
ID ABL32342 standard; DNA; 11534 BP.
DE Human immune system associated gene SEQ ID NO: 315.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 48.8; DB 6; Length 11534;
Best Local Similarity 46.6%; Pred. No. 4;
RESULT 786
ID ABL32467 standard; DNA; 15373 BP.
DE Human immune system associated gene SEQ ID NO: 440.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 48.8; DB 6; Length 15373;
Best Local Similarity 45.3%; Pred. No. 4.2;
RESULT 787
ID AAS46771 standard; DNA; 17280 BP.
DE Tumour suppressor gene derived chemically modified sequence #495.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 48.8; DB 4; Length 17280;
Best Local Similarity 46.4%; Pred. No. 4.2;
RESULT 788
ID ABZ09999 standard; DNA; 5033 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #139.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 48.6; DB 8; Length 5033;
Best Local Similarity 47.9%; Pred. No. 3.9;
RESULT 789
ID ABK33920 standard; DNA; 7001 BP.
DE Human DNA for staging of Astrocytomas, complement, #1.
PN WO200202808-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 48.6; DB 6; Length 7001;
Best Local Similarity 43.4%; Pred. No. 4.1;
RESULT 790
ID ADA20395 standard; DNA; 7001 BP.
DE Prostate tumour related genomic DNA complement sample #30.
PN WO2002103042-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 48.6; DB 8; Length 7001;
Best Local Similarity 43.4%; Pred. No. 4.1;
RESULT 791
ID ADA84202 standard; DNA; 7001 BP.
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:60.
PN WO2002103041-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 48.6; DB 8; Length 7001;
Best Local Similarity 43.4%; Pred. No. 4.1;
RESULT 792
ID AAS46307 standard; DNA; 8033 BP.
DE Tumour suppressor gene derived chemically modified sequence #29.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 48.6; DB 4; Length 8033;
Best Local Similarity 47.9%; Pred. No. 4.1;
RESULT 793
ID ABK31202 standard; DNA; 8033 BP.
DE Signal transduction associated gene modified DNA #23.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 48.6; DB 6; Length 8033;
Best Local Similarity 47.9%; Pred. No. 4.1;
RESULT 794
ID ABL70169 standard; DNA; 8033 BP.
DE Chemically treated cell signalling DNA sequence#30.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 48.6; DB 6; Length 8033;
Best Local Similarity 47.9%; Pred. No. 4.1;
RESULT 795
ID AAS61116 standard; DNA; 8033 BP.
DE Human gene regulation-associated gene oligonucleotide #71.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 48.6; DB 6; Length 8033;
Best Local Similarity 47.9%; Pred. No. 4.1;
RESULT 796
ID ADB54330 standard; DNA; 11787 BP.
DE Pretreated genomic DNA region 254.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 48.6; DB 10; Length 11787;
Best Local Similarity 47.1%; Pred. No. 4.4;
RESULT 797
ID ABL33032 standard; DNA; 14798 BP.
DE Human immune system associated gene SEQ ID NO: 1005.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 48.6; DB 6; Length 14798;
Best Local Similarity 50.2%; Pred. No. 4.5;
RESULT 798
ID AAS61426 standard; DNA; 19380 BP.
DE Human gene regulation-associated gene oligonucleotide #381.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 48.6; DB 6; Length 19380;
Best Local Similarity 44.2%; Pred. No. 4.7;
RESULT 799
ID ABL55644 standard; DNA; 50000 BP.
DE AmEPV genome fragment#2.
PN WO200212526-A2.

PD 14-FEB-2002.
PA (UYFL) UNIV FLORIDA.
Query Match 3.6%; Score 48.6; DB 6; Length 50000;
Best Local Similarity 44.7%; Pred. No. 5.5;
RESULT 800
ID ABL33036 standard; DNA; 6123 BP.
DE Human immune system associated gene SEQ ID NO: 1009.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 48.4; DB 6; Length 6123;
Best Local Similarity 50.4%; Pred. No. 4.4;
RESULT 801
ID ABL32257 standard; DNA; 7498 BP.
DE Human immune system associated gene SEQ ID NO: 230.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 48.4; DB 6; Length 7498;
Best Local Similarity 44.8%; Pred. No. 4.5;
RESULT 802
ID ABK31275 standard; DNA; 10205 BP.
DE Signal transduction associated gene modified complementary DNA #59.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 48.4; DB 6; Length 10205;
Best Local Similarity 51.4%; Pred. No. 4.7;
RESULT 803
ID ABL70236 standard; DNA; 10205 BP.
DE Chemically treated cell signalling DNA sequence complementary to#63.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 48.4; DB 6; Length 10205;
Best Local Similarity 51.4%; Pred. No. 4.7;
RESULT 804
ID AAK73165 standard; DNA; 20420 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27977.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.6%; Score 48.4; DB 4; Length 20420;
Best Local Similarity 51.4%; Pred. No. 5.2;
RESULT 805
ID ABK69933 standard; DNA; 20420 BP.
DE Human secreted protein gene 68 genomic DNA fragment #21.
PN WO200226931-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.6%; Score 48.4; DB 6; Length 20420;
Best Local Similarity 51.4%; Pred. No. 5.2;
RESULT 806
ID ADQ97050 standard; DNA; 687411 BP.
DE Human cancer associated sequence HD08-001, SEQ ID 26.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.6%; Score 48.4; DB 12; Length 110000;
Best Local Similarity 42.2%; Pred. No. 6.7;
RESULT 807
ID ADA71938 standard; DNA; 2000 BP.
DE Rice gene, SEQ ID 5263.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 3.6%; Score 48.2; DB 8; Length 2000;
Best Local Similarity 14.5%; Pred. No. 4;
RESULT 808
ID ADL63811 standard; DNA; 4240 BP.
DE Human ovarian cancer DNA marker #22023.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.6%; Score 48.2; DB 5; Length 4240;
Best Local Similarity 46.5%; Pred. No. 4.5;
RESULT 809
ID AAS45456 standard; DNA; 6030 BP.
DE Chemically pretreated genomic DNA associated with cell cycle #81.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 48.2; DB 4; Length 6030;
Best Local Similarity 44.4%; Pred. No. 4.8;
RESULT 810
ID ABK28312 standard; DNA; 6030 BP.
DE DNA transcription associated complementary genomic DNA #93.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 48.2; DB 6; Length 6030;
Best Local Similarity 44.4%; Pred. No. 4.8;
RESULT 811
ID AAS61348 standard; DNA; 6030 BP.
DE Human gene regulation-associated gene oligonucleotide #303.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 48.2; DB 6; Length 6030;
Best Local Similarity 44.4%; Pred. No. 4.8;
RESULT 812
ID ABL54314 standard; DNA; 6314 BP.
DE Chemically treated apoptosis gene complementary to gene #7.
PN WO200177164-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 48.2; DB 6; Length 6314;
Best Local Similarity 45.0%; Pred. No. 4.8;
RESULT 813
ID ABK39963 standard; DNA; 6731 BP.
DE Human chemically pretreated gene sequence #22 strand 2.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 48.2; DB 6; Length 6731;
Best Local Similarity 51.3%; Pred. No. 4.9;
RESULT 814
ID ABL34240 standard; DNA; 11691 BP.
DE Human immune system associated gene SEQ ID NO: 2213.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 48.2; DB 6; Length 11691;
Best Local Similarity 44.4%; Pred. No. 5.3;
RESULT 815
ID ADB54330 standard; DNA; 11787 BP.
DE Pretreated genomic DNA region 254.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 48.2; DB 10; Length 11787;
Best Local Similarity 44.4%; Pred. No. 5.3;
RESULT 816
ID ABK39920 standard; DNA; 17869 BP.
DE Human chemically pretreated gene sequence #1 strand 1.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 48.2; DB 6; Length 17869;
Best Local Similarity 49.8%; Pred. No. 5.6;
RESULT 817
ID ABL32104 standard; DNA; 17869 BP.
DE Human immune system associated gene SEQ ID NO: 77.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.

Query Match 3.6%; Score 48.2; DB 6; Length 17869;
Best Local Similarity 49.8%; Pred. No. 5.6;
RESULT 818
ID ADE43862 standard; DNA; 40178 BP.
DE Human LIPA genomic sequence, SEQ ID 467.
PN WO2003054143-A2.
PD 03-JUL-2003.
PA (NEUR-) NEUROGENETICS INC.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 3.6%; Score 48.2; DB 10; Length 40178;
Best Local Similarity 44.3%; Pred. No. 6.4;
RESULT 819
ID ADE43863 standard; DNA; 40178 BP.
DE Polymorphic human LIPA genomic sequence, SEQ ID 468.
PN WO2003054143-A2.
PD 03-JUL-2003.
PA (NEUR-) NEUROGENETICS INC.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 3.6%; Score 48.2; DB 10; Length 40178;
Best Local Similarity 44.3%; Pred. No. 6.4;
RESULT 820
ID ADH54341 standard; DNA; 40178 BP.
DE Human LIPA gene variant DNA sequence SeqID468.
PN US2003224380-A1.
PD 04-DEC-2003.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 3.6%; Score 48.2; DB 12; Length 40178;
Best Local Similarity 44.3%; Pred. No. 6.4;
RESULT 821
ID ADH54340 standard; DNA; 40178 BP.
DE Human LIPA gene DNA sequence SeqID467.
PN US2003224380-A1.
PD 04-DEC-2003.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 3.6%; Score 48.2; DB 12; Length 40178;
Best Local Similarity 44.3%; Pred. No. 6.4;
RESULT 822
ID ABL34073 standard; DNA; 40862 BP.
DE Human immune system associated gene SEQ ID NO: 2046.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 48.2; DB 6; Length 40862;
Best Local Similarity 45.0%; Pred. No. 6.4;
RESULT 823
Query Match 3.6%; Score 48.2; DB 13; Length 110000;
Best Local Similarity 43.7%; Pred. No. 7.4;
RESULT 824
ID ABN53251 standard; DNA; 65 BP.
DE Mouse spliced transcript detection oligonucleotide SEQ ID NO:25999.
PN WO200210449-A2.
PD 07-FEB-2002.
PA (COMP-) COMPUGEN INC.
Query Match 3.6%; Score 48; DB 6; Length 65;
Best Local Similarity 84.4%; Pred. No. 2.7;
RESULT 825
ID ABK63918 standard; cDNA; 800 BP.
DE cDNA encoding human secreted protein sequence #3.
PN WO200216388-A1.
PD 28-FEB-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.6%; Score 48; DB 6; Length 800;
Best Local Similarity 60.9%; Pred. No. 3.9;
RESULT 826
ID ABK63942 standard; cDNA; 801 BP.
DE cDNA encoding human secreted protein sequence #27.
PN WO200216388-A1.
PD 28-FEB-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.6%; Score 48; DB 6; Length 801;
Best Local Similarity 60.9%; Pred. No. 3.9;
RESULT 827
ID ACC62484 standard; cDNA; 834 BP.
DE Human secreted protein #10 coding sequence SEQ ID 20.
PN WO200299066-A2.
PD 12-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.6%; Score 48; DB 8; Length 834;
Best Local Similarity 60.9%; Pred. No. 3.9;
RESULT 828
ID AAV73003 standard; cDNA; 3076 BP.
DE Human adult brain secreted protein dm26_2 cDNA.
PN WO9842741-A2.
PD 01-OCT-1998.
PA (GEMY) GENETICS INST INC.
Query Match 3.6%; Score 48; DB 2; Length 3076;
Best Local Similarity 60.9%; Pred. No. 4.7;
RESULT 829
ID ABQ92028 standard; cDNA; 3076 BP.
DE Human polynucleotide SEQ ID NO 25.
PN US2002065394-A1.
PD 30-MAY-2002.
PA (JACO/) JACOBS K.
PA (MCCO/) MCCOY J M.
PA (LAVA/) LAVALLIE E R.
PA (COLL/) COLLINS-RACIE L A.
PA (EVAN/) EVANS C.
PA (MERB/) MERBERG D.
PA (TREA/) TREACY M.
PA (SPAU/) SPAULDING V.
Query Match 3.6%; Score 48; DB 6; Length 3076;
Best Local Similarity 60.9%; Pred. No. 4.7;
RESULT 830
ID ABL32400 standard; DNA; 7167 BP.
DE Human immune system associated gene SEQ ID NO: 373.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 48; DB 6; Length 7167;
Best Local Similarity 43.6%; Pred. No. 5.4;
RESULT 831
ID ABL34105 standard; DNA; 14023 BP.
DE Human immune system associated gene SEQ ID NO: 2078.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 48; DB 6; Length 14023;
Best Local Similarity 48.2%; Pred. No. 6;
RESULT 832
ID ABL70576 standard; DNA; 19576 BP.
DE Chemically treated cell signalling DNA sequence complementary to#233.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 48; DB 6; Length 19576;
Best Local Similarity 46.6%; Pred. No. 6.3;
RESULT 833
ID AAS61259 standard; DNA; 19576 BP.
DE Human gene regulation-associated gene oligonucleotide #214.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 48; DB 6; Length 19576;
Best Local Similarity 46.6%; Pred. No. 6.3;
RESULT 834
ID ABQ66998 standard; DNA; 37515 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 28.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 48; DB 6; Length 37515;
Best Local Similarity 44.3%; Pred. No. 6.9;
RESULT 835
ID ABQ67094 standard; DNA; 83391 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 124.
PN WO200246454-A2.

PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 48; DB 6; Length 83391;
Best Local Similarity 44.7%; Pred. No. 7.8;
RESULT 836
ID ACA64845 standard; DNA; 115218 BP.
DE Human HNRNP GP43 DNA corresponding to AL034397.
PN DE10127572-A1.
PD 05-DEC-2002.
PA (PATH-) PATHOARRAY GMBH.
Query Match 3.6%; Score 48; DB 8; Length 115218;
Best Local Similarity 44.8%; Pred. No. 8.2;
RESULT 837
ID ADR02445 standard; DNA; 636 BP.
DE A. gossypii genomic DNA PAG1692RP.
PN US6239264-B1.
PD 29-MAY-2001.
PA (SYNG-) SYNGENTA PARTICIPATIONS AG.
Query Match 3.6%; Score 47.8; DB 2; Length 636;
Best Local Similarity 43.2%; Pred. No. 4.1;
RESULT 838
ID AAS63366 standard; DNA; 3586 BP.
DE Chemically pretreated metabolism associated gene #61.
PN WO200176451-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 47.8; DB 6; Length 3586;
Best Local Similarity 47.0%; Pred. No. 5.3;
RESULT 839
ID ABK31451 standard; DNA; 7131 BP.
DE Signal transduction associated gene modified complementary DNA #147.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 47.8; DB 6; Length 7131;
Best Local Similarity 44.7%; Pred. No. 5.9;
RESULT 840
ID ABL70428 standard; DNA; 7131 BP.
DE Chemically treated cell signalling DNA sequence complementary to#159.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 47.8; DB 6; Length 7131;
Best Local Similarity 44.7%; Pred. No. 5.9;
RESULT 841
ID AAS61361 standard; DNA; 7131 BP.
DE Human gene regulation-associated gene oligonucleotide #316.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 47.8; DB 6; Length 7131;
Best Local Similarity 44.7%; Pred. No. 5.9;
RESULT 842
ID ABL33989 standard; DNA; 8238 BP.
DE Human immune system associated gene SEQ ID NO: 1962.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 47.8; DB 6; Length 8238;
Best Local Similarity 45.6%; Pred. No. 6;
RESULT 843
ID AAS63349 standard; DNA; 8238 BP.
DE Chemically pretreated metabolism associated gene #44.
PN WO200176451-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 47.8; DB 6; Length 8238;
Best Local Similarity 45.6%; Pred. No. 6;
RESULT 844
ID ABL34293 standard; DNA; 10020 BP.
DE Human immune system associated gene SEQ ID NO: 2266.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 47.8; DB 6; Length 10020;
Best Local Similarity 47.6%; Pred. No. 6.2;
RESULT 845
ID ABQ67149 standard; DNA; 40324 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 179.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.6%; Score 47.8; DB 6; Length 40324;
Best Local Similarity 45.6%; Pred. No. 7.7;
RESULT 846
ID AAA01920 standard; cDNA; 875 BP.
DE Human colon cancer cell line polynucleotide sequence SEQ ID NO:1911.
PN WO9958675-A2.
PD 18-NOV-1999.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 3.5%; Score 47.6; DB 3; Length 875;
Best Local Similarity 39.7%; Pred. No. 4.7;
RESULT 847
ID ABL56243 standard; DNA; 1830 BP.
DE AmEPV metalloprotease (AMV256) encoding sequence.
PN WO200212526-A2.
PD 14-FEB-2002.
PA (UYFL) UNIV FLORIDA.
Query Match 3.5%; Score 47.6; DB 6; Length 1830;
Best Local Similarity 44.1%; Pred. No. 5.3;
RESULT 848
ID ADR07247 standard; cDNA; 2187 BP.
DE Full length human cDNA useful for treating neurological disease Seq 753.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.5%; Score 47.6; DB 13; Length 2187;
Best Local Similarity 46.7%; Pred. No. 5.4;
RESULT 849
ID ABL55640 standard; DNA; 4152 BP.
DE AmEPV ABC transporter-like protein (AMV130) coding sequence.
PN WO200212526-A2.
PD 14-FEB-2002.
PA (UYFL) UNIV FLORIDA.
Query Match 3.5%; Score 47.6; DB 6; Length 4152;
Best Local Similarity 46.6%; Pred. No. 6;
RESULT 850
ID AAS46429 standard; DNA; 6106 BP.
DE Tumour suppressor gene derived chemically modified sequence #151.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.5%; Score 47.6; DB 4; Length 6106;
Best Local Similarity 45.4%; Pred. No. 6.3;
RESULT 851
ID ABK40031 standard; DNA; 6106 BP.
DE Human chemically pretreated gene sequence #57 strand 1.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.5%; Score 47.6; DB 6; Length 6106;
Best Local Similarity 45.4%; Pred. No. 6.3;
RESULT 852
ID ABL33472 standard; DNA; 6106 BP.
DE Human immune system associated gene SEQ ID NO: 1445.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.5%; Score 47.6; DB 6; Length 6106;
Best Local Similarity 45.4%; Pred. No. 6.3;
RESULT 853
ID ABL34358 standard; DNA; 12237 BP.
DE Human immune system associated gene SEQ ID NO: 2331.
PN WO200200928-A2.
PD 03-JAN-2002.

PA (EPIG-) EPIGENOMICS AG.
Query Match 3.5%; Score 47.6; DB 6; Length 12237;
Best Local Similarity 44.1%; Pred. No. 7;
RESULT 854
ID ABL33531 standard; DNA; 13712 BP.
DE Human immune system associated gene SEQ ID NO: 1504.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.5%; Score 47.6; DB 6; Length 13712;
Best Local Similarity 47.0%; Pred. No. 7.1;
RESULT 855
ID ABL41803 standard; DNA; 15567 BP.
DE Nucleotide sequence of mutacin I operon.
PN US6342385-B1.
PD 29-JAN-2002.
PA (UABR-) UAB RES FOUND.
Query Match 3.5%; Score 47.6; DB 6; Length 15567;
Best Local Similarity 49.2%; Pred. No. 7.3;
RESULT 856
ID ABS58318 standard; DNA; 15567 BP.
DE DNA sequence encoding Streptococcus mutans mutacin (MutA) operon.
PN US2002123105-A1.
PD 05-SEP-2002.
PA (QIFF/) QI F.
PA (CAUF/) CAUFIELD P W.
PA (CHEN/) CHEN P.
Query Match 3.5%; Score 47.6; DB 8; Length 15567;
Best Local Similarity 49.2%; Pred. No. 7.3;
RESULT 857
ID ABL33999 standard; DNA; 21537 BP.
DE Human immune system associated gene SEQ ID NO: 1972.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.5%; Score 47.6; DB 6; Length 21537;
Best Local Similarity 42.6%; Pred. No. 7.6;
RESULT 858
ID ABL56203 standard; DNA; 32392 BP.
DE AmEPV genome fragment#5.
PN WO200212526-A2.
PD 14-FEB-2002.
PA (UYFL) UNIV FLORIDA.
Query Match 3.5%; Score 47.6; DB 6; Length 32392;
Best Local Similarity 44.1%; Pred. No. 8.1;
RESULT 859
ID AAI61371 standard; DNA; 335913 BP.
DE Soybean 240017 region G3, SEQ ID NO: 2.
PN WO200151627-A2.
PD 19-JUL-2001.
PA (MONS) MONSANTO CO.
Query Match 3.5%; Score 47.6; DB 5; Length 335913;
Best Local Similarity 46.8%; Pred. No. 12;
RESULT 860
ID AAI61372 standard; DNA; 335913 BP.
DE Soybean 240017 region G3, SEQ ID NO: 3.
PN WO200151627-A2.
PD 19-JUL-2001.
PA (MONS) MONSANTO CO.
Query Match 3.5%; Score 47.6; DB 5; Length 335913;
Best Local Similarity 46.8%; Pred. No. 12;
RESULT 861
ID AAH93353 standard; DNA; 402 BP.
DE Human chromosome 16 BAC clone CIT987SK-A-248F7 SEQ ID NO 74.
PN WO200152616-A2.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.5%; Score 47.4; DB 4; Length 402;
Best Local Similarity 45.9%; Pred. No. 4.6;
RESULT 862
ID ADN04895 standard; cDNA; 2559 BP.
DE Antipsoriatic cDNA sequence #662.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 3.5%; Score 47.4; DB 12; Length 2559;
Best Local Similarity 49.4%; Pred. No. 6.1;
RESULT 863
ID ABK31193 standard; DNA; 5768 BP.
DE Signal transduction associated gene modified complementary DNA #18.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.5%; Score 47.4; DB 6; Length 5768;
Best Local Similarity 47.1%; Pred. No. 6.9;
RESULT 864
ID ABL70518 standard; DNA; 5768 BP.
DE Chemically treated cell signalling DNA sequence complementary to#204.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.5%; Score 47.4; DB 6; Length 5768;
Best Local Similarity 47.1%; Pred. No. 6.9;
RESULT 865
ID AAS45477 standard; DNA; 7657 BP.
DE Chemically pretreated complementary DNA associated with cell cycle #91.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.5%; Score 47.4; DB 4; Length 7657;
Best Local Similarity 48.7%; Pred. No. 7.2;
RESULT 866
ID ABL34022 standard; DNA; 7657 BP.
DE Human immune system associated gene SEQ ID NO: 1995.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.5%; Score 47.4; DB 6; Length 7657;
Best Local Similarity 48.7%; Pred. No. 7.2;
RESULT 867
ID ABL70458 standard; DNA; 15161 BP.
DE Chemically treated cell signalling DNA sequence complementary to#174.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.5%; Score 47.4; DB 6; Length 15161;
Best Local Similarity 48.0%; Pred. No. 8;
RESULT 868
ID AAS61423 standard; DNA; 15161 BP.
DE Human gene regulation-associated gene oligonucleotide #378.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.5%; Score 47.4; DB 6; Length 15161;
Best Local Similarity 48.0%; Pred. No. 8;
RESULT 869
ID ABL32467 standard; DNA; 15373 BP.
DE Human immune system associated gene SEQ ID NO: 440.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.5%; Score 47.4; DB 6; Length 15373;
Best Local Similarity 46.5%; Pred. No. 8;
RESULT 870
ID ABD32715 standard; DNA; 337344 BP.
DE Human cancer-associated genomic DNA HD14-044.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.5%; Score 47.4; DB 13; Length 337344;
Best Local Similarity 45.4%; Pred. No. 13;
RESULT 871
ID ADM82157 standard; cDNA; 1219 BP.
DE Goldfish testis development factor Tdf2-encoding cDNA.
PN CN1401657-A.
PD 12-MAR-2003.

PA (HYDR-) INST HYDROBIOLOGY CHINESE ACAD SCI.
Query Match 3.5%; Score 47.2; DB 11; Length 1219;
Best Local Similarity 50.9%; Pred. No. 6;
RESULT 872
ID ABL32821 standard; DNA; 6123 BP.
DE Human immune system associated gene SEQ ID NO: 794.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.5%; Score 47.2; DB 6; Length 6123;
Best Local Similarity 45.8%; Pred. No. 7.6;
RESULT 873
ID ABL32315 standard; DNA; 6641 BP.
DE Human immune system associated gene SEQ ID NO: 288.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.5%; Score 47.2; DB 6; Length 6641;
Best Local Similarity 43.7%; Pred. No. 7.7;
RESULT 874
ID ABL54336 standard; DNA; 6641 BP.
DE Chemically treated apoptosis gene complementary to gene #18.
PN WO200177164-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.5%; Score 47.2; DB 6; Length 6641;
Best Local Similarity 43.7%; Pred. No. 7.7;
RESULT 875
ID ABK40010 standard; DNA; 7445 BP.
DE Human chemically pretreated gene sequence #46 strand 2.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.5%; Score 47.2; DB 6; Length 7445;
Best Local Similarity 50.4%; Pred. No. 7.9;
RESULT 876
ID ABL32851 standard; DNA; 7445 BP.
DE Human immune system associated gene SEQ ID NO: 824.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.5%; Score 47.2; DB 6; Length 7445;
Best Local Similarity 50.4%; Pred. No. 7.9;
RESULT 877
ID ADB54312 standard; DNA; 7833 BP.
DE Pretreated genomic DNA region 236.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.5%; Score 47.2; DB 10; Length 7833;
Best Local Similarity 45.7%; Pred. No. 7.9;
RESULT 878
ID ADE37779 standard; DNA; 7833 BP.
DE Human chemically treated EYA4 nucleotide sequence SEQ ID NO:25.
PN WO2003072820-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.5%; Score 47.2; DB 10; Length 7833;
Best Local Similarity 45.7%; Pred. No. 7.9;
RESULT 879
ID ADS89608 standard; DNA; 7833 BP.
DE Oligonucleotide of the invention SEQ ID NO:624.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.5%; Score 47.2; DB 13; Length 7833;
Best Local Similarity 45.7%; Pred. No. 7.9;
RESULT 880
ID ABL70227 standard; DNA; 8897 BP.
DE Chemically treated cell signalling DNA sequence#59.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.5%; Score 47.2; DB 6; Length 8897;
Best Local Similarity 47.3%; Pred. No. 8.1;
RESULT 881
ID ABL32669 standard; DNA; 11049 BP.
DE Human immune system associated gene SEQ ID NO: 642.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.5%; Score 47.2; DB 6; Length 11049;
Best Local Similarity 44.7%; Pred. No. 8.3;
RESULT 882
ID ABL92219 standard; DNA; 11049 BP.
DE Chemically treated DNA repair gene fragment complementary to#14.
PN WO200181622-A2.
PD 01-NOV-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.5%; Score 47.2; DB 6; Length 11049;
Best Local Similarity 44.7%; Pred. No. 8.3;
RESULT 883
ID ABL49322 standard; DNA; 11049 BP.
DE Human polynucleotide associated with DNA replication SEQ ID NO 22.
PN WO200177377-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.5%; Score 47.2; DB 6; Length 11049;
Best Local Similarity 44.7%; Pred. No. 8.3;
RESULT 884
ID ABL32624 standard; DNA; 16217 BP.
DE Human immune system associated gene SEQ ID NO: 597.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.5%; Score 47.2; DB 6; Length 16217;
Best Local Similarity 45.5%; Pred. No. 8.8;
RESULT 885
ID ABL34006 standard; DNA; 18434 BP.
DE Human immune system associated gene SEQ ID NO: 1979.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.5%; Score 47.2; DB 6; Length 18434;
Best Local Similarity 45.2%; Pred. No. 9;
RESULT 886
ID ABL32875 standard; DNA; 5273 BP.
DE Human immune system associated gene SEQ ID NO: 848.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.5%; Score 47; DB 6; Length 5273;
Best Local Similarity 45.0%; Pred. No. 8.2;
RESULT 887
ID ABN80294 standard; DNA; 6661 BP.
DE Human chemically modified disease associated gene SEQ ID NO 311.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.5%; Score 47; DB 6; Length 6661;
Best Local Similarity 48.1%; Pred. No. 8.5;
RESULT 888
ID ABL92243 standard; DNA; 11787 BP.
DE Chemically treated DNA repair gene fragment complementary to#26.
PN WO200181622-A2.
PD 01-NOV-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.5%; Score 47; DB 6; Length 11787;
Best Local Similarity 46.9%; Pred. No. 9.2;
RESULT 889
ID ADB54202 standard; DNA; 11787 BP.
DE Pretreated genomic DNA region 126.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.5%; Score 47; DB 10; Length 11787;

Best Local Similarity 46.9%; Pred. No. 9.2;
RESULT 890
ID ABL33927 standard; DNA; 13427 BP.
DE Human immune system associated gene SEQ ID NO: 1900.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.5%; Score 47; DB 6; Length 13427;
Best Local Similarity 42.3%; Pred. No. 9.4;
RESULT 891
ID AAH70049 standard; cDNA; 300 BP.
DE Human cervical cancer marker nucleic acid 1323.
PN WO200142467-A2.
PD 14-JUN-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.5%; Score 46.8; DB 4; Length 300;
Best Local Similarity 53.8%; Pred. No. 5.8;
RESULT 892
ID AAL15924 standard; cDNA; 422 BP.
DE Human breast cancer expressed polynucleotide 8381.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.5%; Score 46.8; DB 4; Length 422;
Best Local Similarity 43.5%; Pred. No. 6.1;
RESULT 893
ID ACN85885 standard; DNA; 858 BP.
DE Breast cancer related marker, seq id 7035.
PN US2003099974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 3.5%; Score 46.8; DB 11; Length 858;
Best Local Similarity 43.5%; Pred. No. 6.8;
RESULT 894
ID ABK31517 standard; DNA; 1335 BP.
DE Signal transduction associated gene modified complementary DNA #180.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.5%; Score 46.8; DB 6; Length 1335;
Best Local Similarity 50.0%; Pred. No. 7.3;
RESULT 895
ID ABL70486 standard; DNA; 1335 BP.
DE Chemically treated cell signalling DNA sequence complementary to#188.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.5%; Score 46.8; DB 6; Length 1335;
Best Local Similarity 50.0%; Pred. No. 7.3;
RESULT 896
ID ABQ54403 standard; cDNA; 2911 BP.
DE Human ovarian antigen HAPOE30 cDNA, SEQ ID NO:283.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.5%; Score 46.8; DB 6; Length 2911;
Best Local Similarity 63.2%; Pred. No. 8.2;
RESULT 897
ID AAV42653 standard; cDNA to mRNA; 4358 BP.
DE Nucleotide sequence of p102, a protein present in SA-17S complex.
PN WO9828419-A2.
PD 02-JUL-1998.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Query Match 3.5%; Score 46.8; DB 2; Length 4358;
Best Local Similarity 67.3%; Pred. No. 8.7;
RESULT 898
ID ABL70494 standard; DNA; 5126 BP.
DE Chemically treated cell signalling DNA sequence complementary to#192.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.5%; Score 46.8; DB 6; Length 5126;
Best Local Similarity 46.1%; Pred. No. 8.9;
RESULT 899
ID ABL33614 standard; DNA; 6127 BP.
DE Human immune system associated gene SEQ ID NO: 1587.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.5%; Score 46.8; DB 6; Length 6127;
Best Local Similarity 48.5%; Pred. No. 9.2;
RESULT 900
ID ABL33303 standard; DNA; 6609 BP.
DE Human immune system associated gene SEQ ID NO: 1276.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.5%; Score 46.8; DB 6; Length 6609;
Best Local Similarity 45.7%; Pred. No. 9.3;
RESULT 901
ID AAZ29911 standard; DNA; 8310 BP.
DE cDNA encoding a SC4 protein of soybean.
PN WO9953067-A2.
PD 21-OCT-1999.
PA (MIAC) CANADA MIN AGRIC & AGRI-FOOD CANADA.
Query Match 3.5%; Score 46.8; DB 2; Length 8310;
Best Local Similarity 46.7%; Pred. No. 9.6;
RESULT 902
ID ABL32426 standard; DNA; 9810 BP.
DE Human immune system associated gene SEQ ID NO: 399.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.5%; Score 46.8; DB 6; Length 9810;
Best Local Similarity 47.9%; Pred. No. 9.9;
RESULT 903
ID ABK39964 standard; DNA; 15479 BP.
DE Human chemically pretreated gene sequence #23 strand 1.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.5%; Score 46.8; DB 6; Length 15479;
Best Local Similarity 44.9%; Pred. No. 11;
RESULT 904
ID ABL33728 standard; DNA; 17721 BP.
DE Human immune system associated gene SEQ ID NO: 1701.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.5%; Score 46.8; DB 6; Length 17721;
Best Local Similarity 58.7%; Pred. No. 11;
RESULT 905
ID ABD32992 standard; DNA; 99764 BP.
DE Human cancer-associated genomic DNA HD21-017.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.5%; Score 46.8; DB 13; Length 99764;
Best Local Similarity 42.8%; Pred. No. 14;
RESULT 906
ID ADH10017 standard; DNA; 365186 BP.
DE Human chromosome 2p21-22 fragment containing the DRIP gene.
PN WO2003093310-A1.
PD 13-NOV-2003.
PA (UYBR-) UNIV BREMEN.
Query Match 3.5%; Score 46.8; DB 10; Length 110000;
Best Local Similarity 47.4%; Pred. No. 14;
RESULT 907
ID ADD34713 standard; DNA; 300 BP.
DE Mouse mitochondrial DNA sequence SEQ ID NO:2492.
PN WO2003020220-A2.
PD 13-MAR-2003.
PA (UYEM-) UNIV EMORY.
Query Match 3.5%; Score 46.6; DB 10; Length 300;
Best Local Similarity 62.4%; Pred. No. 6.4;
RESULT 908

ID ACN85231 standard; DNA; 960 BP.
DE Breast cancer related marker, seq id 6381.
PN US2003099974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 3.5%; Score 46.6; DB 11; Length 960;
Best Local Similarity 40.3%; Pred. No. 7.6;
RESULT 909
ID ABL92243 standard; DNA; 11787 BP.
DE Chemically treated DNA repair gene fragment complementary to#26.
PN WO200181622-A2.
PD 01-NOV-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.5%; Score 46.6; DB 6; Length 11787;
Best Local Similarity 44.2%; Pred. No. 11;
RESULT 910
ID ADB54202 standard; DNA; 11787 BP.
DE Pretreated genomic DNA region 126.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.5%; Score 46.6; DB 10; Length 11787;
Best Local Similarity 44.2%; Pred. No. 11;
RESULT 911
ID ABL32298 standard; DNA; 12507 BP.
DE Human immune system associated gene SEQ ID NO: 271.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.5%; Score 46.6; DB 6; Length 12507;
Best Local Similarity 46.3%; Pred. No. 11;
RESULT 912
ID ABL32729 standard; DNA; 14307 BP.
DE Human immune system associated gene SEQ ID NO: 702.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.5%; Score 46.6; DB 6; Length 14307;
Best Local Similarity 44.0%; Pred. No. 11;
RESULT 913
ID ABL92212 standard; DNA; 18060 BP.
DE Chemically treated DNA repair gene fragment#11.
PN WO200181622-A2.
PD 01-NOV-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.5%; Score 46.6; DB 6; Length 18060;
Best Local Similarity 45.3%; Pred. No. 12;
RESULT 914
ID AAD22313 standard; DNA; 18060 BP.
DE Chemically treated human genomic DNA #3 associated with DNA adducts.
PN WO200177378-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.5%; Score 46.6; DB 6; Length 18060;
Best Local Similarity 45.3%; Pred. No. 12;
RESULT 915
ID AAL15210 standard; cDNA; 883 BP.
DE Human breast cancer expressed polynucleotide 7667.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.4%; Score 46.4; DB 4; Length 883;
Best Local Similarity 40.5%; Pred. No. 8.3;
RESULT 916
ID ADS89680 standard; DNA; 4394 BP.
DE Oligonucleotide of the invention SEQ ID NO:696.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 46.4; DB 13; Length 4394;
Best Local Similarity 46.8%; Pred. No. 11;
RESULT 917
ID ABK28306 standard; DNA; 5518 BP.
DE DNA transcription associated complementary genomic DNA #90.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 46.4; DB 6; Length 5518;
Best Local Similarity 45.1%; Pred. No. 11;
RESULT 918
ID ABL70157 standard; DNA; 5551 BP.
DE Chemically treated cell signalling DNA sequence#24.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 46.4; DB 6; Length 5551;
Best Local Similarity 45.2%; Pred. No. 11;
RESULT 919
ID AAS61099 standard; DNA; 5551 BP.
DE Human gene regulation-associated gene oligonucleotide #54.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 46.4; DB 6; Length 5551;
Best Local Similarity 45.2%; Pred. No. 11;
RESULT 920
ID ABL33567 standard; DNA; 5647 BP.
DE Human immune system associated gene SEQ ID NO: 1540.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 46.4; DB 6; Length 5647;
Best Local Similarity 43.8%; Pred. No. 11;
RESULT 921
ID ABL70356 standard; DNA; 5647 BP.
DE Chemically treated cell signalling DNA sequence complementary to#123.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 46.4; DB 6; Length 5647;
Best Local Similarity 43.8%; Pred. No. 11;
RESULT 922
ID AAS61321 standard; DNA; 5647 BP.
DE Human gene regulation-associated gene oligonucleotide #276.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 46.4; DB 6; Length 5647;
Best Local Similarity 43.8%; Pred. No. 11;
RESULT 923
ID ABL33106 standard; DNA; 5696 BP.
DE Human immune system associated gene SEQ ID NO: 1079.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 46.4; DB 6; Length 5696;
Best Local Similarity 49.6%; Pred. No. 11;
RESULT 924
ID ABK31288 standard; DNA; 5696 BP.
DE Signal transduction associated gene modified DNA #66.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 46.4; DB 6; Length 5696;
Best Local Similarity 49.6%; Pred. No. 11;
RESULT 925
ID AAN50530 standard; DNA; 5760 BP.
DE Sequence encoding the P195 protein of Plasmodium falciparum.
PN EP154454-A.
PD 11-SEP-1985.
PA (WELL) WELLCOME FOUND LTD.
Query Match 3.4%; Score 46.4; DB 1; Length 5760;
Best Local Similarity 45.0%; Pred. No. 11;
RESULT 926
ID AAD46980 standard; DNA; 5917 BP.
DE Plasmodium falciparum merozoite surface protein-1 (MSP-1) DNA.

PN WO200270542-A2.
PD 12-SEP-2002.
PA (SELI-) ST ELIZABETH'S MEDICAL CENT INC.
Query Match 3.4%; Score 46.4; DB 6; Length 5917;
Best Local Similarity 45.0%; Pred. No. 11;
RESULT 927
ID ABL32088 standard; DNA; 6283 BP.
DE Human immune system associated gene SEQ ID NO: 61.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 46.4; DB 6; Length 6283;
Best Local Similarity 44.6%; Pred. No. 11;
RESULT 928
ID ABL33549 standard; DNA; 7503 BP.
DE Human immune system associated gene SEQ ID NO: 1522.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 46.4; DB 6; Length 7503;
Best Local Similarity 45.7%; Pred. No. 11;
RESULT 929
ID ABQ67010 standard; DNA; 7503 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 40.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 46.4; DB 6; Length 7503;
Best Local Similarity 45.7%; Pred. No. 11;
RESULT 930
ID ABK28332 standard; DNA; 11745 BP.
DE DNA transcription associated complementary genomic DNA #103.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 46.4; DB 6; Length 11745;
Best Local Similarity 46.1%; Pred. No. 12;
RESULT 931
ID ABL34493 standard; DNA; 11996 BP.
DE Human metastasis associated gene SEQ ID NO: 46.
PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 46.4; DB 6; Length 11996;
Best Local Similarity 44.2%; Pred. No. 12;
RESULT 932
ID ADS99754 standard; DNA; 11996 BP.
DE Complement of bisulphite treated metastasis-associated human gene #23.
PN US2003148327-A1.
PD 07-AUG-2003.
PA (OLEK/) OLEK A.
PA (PIEP/) PIEPENBROCK C.
PA (BERL/) BERLIN K.
Query Match 3.4%; Score 46.4; DB 7; Length 11996;
Best Local Similarity 44.2%; Pred. No. 12;
RESULT 933
ID ABL56203 standard; DNA; 32392 BP.
DE AmEPV genome fragment#5.
PN WO200212526-A2.
PD 14-FEB-2002.
PA (UYFL) UNIV FLORIDA.
Query Match 3.4%; Score 46.4; DB 6; Length 32392;
Best Local Similarity 44.0%; Pred. No. 14;
RESULT 934
ID ADE13891 standard; DNA; 46951 BP.
DE Human optineurin gene.
PN US2003190617-A1.
PD 09-OCT-2003.
PA (SIEE/) SI E.
PA (RAYM/) RAYMOND V.
PA (MORI/) MORISSETTE J.
Query Match 3.4%; Score 46.4; DB 10; Length 46951;
Best Local Similarity 46.0%; Pred. No. 15;

RESULT 935
ID ABL55643 standard; DNA; 50000 BP.
DE AmEPV genome fragment#1.
PN WO200212526-A2.
PD 14-FEB-2002.
PA (UYFL) UNIV FLORIDA.
Query Match 3.4%; Score 46.4; DB 6; Length 50000;
Best Local Similarity 44.0%; Pred. No. 15;
RESULT 936
ID ADL44075 standard; DNA; 469 BP.
DE Human ovarian cancer DNA marker #17965.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.4%; Score 46.2; DB 5; Length 469;
Best Local Similarity 54.1%; Pred. No. 8.2;
RESULT 937
ID AAS45384 standard; DNA; 5689 BP.
DE Chemically pretreated genomic DNA associated with cell cycle #45.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 46.2; DB 4; Length 5689;
Best Local Similarity 44.3%; Pred. No. 12;
RESULT 938
ID AAS46426 standard; DNA; 5689 BP.
DE Tumour suppressor gene derived chemically modified sequence #148.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 46.2; DB 4; Length 5689;
Best Local Similarity 44.3%; Pred. No. 12;
RESULT 939
ID ABK28226 standard; DNA; 5689 BP.
DE DNA transcription associated complementary genomic DNA #50.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 46.2; DB 6; Length 5689;
Best Local Similarity 44.3%; Pred. No. 12;
RESULT 940
ID ABL70598 standard; DNA; 5706 BP.
DE Chemically treated cell signalling DNA sequence complementary to#244.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 46.2; DB 6; Length 5706;
Best Local Similarity 48.3%; Pred. No. 12;
RESULT 941
ID AAS61319 standard; DNA; 5706 BP.
DE Human gene regulation-associated gene oligonucleotide #274.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 46.2; DB 6; Length 5706;
Best Local Similarity 48.3%; Pred. No. 12;
RESULT 942
ID AAS61176 standard; DNA; 6223 BP.
DE Human gene regulation-associated gene oligonucleotide #131.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 46.2; DB 6; Length 6223;
Best Local Similarity 44.9%; Pred. No. 12;
RESULT 943
ID ABL32281 standard; DNA; 13511 BP.
DE Human immune system associated gene SEQ ID NO: 254.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 46.2; DB 6; Length 13511;
Best Local Similarity 45.8%; Pred. No. 14;
RESULT 944

ID ABQ66975 standard; DNA; 13627 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 5.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 46.2; DB 6; Length 13627;
Best Local Similarity 44.5%; Pred. No. 14;
RESULT 945
ID AAK73166 standard; DNA; 19965 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27978.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.4%; Score 46.2; DB 4; Length 19965;
Best Local Similarity 48.8%; Pred. No. 15;
RESULT 946
ID ABK69932 standard; DNA; 19965 BP.
DE Human secreted protein gene 68 genomic DNA fragment #20.
PN WO200226931-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.4%; Score 46.2; DB 6; Length 19965;
Best Local Similarity 48.8%; Pred. No. 15;
RESULT 947
ID ABX35839 standard; cDNA; 298 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #1004.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 3.4%; Score 46; DB 8; Length 298;
Best Local Similarity 53.6%; Pred. No. 8.5;
RESULT 948
ID ABN80073 standard; DNA; 5771 BP.
DE Human chemically modified disease associated gene SEQ ID NO 90.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 46; DB 6; Length 5771;
Best Local Similarity 46.6%; Pred. No. 13;
RESULT 949
ID ABL33155 standard; DNA; 5807 BP.
DE Human immune system associated gene SEQ ID NO: 1128.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 46; DB 6; Length 5807;
Best Local Similarity 44.9%; Pred. No. 13;
RESULT 950
ID ABL33216 standard; DNA; 6191 BP.
DE Human immune system associated gene SEQ ID NO: 1189.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 46; DB 6; Length 6191;
Best Local Similarity 43.6%; Pred. No. 13;
RESULT 951
ID ABK31306 standard; DNA; 6191 BP.
DE Signal transduction associated gene modified DNA #75.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 46; DB 6; Length 6191;
Best Local Similarity 43.6%; Pred. No. 13;
RESULT 952
ID ABL70281 standard; DNA; 6191 BP.
DE Chemically treated cell signalling DNA sequence#86.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 46; DB 6; Length 6191;
Best Local Similarity 43.6%; Pred. No. 13;
RESULT 953
ID ABN80160 standard; DNA; 6191 BP.
DE Human chemically modified disease associated gene SEQ ID NO 177.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 46; DB 6; Length 6191;
Best Local Similarity 43.6%; Pred. No. 13;
RESULT 954
ID ABL33380 standard; DNA; 6881 BP.
DE Human immune system associated gene SEQ ID NO: 1353.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 46; DB 6; Length 6881;
Best Local Similarity 44.0%; Pred. No. 14;
RESULT 955
ID ABK28249 standard; DNA; 6881 BP.
DE DNA transcription associated genomic DNA #62.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 46; DB 6; Length 6881;
Best Local Similarity 44.0%; Pred. No. 14;
RESULT 956
ID AAS46530 standard; DNA; 7814 BP.
DE Tumour suppressor gene derived chemically modified sequence #252.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 46; DB 4; Length 7814;
Best Local Similarity 43.3%; Pred. No. 14;
RESULT 957
ID ABK28257 standard; DNA; 8170 BP.
DE DNA transcription associated genomic DNA #66.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 46; DB 6; Length 8170;
Best Local Similarity 44.9%; Pred. No. 14;
RESULT 958
ID AAK86270 standard; DNA; 9706 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41082.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.4%; Score 46; DB 4; Length 9706;
Best Local Similarity 51.7%; Pred. No. 14;
RESULT 959
ID ABL32793 standard; DNA; 19087 BP.
DE Human immune system associated gene SEQ ID NO: 766.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 46; DB 6; Length 19087;
Best Local Similarity 47.4%; Pred. No. 16;
RESULT 960
ID ABD32684 standard; DNA; 41991 BP.
DE Human cancer-associated genomic DNA HD13-117.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.4%; Score 46; DB 13; Length 41991;
Best Local Similarity 51.7%; Pred. No. 18;
RESULT 961
ID ABL93743 standard; cDNA; 457 BP.
DE Arabidopsis thaliana nucleic acid sequence Ref:2027508 SEQ ID NO:508.
PN US2002023280-A1.
PD 21-FEB-2002.
PA (GORL/) GORLACH J.
PA (ANYY/) AN Y.
PA (HAMI/) HAMILTON C M.

PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T M.
PA (YUYY/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHEW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
PA (KRIC/) KRICKER M.
PA (SLAT/) SLATER T.
PA (DAVI/) DAVIS K R.
PA (ALLE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURB/) HURBAN P.
Query Match 3.4%; Score 45.8; DB 6; Length 457;
Best Local Similarity 61.2%; Pred. No. 9.9;
RESULT 962
ID ADL45106 standard; DNA; 531 BP.
DE Human ovarian cancer DNA marker #18996.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.4%; Score 45.8; DB 5; Length 531;
Best Local Similarity 59.7%; Pred. No. 10;
RESULT 963
ID AAH93026 standard; DNA; 700 BP.
DE Human inflammatory bowel disease related gene fragment IGR3319a.
PN WO200142511-A2.
PD 14-JUN-2001.
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
PA (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.
Query Match 3.4%; Score 45.8; DB 4; Length 700;
Best Local Similarity 45.2%; Pred. No. 11;
RESULT 964
ID AAA26377 standard; cDNA; 1559 BP.
DE Human secreted protein gene 32 SEQ ID NO:42.
PN WO200006698-A1.
PD 10-FEB-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.4%; Score 45.8; DB 3; Length 1559;
Best Local Similarity 57.2%; Pred. No. 12;
RESULT 965
ID ADL71438 standard; cDNA; 1559 BP.
DE Novel human secreted protein cDNA seqid 42.
PN US2004034196-A1.
PD 19-FEB-2004.
PA (KOMA/) KOMATSOULIS G A.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (DUAN/) DUAN D R.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (LAFL/) LAFLEUR D W.
PA (WEIY/) WEI Y.
Query Match 3.4%; Score 45.8; DB 12; Length 1559;
Best Local Similarity 57.2%; Pred. No. 12;
RESULT 966
ID AAS01496 standard; DNA; 2056 BP.
DE Human secreted protein gene #37.
PN WO200123402-A1.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.4%; Score 45.8; DB 4; Length 2056;
Best Local Similarity 57.2%; Pred. No. 12;
RESULT 967
ID AAH34935 standard; cDNA; 2056 BP.
DE Human colon cancer antigen encoding cDNA SEQ ID NO:2017.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.4%; Score 45.8; DB 4; Length 2056;
Best Local Similarity 57.2%; Pred. No. 12;
RESULT 968
ID AAD08390 standard; cDNA; 2166 BP.
DE Human secreted protein-encoding gene 46 cDNA clone HCQCC96, SEQ ID NO:56.
PN WO200077022-A1.
PD 21-DEC-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.4%; Score 45.8; DB 4; Length 2166;
Best Local Similarity 57.2%; Pred. No. 13;
RESULT 969
ID ABZ73348 standard; cDNA; 2166 BP.
DE Secreted protein-encoding gene 68 cDNA clone HCQCC96, SEQ ID NO:78.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.4%; Score 45.8; DB 8; Length 2166;
Best Local Similarity 57.2%; Pred. No. 13;
RESULT 970
ID ADA97953 standard; cDNA; 2166 BP.
DE Human secreted protein cDNA sequence #47.
PN WO2003004623-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.4%; Score 45.8; DB 8; Length 2166;
Best Local Similarity 57.2%; Pred. No. 13;
RESULT 971
ID ADA43859 standard; cDNA; 2166 BP.
DE Human secreted protein cDNA SEQ ID 47.
PN WO2003000865-A2.
PD 03-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.4%; Score 45.8; DB 8; Length 2166;
Best Local Similarity 57.2%; Pred. No. 13;
RESULT 972
ID ADC20109 standard; DNA; 2166 BP.
DE Human secreted protein coding sequence #48.
PN WO200292787-A2.
PD 21-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.4%; Score 45.8; DB 10; Length 2166;
Best Local Similarity 57.2%; Pred. No. 13;
RESULT 973
ID ADF10572 standard; DNA; 2166 BP.
DE Human secreted protein encoding sequence #25.
PN WO200299085-A2.
PD 12-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.4%; Score 45.8; DB 10; Length 2166;
Best Local Similarity 57.2%; Pred. No. 13;
RESULT 974
ID AAC89670 standard; DNA; 2500 BP.
DE P. gallinaceum chitinase coding sequence SEQ ID NO: 5.
PN WO200073488-A1.
PD 07-DEC-2000.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 3.4%; Score 45.8; DB 4; Length 2500;
Best Local Similarity 42.7%; Pred. No. 13;
RESULT 975
ID ABL17264 standard; DNA; 3296 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 3265.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.4%; Score 45.8; DB 4; Length 3296;
Best Local Similarity 45.6%; Pred. No. 13;
RESULT 976
ID ABL33768 standard; DNA; 5795 BP.
DE Human immune system associated gene SEQ ID NO: 1741.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.8; DB 6; Length 5795;
Best Local Similarity 51.1%; Pred. No. 15;

RESULT 977
ID ABN80232 standard; DNA; 5795 BP.
DE Human chemically modified disease associated gene SEQ ID NO 249.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.8; DB 6; Length 5795;
Best Local Similarity 51.1%; Pred. No. 15;
RESULT 978
ID ABL32267 standard; DNA; 6419 BP.
DE Human immune system associated gene SEQ ID NO: 240.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.8; DB 6; Length 6419;
Best Local Similarity 46.6%; Pred. No. 15;
RESULT 979
ID ABL32463 standard; DNA; 9155 BP.
DE Human immune system associated gene SEQ ID NO: 436.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.8; DB 6; Length 9155;
Best Local Similarity 47.9%; Pred. No. 16;
RESULT 980
ID ABL33421 standard; DNA; 9707 BP.
DE Human immune system associated gene SEQ ID NO: 1394.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.8; DB 6; Length 9707;
Best Local Similarity 44.8%; Pred. No. 16;
RESULT 981
ID ABK31173 standard; DNA; 11178 BP.
DE Signal transduction associated gene modified complementary DNA #8.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.8; DB 6; Length 11178;
Best Local Similarity 46.9%; Pred. No. 16;
RESULT 982
ID ABL70508 standard; DNA; 11178 BP.
DE Chemically treated cell signalling DNA sequence complementary to#199.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.8; DB 6; Length 11178;
Best Local Similarity 46.9%; Pred. No. 16;
RESULT 983
ID AAS61060 standard; DNA; 11178 BP.
DE Human gene regulation-associated gene oligonucleotide #15.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.8; DB 6; Length 11178;
Best Local Similarity 46.9%; Pred. No. 16;
RESULT 984
ID ABK31320 standard; DNA; 11907 BP.
DE Signal transduction associated gene modified DNA #82.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.8; DB 6; Length 11907;
Best Local Similarity 45.7%; Pred. No. 16;
RESULT 985
ID AAS46453 standard; DNA; 15592 BP.
DE Tumour suppressor gene derived chemically modified sequence #175.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.8; DB 4; Length 15592;
Best Local Similarity 43.6%; Pred. No. 17;
RESULT 986
ID ABL33326 standard; DNA; 15592 BP.
DE Human immune system associated gene SEQ ID NO: 1299.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.8; DB 6; Length 15592;
Best Local Similarity 43.6%; Pred. No. 17;
RESULT 987
ID ADL02342 standard; DNA; 255 BP.
DE DNA encoding a M. catarrhalis protein #28.
PN US6673910-B1.
PD 06-JAN-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 3.4%; Score 45.6; DB 12; Length 255;
Best Local Similarity 47.1%; Pred. No. 9.9;
RESULT 988
ID AAL15484 standard; cDNA; 711 BP.
DE Human breast cancer expressed polynucleotide 7941.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.4%; Score 45.6; DB 4; Length 711;
Best Local Similarity 51.2%; Pred. No. 12;
RESULT 989
ID ACN85475 standard; DNA; 950 BP.
DE Breast cancer related marker, seq id 6625.
PN US2003099974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 3.4%; Score 45.6; DB 11; Length 950;
Best Local Similarity 51.2%; Pred. No. 12;
RESULT 990
ID ADS50927 standard; cDNA; 1730 BP.
DE Bacterial polynucleotide #5670.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 3.4%; Score 45.6; DB 13; Length 1730;
Best Local Similarity 43.6%; Pred. No. 13;
RESULT 991
ID AAS46781 standard; DNA; 4654 BP.
DE Tumour suppressor gene derived chemically modified sequence #506.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.6; DB 4; Length 4654;
Best Local Similarity 44.9%; Pred. No. 15;
RESULT 992
ID ABL34223 standard; DNA; 4654 BP.
DE Human immune system associated gene SEQ ID NO: 2196.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.6; DB 6; Length 4654;
Best Local Similarity 44.9%; Pred. No. 15;
RESULT 993
ID ABQ75107 standard; cDNA; 4985 BP.
DE Anopheles gambiae odourant receptor 2 genomic DNA SEQ ID NO:10.
PN WO200259274-A2.
PD 01-AUG-2002.
PA (UYVA-) UNIV VANDERBILT.
Query Match 3.4%; Score 45.6; DB 6; Length 4985;
Best Local Similarity 43.3%; Pred. No. 16;
RESULT 994
ID ACF79720 standard; DNA; 4985 BP.
DE Mosquito odorant receptor 2 genomic DNA.
PN WO2003076590-A2.
PD 18-SEP-2003.
PA (UYVA-) UNIV VANDERBILT.

Query Match 3.4%; Score 45.6; DB 10; Length 4985;
Best Local Similarity 43.3%; Pred. No. 16;
RESULT 995
ID ABK31344 standard; DNA; 5388 BP.
DE Signal transduction associated gene modified DNA #94.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.6; DB 6; Length 5388;
Best Local Similarity 43.1%; Pred. No. 16;
RESULT 996
ID ABL70305 standard; DNA; 5388 BP.
DE Chemically treated cell signalling DNA sequence#98.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.6; DB 6; Length 5388;
Best Local Similarity 43.1%; Pred. No. 16;
RESULT 997
ID AAS61239 standard; DNA; 5388 BP.
DE Human gene regulation-associated gene oligonucleotide #194.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.6; DB 6; Length 5388;
Best Local Similarity 43.1%; Pred. No. 16;
RESULT 998
ID ABL32712 standard; DNA; 5427 BP.
DE Human immune system associated gene SEQ ID NO: 685.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.6; DB 6; Length 5427;
Best Local Similarity 49.6%; Pred. No. 16;
RESULT 999
ID ABL32676 standard; DNA; 6015 BP.
DE Human immune system associated gene SEQ ID NO: 649.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.6; DB 6; Length 6015;
Best Local Similarity 45.7%; Pred. No. 16;
RESULT 1000
ID AAS46439 standard; DNA; 7040 BP.
DE Tumour suppressor gene derived chemically modified sequence #161.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.6; DB 4; Length 7040;
Best Local Similarity 44.2%; Pred. No. 16;
RESULT 1001
ID ABK33963 standard; DNA; 7040 BP.
DE Human DNA for staging of Astrocytomas #24.
PN WO200202808-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.6; DB 6; Length 7040;
Best Local Similarity 44.2%; Pred. No. 16;
RESULT 1002
ID ABZ10179 standard; DNA; 7040 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #319.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.6; DB 8; Length 7040;
Best Local Similarity 44.2%; Pred. No. 16;
RESULT 1003
ID ABZ10033 standard; DNA; 7040 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #173.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.6; DB 8; Length 7040;
Best Local Similarity 44.2%; Pred. No. 16;
RESULT 1004
ID ADA20348 standard; DNA; 7040 BP.
DE Prostate tumour related genomic DNA sample #7.
PN WO2002103042-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.6; DB 8; Length 7040;
Best Local Similarity 44.2%; Pred. No. 16;
RESULT 1005
ID ADA84155 standard; DNA; 7040 BP.
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:13.
PN WO2002103041-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.6; DB 8; Length 7040;
Best Local Similarity 44.2%; Pred. No. 16;
RESULT 1006
ID ADE84191 standard; DNA; 7040 BP.
DE Human lymphoid cell proliferative disorder gene derived DNA #127.
PN WO2003044226-A2.
PD 30-MAY-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.6; DB 10; Length 7040;
Best Local Similarity 44.2%; Pred. No. 16;
RESULT 1007
ID ADE84115 standard; DNA; 7040 BP.
DE Human lymphoid cell proliferative disorder gene derived DNA #51.
PN WO2003044226-A2.
PD 30-MAY-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.6; DB 10; Length 7040;
Best Local Similarity 44.2%; Pred. No. 16;
RESULT 1008
ID ADB54184 standard; DNA; 7833 BP.
DE Pretreated genomic DNA region 108.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.6; DB 10; Length 7833;
Best Local Similarity 45.5%; Pred. No. 17;
RESULT 1009
ID ADE37769 standard; DNA; 7833 BP.
DE Human chemically treated EYA4 nucleotide sequence SEQ ID NO:15.
PN WO2003072820-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.6; DB 10; Length 7833;
Best Local Similarity 45.5%; Pred. No. 17;
RESULT 1010
ID ADS89334 standard; DNA; 7833 BP.
DE Oligonucleotide of the invention SEQ ID NO:350.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.6; DB 13; Length 7833;
Best Local Similarity 45.5%; Pred. No. 17;
RESULT 1011
ID ABL32158 standard; DNA; 7990 BP.
DE Human immune system associated gene SEQ ID NO: 131.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.6; DB 6; Length 7990;
Best Local Similarity 44.2%; Pred. No. 17;
RESULT 1012
ID ABL54307 standard; DNA; 7990 BP.
DE Chemically treated apoptosis gene #4.
PN WO200177164-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.6; DB 6; Length 7990;
Best Local Similarity 44.2%; Pred. No. 17;

RESULT 1013
ID ABL33568 standard; DNA; 8305 BP.
DE Human immune system associated gene SEQ ID NO: 1541.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.6; DB 6; Length 8305;
Best Local Similarity 47.7%; Pred. No. 17;
RESULT 1014
ID AAS45314 standard; DNA; 11260 BP.
DE Chemically pretreated genomic DNA associated with cell cycle #10.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.6; DB 4; Length 11260;
Best Local Similarity 68.5%; Pred. No. 18;
RESULT 1015
ID ABK28153 standard; DNA; 11260 BP.
DE DNA transcription associated genomic DNA #14.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.6; DB 6; Length 11260;
Best Local Similarity 68.5%; Pred. No. 18;
RESULT 1016
ID ABN80038 standard; DNA; 11260 BP.
DE Human chemically modified disease associated gene SEQ ID NO 55.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.6; DB 6; Length 11260;
Best Local Similarity 68.5%; Pred. No. 18;
RESULT 1017
ID ABL33262 standard; DNA; 12393 BP.
DE Human immune system associated gene SEQ ID NO: 1235.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.6; DB 6; Length 12393;
Best Local Similarity 44.1%; Pred. No. 18;
RESULT 1018
ID ABL33453 standard; DNA; 14032 BP.
DE Human immune system associated gene SEQ ID NO: 1426.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.6; DB 6; Length 14032;
Best Local Similarity 45.3%; Pred. No. 18;
RESULT 1019
ID AAS46506 standard; DNA; 14919 BP.
DE Tumour suppressor gene derived chemically modified sequence #228.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.6; DB 4; Length 14919;
Best Local Similarity 45.0%; Pred. No. 18;
RESULT 1020
ID AAS45348 standard; DNA; 17421 BP.
DE Chemically pretreated genomic DNA associated with cell cycle #27.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.6; DB 4; Length 17421;
Best Local Similarity 46.8%; Pred. No. 19;
RESULT 1021
ID ABK28181 standard; DNA; 17421 BP.
DE DNA transcription associated genomic DNA #28.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.6; DB 6; Length 17421;
Best Local Similarity 46.8%; Pred. No. 19;
RESULT 1022
ID ABK31212 standard; DNA; 19459 BP.
DE Signal transduction associated gene modified DNA #28.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.6; DB 6; Length 19459;
Best Local Similarity 45.2%; Pred. No. 19;
RESULT 1023
ID ABL70527 standard; DNA; 19459 BP.
DE Chemically treated cell signalling DNA sequence#209.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.6; DB 6; Length 19459;
Best Local Similarity 45.2%; Pred. No. 19;
RESULT 1024
Query Match 3.4%; Score 45.6; DB 8; Length 110000;
Best Local Similarity 45.0%; Pred. No. 25;
RESULT 1025
ID ADQ97266 standard; DNA; 355211 BP.
DE Human cancer associated sequence HD08-023, SEQ ID 242.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.4%; Score 45.6; DB 12; Length 110000;
Best Local Similarity 46.7%; Pred. No. 25;
RESULT 1026
ID ADL37508 standard; DNA; 294 BP.
DE Human ovarian cancer DNA marker #11398.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.4%; Score 45.4; DB 5; Length 294;
Best Local Similarity 47.6%; Pred. No. 11;
RESULT 1027
ID ADI72364 standard; DNA; 294 BP.
DE Human ovarian cancer DNA marker #5106.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.4%; Score 45.4; DB 5; Length 294;
Best Local Similarity 47.6%; Pred. No. 11;
RESULT 1028
ID ABV05431 standard; cDNA; 445 BP.
DE Human prostate expression marker cDNA 5422.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.4%; Score 45.4; DB 5; Length 445;
Best Local Similarity 47.5%; Pred. No. 12;
RESULT 1029
ID ADI72375 standard; DNA; 614 BP.
DE Human ovarian cancer DNA marker #5117.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.4%; Score 45.4; DB 5; Length 614;
Best Local Similarity 43.0%; Pred. No. 12;
RESULT 1030
ID ADL37519 standard; DNA; 614 BP.
DE Human ovarian cancer DNA marker #11409.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.4%; Score 45.4; DB 5; Length 614;
Best Local Similarity 43.0%; Pred. No. 12;
RESULT 1031
ID ADR01494 standard; DNA; 615 BP.
DE A. gossypii genomic DNA PAG1074RP.
PN US6239264-B1.
PD 29-MAY-2001.
PA (SYNG-) SYNGENTA PARTICIPATIONS AG.
Query Match 3.4%; Score 45.4; DB 2; Length 615;

Best Local Similarity 44.2%; Pred. No. 12;
RESULT 1032
ID AAL01672 standard; cDNA; 622 BP.
DE Human reproductive system related antigen cDNA SEQ ID NO: 1673.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.4%; Score 45.4; DB 4; Length 622;
Best Local Similarity 70.1%; Pred. No. 12;
RESULT 1033
ID ABA07591 standard; cDNA; 622 BP.
DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 148.
PN WO200155325-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.4%; Score 45.4; DB 4; Length 622;
Best Local Similarity 70.1%; Pred. No. 12;
RESULT 1034
ID AAX37474 standard; cDNA; 1014 BP.
DE Human secreted protein cDNA fragment containing gene 24.
PN WO9918208-A1.
PD 15-APR-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.4%; Score 45.4; DB 2; Length 1014;
Best Local Similarity 51.2%; Pred. No. 13;
RESULT 1035
ID AAS92198 standard; cDNA; 2482 BP.
DE DNA encoding novel human diagnostic protein #28002.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.4%; Score 45.4; DB 5; Length 2482;
Best Local Similarity 49.4%; Pred. No. 15;
RESULT 1036
ID ABL17264 standard; DNA; 3296 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 3265.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.4%; Score 45.4; DB 4; Length 3296;
Best Local Similarity 45.8%; Pred. No. 16;
RESULT 1037
ID AAV52396 standard; DNA; 3744 BP.
DE Streptococcus pneumoniae genome fragment SEQ ID NO:263.
PN WO9818931-A2.
PD 07-MAY-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.4%; Score 45.4; DB 2; Length 3744;
Best Local Similarity 47.7%; Pred. No. 16;
RESULT 1038
ID ADS89612 standard; DNA; 4930 BP.
DE Oligonucleotide of the invention SEQ ID NO:628.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.4; DB 13; Length 4930;
Best Local Similarity 47.2%; Pred. No. 17;
RESULT 1039
ID ABQ75107 standard; cDNA; 4985 BP.
DE Anopheles gambiae odourant receptor 2 genomic DNA SEQ ID NO:10.
PN WO200259274-A2.
PD 01-AUG-2002.
PA (UYVA-) UNIV VANDERBILT.
Query Match 3.4%; Score 45.4; DB 6; Length 4985;
Best Local Similarity 45.8%; Pred. No. 17;
RESULT 1040
ID ACF79720 standard; DNA; 4985 BP.
DE Mosquito odorant receptor 2 genomic DNA.
PN WO2003076590-A2.
PD 18-SEP-2003.
PA (UYVA-) UNIV VANDERBILT.
Query Match 3.4%; Score 45.4; DB 10; Length 4985;
Best Local Similarity 45.8%; Pred. No. 17;
RESULT 1041
ID ABZ10145 standard; DNA; 5033 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #285.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.4; DB 8; Length 5033;
Best Local Similarity 47.3%; Pred. No. 17;
RESULT 1042
ID ABL33266 standard; DNA; 5218 BP.
DE Human immune system associated gene SEQ ID NO: 1239.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.4; DB 6; Length 5218;
Best Local Similarity 43.5%; Pred. No. 17;
RESULT 1043
ID ABL34150 standard; DNA; 5376 BP.
DE Human immune system associated gene SEQ ID NO: 2123.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.4; DB 6; Length 5376;
Best Local Similarity 50.2%; Pred. No. 17;
RESULT 1044
ID ABL32713 standard; DNA; 5427 BP.
DE Human immune system associated gene SEQ ID NO: 686.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.4; DB 6; Length 5427;
Best Local Similarity 45.5%; Pred. No. 17;
RESULT 1045
ID ABL33276 standard; DNA; 5675 BP.
DE Human immune system associated gene SEQ ID NO: 1249.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.4; DB 6; Length 5675;
Best Local Similarity 44.0%; Pred. No. 17;
RESULT 1046
ID ABN80142 standard; DNA; 5721 BP.
DE Human chemically modified disease associated gene SEQ ID NO 159.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.4; DB 6; Length 5721;
Best Local Similarity 43.8%; Pred. No. 17;
RESULT 1047
ID ABL33159 standard; DNA; 5909 BP.
DE Human immune system associated gene SEQ ID NO: 1132.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.4; DB 6; Length 5909;
Best Local Similarity 55.3%; Pred. No. 18;
RESULT 1048
ID ADS89769 standard; DNA; 6001 BP.
DE Oligonucleotide of the invention SEQ ID NO:785.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.4; DB 13; Length 6001;
Best Local Similarity 47.2%; Pred. No. 18;
RESULT 1049
ID ABL32913 standard; DNA; 6621 BP.
DE Human immune system associated gene SEQ ID NO: 886.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.4; DB 6; Length 6621;
Best Local Similarity 47.6%; Pred. No. 18;
RESULT 1050

ID AAA70132 standard; DNA; 7620 BP.
DE Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:265.
PN WO200025728-A2.
PD 11-MAY-2000.
PA (HOFF/) HOFFMAN S.
PA (CARU/) CARUCCI D.
PA (GARD/) GARDNER M.
PA (VENT/) VENTER J C.
Query Match 3.4%; Score 45.4; DB 3; Length 7620;
Best Local Similarity 47.3%; Pred. No. 18;
RESULT 1051
ID AAS45391 standard; DNA; 7906 BP.
DE Chemically pretreated complementary DNA associated with cell cycle #48.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.4; DB 4; Length 7906;
Best Local Similarity 48.2%; Pred. No. 18;
RESULT 1052
ID ABK28236 standard; DNA; 7906 BP.
DE DNA transcription associated complementary genomic DNA #55.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.4; DB 6; Length 7906;
Best Local Similarity 48.2%; Pred. No. 18;
RESULT 1053
ID ABN80179 standard; DNA; 7906 BP.
DE Human chemically modified disease associated gene SEQ ID NO 196.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.4; DB 6; Length 7906;
Best Local Similarity 48.2%; Pred. No. 18;
RESULT 1054
ID ABQ67125 standard; DNA; 8227 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 155.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.4; DB 6; Length 8227;
Best Local Similarity 46.4%; Pred. No. 18;
RESULT 1055
ID AAS46588 standard; DNA; 8524 BP.
DE Tumour suppressor gene derived chemically modified sequence #310.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.4; DB 4; Length 8524;
Best Local Similarity 48.6%; Pred. No. 19;
RESULT 1056
ID ABL33841 standard; DNA; 8524 BP.
DE Human immune system associated gene SEQ ID NO: 1814.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.4; DB 6; Length 8524;
Best Local Similarity 48.6%; Pred. No. 19;
RESULT 1057
ID ABL33317 standard; DNA; 13574 BP.
DE Human immune system associated gene SEQ ID NO: 1290.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.4; DB 6; Length 13574;
Best Local Similarity 46.9%; Pred. No. 20;
RESULT 1058
ID ABL70466 standard; DNA; 15853 BP.
DE Chemically treated cell signalling DNA sequence complementary to#178.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.4; DB 6; Length 15853;
Best Local Similarity 44.8%; Pred. No. 20;
RESULT 1059
ID AAS61457 standard; DNA; 15853 BP.
DE Human gene regulation-associated gene oligonucleotide #412.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.4; DB 6; Length 15853;
Best Local Similarity 44.8%; Pred. No. 20;
RESULT 1060
ID ABL33949 standard; DNA; 18218 BP.
DE Human immune system associated gene SEQ ID NO: 1922.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.4; DB 6; Length 18218;
Best Local Similarity 46.4%; Pred. No. 21;
RESULT 1061
ID ABL32610 standard; DNA; 18855 BP.
DE Human immune system associated gene SEQ ID NO: 583.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.4; DB 6; Length 18855;
Best Local Similarity 48.3%; Pred. No. 21;
RESULT 1062
Query Match 3.4%; Score 45.4; DB 10; Length 110000;
Best Local Similarity 47.7%; Pred. No. 27;
RESULT 1063
Query Match 3.4%; Score 45.4; DB 10; Length 110000;
Best Local Similarity 46.8%; Pred. No. 27;
RESULT 1064
ID ADL17884 standard; cDNA; 158001 BP.
DE Human phosphotyrosyl phosphatase activator, PTPA, gene.
PN US2004023906-A1.
PD 05-FEB-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 3.4%; Score 45.4; DB 12; Length 158001;
Best Local Similarity 45.1%; Pred. No. 29;
RESULT 1065
ID ADL38882 standard; DNA; 420 BP.
DE Human ovarian cancer DNA marker #12772.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.4%; Score 45.2; DB 5; Length 420;
Best Local Similarity 41.7%; Pred. No. 13;
RESULT 1066
ID ADI72427 standard; DNA; 421 BP.
DE Human ovarian cancer DNA marker #5169.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.4%; Score 45.2; DB 5; Length 421;
Best Local Similarity 41.7%; Pred. No. 13;
RESULT 1067
ID ABV97199 standard; cDNA; 505 BP.
DE Human pancreatic cancer expressed cDNA SEQ ID NO 2607.
PN WO200260317-A2.
PD 08-AUG-2002.
PA (CORI-) CORIXA CORP.
Query Match 3.4%; Score 45.2; DB 6; Length 505;
Best Local Similarity 57.5%; Pred. No. 13;
RESULT 1068
ID ABK33950 standard; DNA; 5001 BP.
DE Human DNA for staging of Astrocytomas #17.
PN WO200202808-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.2; DB 6; Length 5001;
Best Local Similarity 46.3%; Pred. No. 19;
RESULT 1069
ID ABL54373 standard; DNA; 5001 BP.

DE Chemically treated apoptosis gene #37.
PN WO200177164-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.2; DB 6; Length 5001;
Best Local Similarity 46.3%; Pred. No. 19;
RESULT 1070
ID ADA20404 standard; DNA; 5001 BP.
DE Prostate tumour related genomic DNA sample #35.
PN WO2002103042-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.2; DB 8; Length 5001;
Best Local Similarity 46.3%; Pred. No. 19;
RESULT 1071
ID ADA84211 standard; DNA; 5001 BP.
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:69.
PN WO2002103041-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.2; DB 8; Length 5001;
Best Local Similarity 46.3%; Pred. No. 19;
RESULT 1072
ID ABL32560 standard; DNA; 5328 BP.
DE Human immune system associated gene SEQ ID NO: 533.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.2; DB 6; Length 5328;
Best Local Similarity 46.1%; Pred. No. 19;
RESULT 1073
ID ABK39970 standard; DNA; 5519 BP.
DE Human chemically pretreated gene sequence #26 strand 1.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.2; DB 6; Length 5519;
Best Local Similarity 42.3%; Pred. No. 19;
RESULT 1074
ID ABL32517 standard; DNA; 5930 BP.
DE Human immune system associated gene SEQ ID NO: 490.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.2; DB 6; Length 5930;
Best Local Similarity 44.3%; Pred. No. 19;
RESULT 1075
ID ABL32788 standard; DNA; 6171 BP.
DE Human immune system associated gene SEQ ID NO: 761.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.2; DB 6; Length 6171;
Best Local Similarity 53.2%; Pred. No. 19;
RESULT 1076
ID ABL34215 standard; DNA; 6200 BP.
DE Human immune system associated gene SEQ ID NO: 2188.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.2; DB 6; Length 6200;
Best Local Similarity 44.8%; Pred. No. 19;
RESULT 1077
ID ABL32345 standard; DNA; 7346 BP.
DE Human immune system associated gene SEQ ID NO: 318.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.2; DB 6; Length 7346;
Best Local Similarity 46.5%; Pred. No. 20;
RESULT 1078
ID ABK40056 standard; DNA; 7892 BP.
DE Human chemically pretreated gene sequence #69 strand 2.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.2; DB 6; Length 7892;
Best Local Similarity 49.4%; Pred. No. 20;
RESULT 1079
ID ABL34152 standard; DNA; 9255 BP.
DE Human immune system associated gene SEQ ID NO: 2125.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.2; DB 6; Length 9255;
Best Local Similarity 45.9%; Pred. No. 21;
RESULT 1080
ID AAS63354 standard; DNA; 9265 BP.
DE Chemically pretreated metabolism associated gene #49.
PN WO200176451-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.2; DB 6; Length 9265;
Best Local Similarity 45.9%; Pred. No. 21;
RESULT 1081
ID AAS61102 standard; DNA; 12592 BP.
DE Human gene regulation-associated gene oligonucleotide #57.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.2; DB 6; Length 12592;
Best Local Similarity 50.0%; Pred. No. 22;
RESULT 1082
ID AAS61427 standard; DNA; 19380 BP.
DE Human gene regulation-associated gene oligonucleotide #382.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.2; DB 6; Length 19380;
Best Local Similarity 43.9%; Pred. No. 23;
RESULT 1083
ID ABQ67150 standard; DNA; 40324 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 180.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.4%; Score 45.2; DB 6; Length 40324;
Best Local Similarity 44.2%; Pred. No. 26;
RESULT 1084
Query Match 3.4%; Score 45.2; DB 6; Length 110000;
Best Local Similarity 45.9%; Pred. No. 30;
RESULT 1085
ID ABD32659 standard; DNA; 163382 BP.
DE Human cancer-associated genomic DNA HD13-065.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.4%; Score 45.2; DB 13; Length 163382;
Best Local Similarity 45.7%; Pred. No. 32;
RESULT 1086
ID AAL13342 standard; cDNA; 297 BP.
DE Human breast cancer expressed polynucleotide 5799.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.3%; Score 45; DB 4; Length 297;
Best Local Similarity 42.5%; Pred. No. 13;
RESULT 1087
ID AAI82669 standard; cDNA; 350 BP.
DE Human polynucleotide SEQ ID NO 2729.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.3%; Score 45; DB 4; Length 350;
Best Local Similarity 60.0%; Pred. No. 14;
RESULT 1088

ID AAI87168 standard; cDNA; 361 BP.
DE Human polynucleotide SEQ ID NO 7228.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.3%; Score 45; DB 4; Length 361;
Best Local Similarity 60.0%; Pred. No. 14;
RESULT 1089
ID ACN83440 standard; DNA; 411 BP.
DE Breast cancer related marker, seq id 4590.
PN US2003099974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 3.3%; Score 45; DB 11; Length 411;
Best Local Similarity 42.5%; Pred. No. 14;
RESULT 1090
ID ABZ10188 standard; DNA; 1501 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #328.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 45; DB 8; Length 1501;
Best Local Similarity 46.5%; Pred. No. 17;
RESULT 1091
ID ADE84162 standard; DNA; 1501 BP.
DE Human lymphoid cell proliferative disorder gene derived DNA #98.
PN WO2003044226-A2.
PD 30-MAY-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 45; DB 10; Length 1501;
Best Local Similarity 46.5%; Pred. No. 17;
RESULT 1092
ID ADQ22191 standard; DNA; 1758 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5011.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.3%; Score 45; DB 12; Length 1758;
Best Local Similarity 57.4%; Pred. No. 18;
RESULT 1093
ID ABZ16379 standard; DNA; 2000 BP.
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 4184.
PN WO200216655-A2.
PD 28-FEB-2002.
PA (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 3.3%; Score 45; DB 6; Length 2000;
Best Local Similarity 46.4%; Pred. No. 18;
RESULT 1094
ID ABK31379 standard; DNA; 5338 BP.
DE Signal transduction associated gene modified complementary DNA #111.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 45; DB 6; Length 5338;
Best Local Similarity 46.9%; Pred. No. 21;
RESULT 1095
ID ABL70330 standard; DNA; 5338 BP.
DE Chemically treated cell signalling DNA sequence complementary to#110.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 45; DB 6; Length 5338;
Best Local Similarity 46.9%; Pred. No. 21;
RESULT 1096
ID AAS61281 standard; DNA; 5338 BP.
DE Human gene regulation-associated gene oligonucleotide #236.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 45; DB 6; Length 5338;
Best Local Similarity 46.9%; Pred. No. 21;
RESULT 1097
ID AAA70105 standard; DNA; 5940 BP.
DE Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:238.
PN WO200025728-A2.
PD 11-MAY-2000.
PA (HOFF/) HOFFMAN S.
PA (CARU/) CARUCCI D.
PA (GARD/) GARDNER M.
PA (VENT/) VENTER J C.
Query Match 3.3%; Score 45; DB 3; Length 5940;
Best Local Similarity 44.9%; Pred. No. 21;
RESULT 1098
ID ABL32194 standard; DNA; 6208 BP.
DE Human immune system associated gene SEQ ID NO: 167.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 45; DB 6; Length 6208;
Best Local Similarity 50.2%; Pred. No. 21;
RESULT 1099
ID ABL32087 standard; DNA; 8178 BP.
DE Human immune system associated gene SEQ ID NO: 60.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 45; DB 6; Length 8178;
Best Local Similarity 46.1%; Pred. No. 22;
RESULT 1100
ID AAS46421 standard; DNA; 13321 BP.
DE Tumour suppressor gene derived chemically modified sequence #143.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 45; DB 4; Length 13321;
Best Local Similarity 44.2%; Pred. No. 24;
RESULT 1101
ID ABL32254 standard; DNA; 18154 BP.
DE Human immune system associated gene SEQ ID NO: 227.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 45; DB 6; Length 18154;
Best Local Similarity 45.4%; Pred. No. 25;
RESULT 1102
ID ACA64845 standard; DNA; 115218 BP.
DE Human HNRNP GP43 DNA corresponding to AL034397.
PN DE10127572-A1.
PD 05-DEC-2002.
PA (PATH-) PATHOARRAY GMBH.
Query Match 3.3%; Score 45; DB 8; Length 115218;
Best Local Similarity 45.6%; Pred. No. 33;
RESULT 1103
ID AAC94795 standard; cDNA; 549 BP.
DE Cat flea hindgut and Malpighian tubule (HMT) cDNA, SEQ ID NO:1290.
PN WO200061621-A2.
PD 19-OCT-2000.
PA (HESK-) HESKA CORP.
Query Match 3.3%; Score 44.8; DB 3; Length 549;
Best Local Similarity 49.6%; Pred. No. 16;
RESULT 1104
ID AAC99867 standard; cDNA; 551 BP.
DE Human secreted protein gene 50 SEQ ID NO:60.
PN WO200070042-A1.
PD 23-NOV-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 44.8; DB 3; Length 551;
Best Local Similarity 59.4%; Pred. No. 16;
RESULT 1105
ID ADR01596 standard; DNA; 837 BP.
DE A. gossypii genomic DNA PAG1241RP.
PN US6239264-B1.
PD 29-MAY-2001.
PA (SYNG-) SYNGENTA PARTICIPATIONS AG.
Query Match 3.3%; Score 44.8; DB 2; Length 837;

Best Local Similarity 44.9%; Pred. No. 17;
RESULT 1106
ID ADF82206 standard; DNA; 1114 BP.
DE Leukaemia-related DNA sequence #2762.
PN WO2003039443-A2.
PD 15-MAY-2003.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAFE/) HAFERLACH T.
PA (SCHO/) SCHOCH C.
PA (KERN/) KERN W.
Query Match 3.3%; Score 44.8; DB 10; Length 1114;
Best Local Similarity 56.6%; Pred. No. 18;
RESULT 1107
ID AAA97037 standard; DNA; 2486 BP.
DE Nucleotide sequence encoding 48kD i-antigen.
PN WO200046373-A1.
PD 10-AUG-2000.
PA (UYGE-) UNIV GEORGIA RES FOUND INC.
PA (CORR) CORNELL RES FOUND INC.
PA (CLAR/) CLARK T G.
PA (DICK/) DICKERSON H W.
PA (LINT/) LIN T.
Query Match 3.3%; Score 44.8; DB 3; Length 2486;
Best Local Similarity 46.2%; Pred. No. 20;
RESULT 1108
ID ADS89406 standard; DNA; 4394 BP.
DE Oligonucleotide of the invention SEQ ID NO:422.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.8; DB 13; Length 4394;
Best Local Similarity 46.5%; Pred. No. 22;
RESULT 1109
ID ABZ09959 standard; DNA; 5020 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #99.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.8; DB 8; Length 5020;
Best Local Similarity 46.8%; Pred. No. 23;
RESULT 1110
ID ABZ10105 standard; DNA; 5020 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #245.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.8; DB 8; Length 5020;
Best Local Similarity 46.8%; Pred. No. 23;
RESULT 1111
ID AAA70189 standard; DNA; 5454 BP.
DE Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:322.
PN WO200025728-A2.
PD 11-MAY-2000.
PA (HOFF/) HOFFMAN S.
PA (CARU/) CARUCCI D.
PA (GARD/) GARDNER M.
PA (VENT/) VENTER J C.
Query Match 3.3%; Score 44.8; DB 3; Length 5454;
Best Local Similarity 47.5%; Pred. No. 23;
RESULT 1112
ID AAN50530 standard; DNA; 5760 BP.
DE Sequence encoding the P195 protein of Plasmodium falciparum.
PN EP154454-A.
PD 11-SEP-1985.
PA (WELL) WELLCOME FOUND LTD.
Query Match 3.3%; Score 44.8; DB 1; Length 5760;
Best Local Similarity 62.9%; Pred. No. 23;
RESULT 1113
ID ABL32288 standard; DNA; 5875 BP.
DE Human immune system associated gene SEQ ID NO: 261.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.8; DB 6; Length 5875;
Best Local Similarity 43.8%; Pred. No. 23;
RESULT 1114
ID AAD46980 standard; DNA; 5917 BP.
DE Plasmodium falciparum merozoite surface protein-1 (MSP-1) DNA.
PN WO200270542-A2.
PD 12-SEP-2002.
PA (SELI-) ST ELIZABETH'S MEDICAL CENT INC.
Query Match 3.3%; Score 44.8; DB 6; Length 5917;
Best Local Similarity 62.9%; Pred. No. 23;
RESULT 1115
ID ABL32238 standard; DNA; 6222 BP.
DE Human immune system associated gene SEQ ID NO: 211.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.8; DB 6; Length 6222;
Best Local Similarity 55.0%; Pred. No. 23;
RESULT 1116
ID ABK31496 standard; DNA; 6228 BP.
DE Signal transduction associated gene modified DNA #170.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.8; DB 6; Length 6228;
Best Local Similarity 55.0%; Pred. No. 23;
RESULT 1117
ID ABL70469 standard; DNA; 6228 BP.
DE Chemically treated cell signalling DNA sequence#180.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.8; DB 6; Length 6228;
Best Local Similarity 55.0%; Pred. No. 23;
RESULT 1118
ID AAS61430 standard; DNA; 6228 BP.
DE Human gene regulation-associated gene oligonucleotide #385.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.8; DB 6; Length 6228;
Best Local Similarity 55.0%; Pred. No. 23;
RESULT 1119
ID ABL32819 standard; DNA; 6397 BP.
DE Human immune system associated gene SEQ ID NO: 792.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.8; DB 6; Length 6397;
Best Local Similarity 49.0%; Pred. No. 23;
RESULT 1120
ID ABL33574 standard; DNA; 6627 BP.
DE Human immune system associated gene SEQ ID NO: 1547.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.8; DB 6; Length 6627;
Best Local Similarity 47.5%; Pred. No. 24;
RESULT 1121
ID ABL32398 standard; DNA; 6662 BP.
DE Human immune system associated gene SEQ ID NO: 371.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.8; DB 6; Length 6662;
Best Local Similarity 45.0%; Pred. No. 24;
RESULT 1122
ID ABQ67014 standard; DNA; 6676 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 44.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.

Query Match 3.3%; Score 44.8; DB 6; Length 6676;
Best Local Similarity 49.7%; Pred. No. 24;
RESULT 1123
ID ABL32212 standard; DNA; 6904 BP.
DE Human immune system associated gene SEQ ID NO: 185.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.8; DB 6; Length 6904;
Best Local Similarity 46.2%; Pred. No. 24;
RESULT 1124
ID ABL32336 standard; DNA; 7201 BP.
DE Human immune system associated gene SEQ ID NO: 309.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.8; DB 6; Length 7201;
Best Local Similarity 45.8%; Pred. No. 24;
RESULT 1125
ID ABL34045 standard; DNA; 7319 BP.
DE Human immune system associated gene SEQ ID NO: 2018.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.8; DB 6; Length 7319;
Best Local Similarity 49.0%; Pred. No. 24;
RESULT 1126
ID AAS45490 standard; DNA; 7823 BP.
DE Chemically pretreated genomic DNA associated with cell cycle #98.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.8; DB 4; Length 7823;
Best Local Similarity 45.1%; Pred. No. 24;
RESULT 1127
ID ABL34061 standard; DNA; 7823 BP.
DE Human immune system associated gene SEQ ID NO: 2034.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.8; DB 6; Length 7823;
Best Local Similarity 45.1%; Pred. No. 24;
RESULT 1128
ID ABK31493 standard; DNA; 7823 BP.
DE Signal transduction associated gene modified complementary DNA #168.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.8; DB 6; Length 7823;
Best Local Similarity 45.1%; Pred. No. 24;
RESULT 1129
ID ABK28418 standard; DNA; 7823 BP.
DE DNA transcription associated complementary genomic DNA #146.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.8; DB 6; Length 7823;
Best Local Similarity 45.1%; Pred. No. 24;
RESULT 1130
ID ADE84209 standard; DNA; 8020 BP.
DE Human lymphoid cell proliferative disorder gene derived DNA #145.
PN WO2003044226-A2.
PD 30-MAY-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.8; DB 10; Length 8020;
Best Local Similarity 46.8%; Pred. No. 24;
RESULT 1131
ID ADE84133 standard; DNA; 8020 BP.
DE Human lymphoid cell proliferative disorder gene derived DNA #69.
PN WO2003044226-A2.
PD 30-MAY-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.8; DB 10; Length 8020;
Best Local Similarity 46.8%; Pred. No. 24;
RESULT 1132
ID ADS89617 standard; DNA; 8020 BP.
DE Oligonucleotide of the invention SEQ ID NO:633.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.8; DB 13; Length 8020;
Best Local Similarity 46.8%; Pred. No. 24;
RESULT 1133
ID ADS89343 standard; DNA; 8020 BP.
DE Oligonucleotide of the invention SEQ ID NO:359.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.8; DB 13; Length 8020;
Best Local Similarity 46.8%; Pred. No. 24;
RESULT 1134
ID AAS46445 standard; DNA; 8952 BP.
DE Tumour suppressor gene derived chemically modified sequence #167.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.8; DB 4; Length 8952;
Best Local Similarity 43.4%; Pred. No. 25;
RESULT 1135
ID ABL32687 standard; DNA; 8962 BP.
DE Human immune system associated gene SEQ ID NO: 660.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.8; DB 6; Length 8962;
Best Local Similarity 43.3%; Pred. No. 25;
RESULT 1136
ID ABL33513 standard; DNA; 11092 BP.
DE Human immune system associated gene SEQ ID NO: 1486.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.8; DB 6; Length 11092;
Best Local Similarity 44.5%; Pred. No. 25;
RESULT 1137
ID ABL70570 standard; DNA; 24939 BP.
DE Chemically treated cell signalling DNA sequence complementary to#230.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.8; DB 6; Length 24939;
Best Local Similarity 41.8%; Pred. No. 29;
RESULT 1138
ID ADE43582 standard; DNA; 128034 BP.
DE Polymorphic human IDE genomic sequence, SEQ ID 187.
PN WO2003054143-A2.
PD 03-JUL-2003.
PA (NEUR-) NEUROGENETICS INC.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 3.3%; Score 44.8; DB 10; Length 128034;
Best Local Similarity 58.1%; Pred. No. 37;
RESULT 1139
ID ADE43581 standard; DNA; 128034 BP.
DE Human IDE genomic sequence, SEQ ID 186.
PN WO2003054143-A2.
PD 03-JUL-2003.
PA (NEUR-) NEUROGENETICS INC.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 3.3%; Score 44.8; DB 10; Length 128034;
Best Local Similarity 58.1%; Pred. No. 37;
RESULT 1140
ID ADH54059 standard; DNA; 128034 BP.
DE Human IDE gene DNA sequence SeqID186.
PN US2003224380-A1.
PD 04-DEC-2003.
PA (GEHO) GEN HOSPITAL CORP.

Query Match 3.3%; Score 44.8; DB 12; Length 128034;
Best Local Similarity 58.1%; Pred. No. 37;
RESULT 1141
ID ADH54060 standard; DNA; 128034 BP.
DE Human IDE gene variant DNA sequence SeqID187.
PN US2003224380-A1.
PD 04-DEC-2003.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 3.3%; Score 44.8; DB 12; Length 128034;
Best Local Similarity 58.1%; Pred. No. 37;
RESULT 1142
ID ADE43315 standard; DNA; 202100 BP.
DE Human IDE/ KNSL1 genomic sequence, SEQ ID 484.
PN WO2003054143-A2.
PD 03-JUL-2003.
PA (NEUR-) NEUROGENETICS INC.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 3.3%; Score 44.8; DB 10; Length 202100;
Best Local Similarity 58.1%; Pred. No. 39;
RESULT 1143
ID ADH54357 standard; DNA; 202100 BP.
DE Human IDE/KNSL1 gene DNA sequence SeqID484.
PN US2003224380-A1.
PD 04-DEC-2003.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 3.3%; Score 44.8; DB 12; Length 202100;
Best Local Similarity 58.1%; Pred. No. 39;
RESULT 1144
ID ADI71847 standard; DNA; 363 BP.
DE Human ovarian cancer DNA marker #4589.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.3%; Score 44.6; DB 5; Length 363;
Best Local Similarity 43.2%; Pred. No. 17;
RESULT 1145
ID ADL36998 standard; DNA; 363 BP.
DE Human ovarian cancer DNA marker #10888.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.3%; Score 44.6; DB 5; Length 363;
Best Local Similarity 43.2%; Pred. No. 17;
RESULT 1146
ID ABX39417 standard; cDNA; 393 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #4582.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 3.3%; Score 44.6; DB 8; Length 393;
Best Local Similarity 48.0%; Pred. No. 17;
RESULT 1147
ID ADL43858 standard; DNA; 465 BP.
DE Human ovarian cancer DNA marker #17748.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.3%; Score 44.6; DB 5; Length 465;
Best Local Similarity 53.8%; Pred. No. 17;
RESULT 1148
ID AAS46621 standard; DNA; 6031 BP.
DE Tumour suppressor gene derived chemically modified sequence #343.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.6; DB 4; Length 6031;
Best Local Similarity 49.2%; Pred. No. 25;
RESULT 1149
ID ABN80275 standard; DNA; 6452 BP.
DE Human chemically modified disease associated gene SEQ ID NO 292.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.6; DB 6; Length 6452;
Best Local Similarity 46.9%; Pred. No. 26;
RESULT 1150
ID ABL32310 standard; DNA; 6853 BP.
DE Human immune system associated gene SEQ ID NO: 283.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.6; DB 6; Length 6853;
Best Local Similarity 46.0%; Pred. No. 26;
RESULT 1151
ID ABL54331 standard; DNA; 6853 BP.
DE Chemically treated apoptosis gene #16.
PN WO200177164-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.6; DB 6; Length 6853;
Best Local Similarity 46.0%; Pred. No. 26;
RESULT 1152
ID ABL32028 standard; DNA; 7351 BP.
DE Human immune system associated gene SEQ ID NO: 1.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.6; DB 6; Length 7351;
Best Local Similarity 44.4%; Pred. No. 26;
RESULT 1153
ID ABZ10245 standard; DNA; 8056 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #385.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.6; DB 8; Length 8056;
Best Local Similarity 45.5%; Pred. No. 27;
RESULT 1154
ID ABL92302 standard; DNA; 8607 BP.
DE Chemically treated DNA repair gene fragment#56.
PN WO200181622-A2.
PD 01-NOV-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.6; DB 6; Length 8607;
Best Local Similarity 53.8%; Pred. No. 27;
RESULT 1155
ID ABL49371 standard; DNA; 8607 BP.
DE Human polynucleotide associated with DNA replication SEQ ID NO 71.
PN WO200177377-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.6; DB 6; Length 8607;
Best Local Similarity 53.8%; Pred. No. 27;
RESULT 1156
ID ABQ67026 standard; DNA; 11964 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 56.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.6; DB 6; Length 11964;
Best Local Similarity 50.2%; Pred. No. 28;
RESULT 1157
ID ABL32631 standard; DNA; 14987 BP.
DE Human immune system associated gene SEQ ID NO: 604.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.6; DB 6; Length 14987;
Best Local Similarity 46.3%; Pred. No. 29;
RESULT 1158
ID AAS45388 standard; DNA; 15732 BP.
DE Chemically pretreated genomic DNA associated with cell cycle #47.
PN WO200168911-A2.

PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.6; DB 4; Length 15732;
Best Local Similarity 44.6%; Pred. No. 29;
RESULT 1159
ID ABK28233 standard; DNA; 15732 BP.
DE DNA transcription associated genomic DNA #54.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.6; DB 6; Length 15732;
Best Local Similarity 44.6%; Pred. No. 29;
RESULT 1160
ID ABL33681 standard; DNA; 15951 BP.
DE Human immune system associated gene SEQ ID NO: 1654.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.6; DB 6; Length 15951;
Best Local Similarity 44.3%; Pred. No. 30;
RESULT 1161
ID ABL34581 standard; DNA; 15951 BP.
DE Human metastasis associated gene SEQ ID NO: 134.
PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.6; DB 6; Length 15951;
Best Local Similarity 44.3%; Pred. No. 30;
RESULT 1162
ID ABL70374 standard; DNA; 15951 BP.
DE Chemically treated cell signalling DNA sequence complementary to#132.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.6; DB 6; Length 15951;
Best Local Similarity 44.3%; Pred. No. 30;
RESULT 1163
ID ADS99842 standard; DNA; 15951 BP.
DE Complement of bisulphite treated metastasis-associated human gene #67.
PN US2003148327-A1.
PD 07-AUG-2003.
PA (OLEK/) OLEK A.
PA (PIEP/) PIEPENBROCK C.
PA (BERL/) BERLIN K.
Query Match 3.3%; Score 44.6; DB 7; Length 15951;
Best Local Similarity 44.3%; Pred. No. 30;
RESULT 1164
ID ABL32575 standard; DNA; 17959 BP.
DE Human immune system associated gene SEQ ID NO: 548.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.6; DB 6; Length 17959;
Best Local Similarity 47.1%; Pred. No. 30;
RESULT 1165
ID ABL54342 standard; DNA; 17959 BP.
DE Chemically treated apoptosis gene complementary to gene #21.
PN WO200177164-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.6; DB 6; Length 17959;
Best Local Similarity 47.1%; Pred. No. 30;
RESULT 1166
ID ABL32626 standard; DNA; 19082 BP.
DE Human immune system associated gene SEQ ID NO: 599.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.6; DB 6; Length 19082;
Best Local Similarity 46.7%; Pred. No. 30;
RESULT 1167
ID AAT72882 standard; cDNA; 19124 BP.
DE Plasmodium var-7 gene.
PN WO9640766-A2.
PD 19-DEC-1996.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 3.3%; Score 44.6; DB 2; Length 19124;
Best Local Similarity 46.1%; Pred. No. 30;
RESULT 1168
ID AAZ98287 standard; DNA; 19124 BP.
DE Plasmodium var-7 polypeptide encoding DNA.
PN US5993827-A.
PD 30-NOV-1999.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 3.3%; Score 44.6; DB 3; Length 19124;
Best Local Similarity 46.1%; Pred. No. 30;
RESULT 1169
ID ABL34124 standard; DNA; 73334 BP.
DE Human immune system associated gene SEQ ID NO: 2097.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.6; DB 6; Length 73334;
Best Local Similarity 43.9%; Pred. No. 37;
RESULT 1170
ID ABL92318 standard; DNA; 73334 BP.
DE Chemically treated DNA repair gene fragment#64.
PN WO200181622-A2.
PD 01-NOV-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.6; DB 6; Length 73334;
Best Local Similarity 43.9%; Pred. No. 37;
RESULT 1171
ID ABL34175 standard; DNA; 113515 BP.
DE Human immune system associated gene SEQ ID NO: 2148.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.6; DB 6; Length 113515;
Best Local Similarity 43.3%; Pred. No. 40;
RESULT 1172
ID ADQ59452 standard; DNA; 168198 BP.
DE Human cancer-associated (CA) gene sequence SEQ ID NO:88.
PN WO2004058288-A1.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.3%; Score 44.6; DB 12; Length 168198;
Best Local Similarity 46.6%; Pred. No. 42;
RESULT 1173
ID ABX48619 standard; cDNA; 397 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #13784.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 3.3%; Score 44.4; DB 8; Length 397;
Best Local Similarity 52.7%; Pred. No. 19;
RESULT 1174
ID ADI72227 standard; DNA; 647 BP.
DE Human ovarian cancer DNA marker #4969.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.3%; Score 44.4; DB 5; Length 647;
Best Local Similarity 42.9%; Pred. No. 20;
RESULT 1175
ID ADL37372 standard; DNA; 647 BP.
DE Human ovarian cancer DNA marker #11262.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.3%; Score 44.4; DB 5; Length 647;
Best Local Similarity 42.9%; Pred. No. 20;
RESULT 1176

ID ADB59228 standard; DNA; 2217 BP.
DE Toxicity-related gene, SEQ ID 4254.
PN WO2003064624-A2.
PD 07-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 3.3%; Score 44.4; DB 10; Length 2217;
Best Local Similarity 54.2%; Pred. No. 24;
RESULT 1177
ID ABT42483 standard; DNA; 2217 BP.
DE Toxicity modelling related rat gene SEQ ID No 2185.
PN WO200295000-A2.
PD 28-NOV-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 3.3%; Score 44.4; DB 10; Length 2217;
Best Local Similarity 54.2%; Pred. No. 24;
RESULT 1178
ID ADS89709 standard; DNA; 2526 BP.
DE Oligonucleotide of the invention SEQ ID NO:725.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.4; DB 13; Length 2526;
Best Local Similarity 45.6%; Pred. No. 25;
RESULT 1179
ID ADS91270 standard; DNA; 2648 BP.
DE alpha-1 tubulin coding sequence, SEQ ID 166.
PN WO2004074479-A1.
PD 02-SEP-2004.
PA (PHYL-) PHYLOGICA LTD.
Query Match 3.3%; Score 44.4; DB 13; Length 2648;
Best Local Similarity 44.9%; Pred. No. 25;
RESULT 1180
ID ABL33598 standard; DNA; 5487 BP.
DE Human immune system associated gene SEQ ID NO: 1571.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.4; DB 6; Length 5487;
Best Local Similarity 47.2%; Pred. No. 28;
RESULT 1181
ID ABL32603 standard; DNA; 5912 BP.
DE Human immune system associated gene SEQ ID NO: 576.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.4; DB 6; Length 5912;
Best Local Similarity 45.4%; Pred. No. 28;
RESULT 1182
ID ABL32862 standard; DNA; 6132 BP.
DE Human immune system associated gene SEQ ID NO: 835.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.4; DB 6; Length 6132;
Best Local Similarity 46.4%; Pred. No. 28;
RESULT 1183
ID ABL33587 standard; DNA; 6227 BP.
DE Human immune system associated gene SEQ ID NO: 1560.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.4; DB 6; Length 6227;
Best Local Similarity 46.8%; Pred. No. 28;
RESULT 1184
ID ABL92261 standard; DNA; 6227 BP.
DE Chemically treated DNA repair gene fragment complementary to#35.
PN WO200181622-A2.
PD 01-NOV-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.4; DB 6; Length 6227;
Best Local Similarity 46.8%; Pred. No. 28;
RESULT 1185
ID ABL34025 standard; DNA; 6375 BP.
DE Human immune system associated gene SEQ ID NO: 1998.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.4; DB 6; Length 6375;
Best Local Similarity 43.3%; Pred. No. 28;
RESULT 1186
ID ABL32985 standard; DNA; 6465 BP.
DE Human immune system associated gene SEQ ID NO: 958.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.4; DB 6; Length 6465;
Best Local Similarity 44.5%; Pred. No. 28;
RESULT 1187
ID ABK40036 standard; DNA; 7374 BP.
DE Human chemically pretreated gene sequence #59 strand 2.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.4; DB 6; Length 7374;
Best Local Similarity 48.4%; Pred. No. 29;
RESULT 1188
ID ABL70602 standard; DNA; 7374 BP.
DE Chemically treated cell signalling DNA sequence complementary to#246.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.4; DB 6; Length 7374;
Best Local Similarity 48.4%; Pred. No. 29;
RESULT 1189
ID ABX77219 standard; DNA; 10094 BP.
DE 5' sequence flanking human MDR1 contig.
PN WO200283897-A1.
PD 24-OCT-2002.
PA (GENE-) GENE STREAM PTY LTD.
Query Match 3.3%; Score 44.4; DB 10; Length 10094;
Best Local Similarity 45.5%; Pred. No. 30;
RESULT 1190
ID ABL34122 standard; DNA; 10329 BP.
DE Human immune system associated gene SEQ ID NO: 2095.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.4; DB 6; Length 10329;
Best Local Similarity 46.9%; Pred. No. 30;
RESULT 1191
ID AAS63313 standard; DNA; 12409 BP.
DE Chemically pretreated metabolism associated gene #8.
PN WO200176451-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.4; DB 6; Length 12409;
Best Local Similarity 46.0%; Pred. No. 31;
RESULT 1192
ID ABL33926 standard; DNA; 13427 BP.
DE Human immune system associated gene SEQ ID NO: 1899.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.4; DB 6; Length 13427;
Best Local Similarity 46.2%; Pred. No. 32;
RESULT 1193
ID ABL32615 standard; DNA; 13584 BP.
DE Human immune system associated gene SEQ ID NO: 588.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.4; DB 6; Length 13584;
Best Local Similarity 45.4%; Pred. No. 32;
RESULT 1194
ID ABL32362 standard; DNA; 15674 BP.
DE Human immune system associated gene SEQ ID NO: 335.

PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.4; DB 6; Length 15674;
Best Local Similarity 48.6%; Pred. No. 32;
RESULT 1195
ID ABL34476 standard; DNA; 15674 BP.
DE Human metastasis associated gene SEQ ID NO: 29.
PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.4; DB 6; Length 15674;
Best Local Similarity 48.6%; Pred. No. 32;
RESULT 1196
ID ABL70513 standard; DNA; 15674 BP.
DE Chemically treated cell signalling DNA sequence#202.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.4; DB 6; Length 15674;
Best Local Similarity 48.6%; Pred. No. 32;
RESULT 1197
ID ADS99737 standard; DNA; 15674 BP.
DE Bisulphite treated human gene associated with metastasis #15.
PN US2003148327-A1.
PD 07-AUG-2003.
PA (OLEK/) OLEK A.
PA (PIEP/) PIEPENBROCK C.
PA (BERL/) BERLIN K.
Query Match 3.3%; Score 44.4; DB 7; Length 15674;
Best Local Similarity 48.6%; Pred. No. 32;
RESULT 1198
ID ADB54118 standard; DNA; 16579 BP.
DE Pretreated genomic DNA region 42.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.4; DB 10; Length 16579;
Best Local Similarity 46.0%; Pred. No. 33;
RESULT 1199
ID ADB54246 standard; DNA; 16579 BP.
DE Pretreated genomic DNA region 170.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.4; DB 10; Length 16579;
Best Local Similarity 46.0%; Pred. No. 33;
RESULT 1200
ID ADE37773 standard; DNA; 16579 BP.
DE Human chemically treated TPEF nucleotide sequence SEQ ID NO:19.
PN WO2003072820-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.4; DB 10; Length 16579;
Best Local Similarity 46.0%; Pred. No. 33;
RESULT 1201
ID ADE37763 standard; DNA; 16579 BP.
DE Human chemically treated TPEF nucleotide sequence SEQ ID NO:9.
PN WO2003072820-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.4; DB 10; Length 16579;
Best Local Similarity 46.0%; Pred. No. 33;
RESULT 1202
ID ADS89274 standard; DNA; 16579 BP.
DE Oligonucleotide of the invention SEQ ID NO:290.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.4; DB 13; Length 16579;
Best Local Similarity 46.0%; Pred. No. 33;
RESULT 1203
ID ADS89548 standard; DNA; 16579 BP.
DE Oligonucleotide of the invention SEQ ID NO:564.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.4; DB 13; Length 16579;
Best Local Similarity 46.0%; Pred. No. 33;
RESULT 1204
ID AAS46314 standard; DNA; 16750 BP.
DE Tumour suppressor gene derived chemically modified sequence #36.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.4; DB 4; Length 16750;
Best Local Similarity 46.0%; Pred. No. 33;
RESULT 1205
ID ABL32521 standard; DNA; 16750 BP.
DE Human immune system associated gene SEQ ID NO: 494.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.4; DB 6; Length 16750;
Best Local Similarity 46.0%; Pred. No. 33;
RESULT 1206
ID ABL33053 standard; DNA; 17131 BP.
DE Human immune system associated gene SEQ ID NO: 1026.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.4; DB 6; Length 17131;
Best Local Similarity 46.7%; Pred. No. 33;
RESULT 1207
ID ABL34027 standard; DNA; 17594 BP.
DE Human immune system associated gene SEQ ID NO: 2000.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.4; DB 6; Length 17594;
Best Local Similarity 47.4%; Pred. No. 33;
RESULT 1208
ID AAS45323 standard; DNA; 17848 BP.
DE Chemically pretreated complementary DNA associated with cell cycle #14.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.4; DB 4; Length 17848;
Best Local Similarity 44.6%; Pred. No. 33;
RESULT 1209
ID ABK39976 standard; DNA; 17848 BP.
DE Human chemically pretreated gene sequence #29 strand 2.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.4; DB 6; Length 17848;
Best Local Similarity 44.6%; Pred. No. 33;
RESULT 1210
ID ABK28164 standard; DNA; 17848 BP.
DE DNA transcription associated complementary genomic DNA #19.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.4; DB 6; Length 17848;
Best Local Similarity 44.6%; Pred. No. 33;
RESULT 1211
ID ABL32313 standard; DNA; 18683 BP.
DE Human immune system associated gene SEQ ID NO: 286.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.4; DB 6; Length 18683;
Best Local Similarity 44.3%; Pred. No. 33;
RESULT 1212
ID ABL54334 standard; DNA; 18683 BP.
DE Chemically treated apoptosis gene complementary to gene #17.

PN WO200177164-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.4; DB 6; Length 18683;
Best Local Similarity 44.3%; Pred. No. 33;
RESULT 1213
ID ABN80016 standard; DNA; 19345 BP.
DE Human chemically modified disease associated gene SEQ ID NO 33.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.4; DB 6; Length 19345;
Best Local Similarity 46.5%; Pred. No. 33;
RESULT 1214
ID ABN85767 standard; cDNA; 83698 BP.
DE Arabidopsis yellow stripe1-like 4 encoding cDNA SEQ ID NO 9.
PN WO200240688-A2.
PD 23-MAY-2002.
PA (UYYA) UNIV YALE.
Query Match 3.3%; Score 44.4; DB 6; Length 83698;
Best Local Similarity 62.7%; Pred. No. 42;
RESULT 1215
ID ADQ97050 standard; DNA; 687411 BP.
DE Human cancer associated sequence HD08-001, SEQ ID 26.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.3%; Score 44.4; DB 12; Length 110000;
Best Local Similarity 46.5%; Pred. No. 43;
RESULT 1216
ID ACF62751 standard; DNA; 177380 BP.
DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:683.
PN WO2003013534-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 3.3%; Score 44.4; DB 8; Length 177380;
Best Local Similarity 45.5%; Pred. No. 47;
RESULT 1217
ID ADB20870 standard; DNA; 177380 BP.
DE MRP1 based cancer related nucleic acid SEQ ID NO:683.
PN WO2003013533-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 3.3%; Score 44.4; DB 8; Length 177380;
Best Local Similarity 45.5%; Pred. No. 47;
RESULT 1218
ID ADB87959 standard; DNA; 177380 BP.
DE Human UGT1A1 gene sequence SEQ ID NO:683.
PN WO2003013536-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 3.3%; Score 44.4; DB 10; Length 177380;
Best Local Similarity 45.5%; Pred. No. 47;
RESULT 1219
ID ADB96942 standard; DNA; 177380 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:683.
PN WO2003013537-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 3.3%; Score 44.4; DB 10; Length 177380;
Best Local Similarity 45.5%; Pred. No. 47;
RESULT 1220
ID ADB92133 standard; DNA; 177380 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:683.
PN WO2003013535-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 3.3%; Score 44.4; DB 10; Length 177380;
Best Local Similarity 45.5%; Pred. No. 47;
RESULT 1221
ID ADL37087 standard; DNA; 410 BP.
DE Human ovarian cancer DNA marker #10977.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.3%; Score 44.2; DB 5; Length 410;
Best Local Similarity 43.1%; Pred. No. 20;
RESULT 1222
ID ADI71936 standard; DNA; 410 BP.
DE Human ovarian cancer DNA marker #4678.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.3%; Score 44.2; DB 5; Length 410;
Best Local Similarity 43.1%; Pred. No. 20;
RESULT 1223
ID ADL43834 standard; DNA; 461 BP.
DE Human ovarian cancer DNA marker #17724.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.3%; Score 44.2; DB 5; Length 461;
Best Local Similarity 61.4%; Pred. No. 21;
RESULT 1224
ID ADL10644 standard; cDNA; 495 BP.
DE Cat flea hindgut and malpighian tubule (HMT) protein cDNA #1049.
PN US2004067516-A1.
PD 08-APR-2004.
PA (BRAN/) BRANDT K S.
PA (GAIN/) GAINES P J.
PA (STIN/) STINCHCOMB D T.
PA (WISN/) WISNEWSKI N.
Query Match 3.3%; Score 44.2; DB 12; Length 495;
Best Local Similarity 48.0%; Pred. No. 21;
RESULT 1225
ID ADC20845 standard; DNA; 1238 BP.
DE Human secreted protein-related DNA sequence #263.
PN WO200292787-A2.
PD 21-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 44.2; DB 10; Length 1238;
Best Local Similarity 60.3%; Pred. No. 24;
RESULT 1226
ID ABT16982 standard; DNA; 1238 BP.
DE Human secreted protein-related DNA sequence - SEQ ID No 336.
PN WO200277188-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 44.2; DB 10; Length 1238;
Best Local Similarity 60.3%; Pred. No. 24;
RESULT 1227
ID ABZ67930 standard; DNA; 1238 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1453.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 44.2; DB 10; Length 1238;
Best Local Similarity 60.3%; Pred. No. 24;
RESULT 1228
ID ACA28992 standard; DNA; 1425 BP.
DE Prokaryotic essential gene #10649.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 3.3%; Score 44.2; DB 8; Length 1425;
Best Local Similarity 50.7%; Pred. No. 25;
RESULT 1229
ID AAN80917 standard; cDNA; 1540 BP.
DE Sequence of the 3'-end of the human glucocorticoid receptor beta cDNA
DE (beta-hGR).
PN WO8803168-A.
PD 05-MAY-1988.
PA (SALK) SALK INST BIOLOGICAL STUDIES.
Query Match 3.3%; Score 44.2; DB 1; Length 1540;
Best Local Similarity 75.3%; Pred. No. 25;
RESULT 1230

ID AAV38740 standard; cDNA; 1584 BP.
DE Complementary strand of cDNA nfSPI1-1584 encoding a SPI protein.
PN WO9820034-A2.
PD 14-MAY-1998.
PA (HESK-) HESKA CORP.
Query Match 3.3%; Score 44.2; DB 2; Length 1584;
Best Local Similarity 47.7%; Pred. No. 25;
RESULT 1231
ID AAV38739 standard; cDNA; 1584 BP.
DE cDNA nfSPI1-1584 encoding a flea serine protease inhibitor protein.
PN WO9820034-A2.
PD 14-MAY-1998.
PA (HESK-) HESKA CORP.
Query Match 3.3%; Score 44.2; DB 2; Length 1584;
Best Local Similarity 47.7%; Pred. No. 25;
RESULT 1232
ID ADQ25468 standard; DNA; 2341 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 8288.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.3%; Score 44.2; DB 12; Length 2341;
Best Local Similarity 68.5%; Pred. No. 27;
RESULT 1233
ID ADQ24153 standard; DNA; 2341 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6973.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.3%; Score 44.2; DB 12; Length 2341;
Best Local Similarity 68.5%; Pred. No. 27;
RESULT 1234
ID AAS46320 standard; DNA; 2865 BP.
DE Tumour suppressor gene derived chemically modified sequence #42.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.2; DB 4; Length 2865;
Best Local Similarity 44.9%; Pred. No. 27;
RESULT 1235
ID ABN80051 standard; DNA; 2865 BP.
DE Human chemically modified disease associated gene SEQ ID NO 68.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.2; DB 6; Length 2865;
Best Local Similarity 44.9%; Pred. No. 27;
RESULT 1236
ID ABQ67051 standard; DNA; 3046 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 81.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.2; DB 6; Length 3046;
Best Local Similarity 46.8%; Pred. No. 28;
RESULT 1237
ID ABL32133 standard; DNA; 5421 BP.
DE Human immune system associated gene SEQ ID NO: 106.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.2; DB 6; Length 5421;
Best Local Similarity 49.8%; Pred. No. 30;
RESULT 1238
ID AAD28388 standard; DNA; 6123 BP.
DE Human chemically treated genomic DNA #29.
PN WO200202809-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.2; DB 6; Length 6123;
Best Local Similarity 44.5%; Pred. No. 31;
RESULT 1239
ID ABL32972 standard; DNA; 6145 BP.
DE Human immune system associated gene SEQ ID NO: 945.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.2; DB 6; Length 6145;
Best Local Similarity 51.4%; Pred. No. 31;
RESULT 1240
ID ABZ10060 standard; DNA; 6289 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #200.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.2; DB 8; Length 6289;
Best Local Similarity 46.8%; Pred. No. 31;
RESULT 1241
ID ABZ10194 standard; DNA; 6343 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #334.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.2; DB 8; Length 6343;
Best Local Similarity 49.8%; Pred. No. 31;
RESULT 1242
ID ADS89670 standard; DNA; 6343 BP.
DE Oligonucleotide of the invention SEQ ID NO:686.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.2; DB 13; Length 6343;
Best Local Similarity 49.8%; Pred. No. 31;
RESULT 1243
ID ABQ66987 standard; DNA; 6652 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 17.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.2; DB 6; Length 6652;
Best Local Similarity 45.3%; Pred. No. 31;
RESULT 1244
ID ABL33602 standard; DNA; 6821 BP.
DE Human immune system associated gene SEQ ID NO: 1575.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.2; DB 6; Length 6821;
Best Local Similarity 53.1%; Pred. No. 31;
RESULT 1245
ID ABN80025 standard; DNA; 8453 BP.
DE Human chemically modified disease associated gene SEQ ID NO 42.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.2; DB 6; Length 8453;
Best Local Similarity 46.8%; Pred. No. 32;
RESULT 1246
ID ABL32210 standard; DNA; 8889 BP.
DE Human immune system associated gene SEQ ID NO: 183.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.2; DB 6; Length 8889;
Best Local Similarity 44.7%; Pred. No. 33;
RESULT 1247
ID AAS46502 standard; DNA; 9289 BP.
DE Tumour suppressor gene derived chemically modified sequence #224.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.2; DB 4; Length 9289;
Best Local Similarity 46.8%; Pred. No. 33;
RESULT 1248
ID ADE84122 standard; DNA; 9289 BP.
DE Human lymphoid cell proliferative disorder gene derived DNA #58.

PN WO2003044226-A2.
PD 30-MAY-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.2; DB 10; Length 9289;
Best Local Similarity 46.8%; Pred. No. 33;
RESULT 1249
ID ABL33014 standard; DNA; 17967 BP.
DE Human immune system associated gene SEQ ID NO: 987.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.2; DB 6; Length 17967;
Best Local Similarity 45.3%; Pred. No. 36;
RESULT 1250
ID ABL70502 standard; DNA; 18283 BP.
DE Chemically treated cell signalling DNA sequence complementary to#196.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.2; DB 6; Length 18283;
Best Local Similarity 45.1%; Pred. No. 36;
RESULT 1251
ID AAS61363 standard; DNA; 18283 BP.
DE Human gene regulation-associated gene oligonucleotide #318.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44.2; DB 6; Length 18283;
Best Local Similarity 45.1%; Pred. No. 36;
RESULT 1252
ID AAD36834 standard; DNA; 59215 BP.
DE Human transporter protein genomic DNA.
Query Match 3.3%; Score 44.2; DB 8; Length 59215;
Best Local Similarity 48.2%; Pred. No. 43;
RESULT 1253
Query Match 3.3%; Score 44.2; DB 6; Length 110000;
Best Local Similarity 46.8%; Pred. No. 48;
RESULT 1254
ID ABD32602 standard; DNA; 277616 BP.
DE Human cancer-associated genomic DNA HD7-221.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.3%; Score 44.2; DB 13; Length 277616;
Best Local Similarity 44.4%; Pred. No. 55;
RESULT 1255
ID ADL37437 standard; DNA; 469 BP.
DE Human ovarian cancer DNA marker #11327.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.3%; Score 44; DB 5; Length 469;
Best Local Similarity 60.2%; Pred. No. 23;
RESULT 1256
ID ADI72293 standard; DNA; 469 BP.
DE Human ovarian cancer DNA marker #5035.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.3%; Score 44; DB 5; Length 469;
Best Local Similarity 60.2%; Pred. No. 23;
RESULT 1257
ID ACN47785 standard; cDNA; 557 BP.
DE Cotton primed seed EST Clone ID: LIB3825-015-Q1-N6-A5, SEQ:2566.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 3.3%; Score 44; DB 13; Length 557;
Best Local Similarity 52.8%; Pred. No. 24;
RESULT 1258
ID AAA70232 standard; DNA; 579 BP.
DE Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:365.
PN WO200025728-A2.
PD 11-MAY-2000.
PA (HOFF/) HOFFMAN S.
PA (CARU/) CARUCCI D.
PA (GARD/) GARDNER M.
PA (VENT/) VENTER J C.
Query Match 3.3%; Score 44; DB 3; Length 579;
Best Local Similarity 47.6%; Pred. No. 24;
RESULT 1259
ID AAS00668 standard; cDNA; 1909 BP.
DE Human INTERCEPT 309 cDNA.
PN WO200129088-A1.
PD 26-APR-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 3.3%; Score 44; DB 4; Length 1909;
Best Local Similarity 56.1%; Pred. No. 28;
RESULT 1260
ID ACD66731 standard; cDNA; 1909 BP.
DE Secreted polypeptide-related cDNA #23.
PN US2003022279-A1.
PD 30-JAN-2003.
PA (FRAS/) FRASER C C.
PA (BARN/) BARNES T M.
PA (SHAR/) SHARP J D.
PA (KIRS/) KIRST S J.
PA (MYER/) MYERS P S.
PA (LEIB/) LEIBY K R.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (WRIG/) WRIGHTON N.
PA (MACK/) MACKAY C R.
PA (GOOD/) GOODEARL A D J.
Query Match 3.3%; Score 44; DB 8; Length 1909;
Best Local Similarity 56.1%; Pred. No. 28;
RESULT 1261
ID ADQ10174 standard; cDNA; 1909 BP.
DE Human polynucleotide #24.
PN US2004121396-A1.
PD 24-JUN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 3.3%; Score 44; DB 12; Length 1909;
Best Local Similarity 56.1%; Pred. No. 28;
RESULT 1262
ID ABV23236 standard; cDNA; 2105 BP.
DE Human prostate expression marker cDNA 23227.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.3%; Score 44; DB 5; Length 2105;
Best Local Similarity 56.1%; Pred. No. 29;
RESULT 1263
ID ABV29079 standard; cDNA; 2109 BP.
DE Human prostate expression marker cDNA 29070.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.3%; Score 44; DB 5; Length 2109;
Best Local Similarity 56.1%; Pred. No. 29;
RESULT 1264
ID ABL32178 standard; DNA; 5536 BP.
DE Human immune system associated gene SEQ ID NO: 151.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44; DB 6; Length 5536;
Best Local Similarity 50.4%; Pred. No. 33;
RESULT 1265
ID AAS45313 standard; DNA; 5979 BP.
DE Chemically pretreated complementary DNA associated with cell cycle #9.
PN WO200168911-A2.
PD 20-SEP-2001.

PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44; DB 4; Length 5979;
Best Local Similarity 45.0%; Pred. No. 34;
RESULT 1266
ID ABK28152 standard; DNA; 5979 BP.
DE DNA transcription associated complementary genomic DNA #13.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44; DB 6; Length 5979;
Best Local Similarity 45.0%; Pred. No. 34;
RESULT 1267
ID ABL33679 standard; DNA; 6070 BP.
DE Human immune system associated gene SEQ ID NO: 1652.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44; DB 6; Length 6070;
Best Local Similarity 46.8%; Pred. No. 34;
RESULT 1268
ID ABL34579 standard; DNA; 6070 BP.
DE Human metastasis associated gene SEQ ID NO: 132.
PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44; DB 6; Length 6070;
Best Local Similarity 46.8%; Pred. No. 34;
RESULT 1269
ID ABL70372 standard; DNA; 6070 BP.
DE Chemically treated cell signalling DNA sequence complementary to#131.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44; DB 6; Length 6070;
Best Local Similarity 46.8%; Pred. No. 34;
RESULT 1270
ID ABQ67130 standard; DNA; 6070 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 160.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44; DB 6; Length 6070;
Best Local Similarity 46.8%; Pred. No. 34;
RESULT 1271
ID ADS99840 standard; DNA; 6070 BP.
DE Complement of bisulphite treated metastasis-associated human gene #66.
PN US2003148327-A1.
PD 07-AUG-2003.
PA (OLEK/) OLEK A.
PA (PIEP/) PIEPENBROCK C.
PA (BERL/) BERLIN K.
Query Match 3.3%; Score 44; DB 7; Length 6070;
Best Local Similarity 46.8%; Pred. No. 34;
RESULT 1272
ID ABL34218 standard; DNA; 6077 BP.
DE Human immune system associated gene SEQ ID NO: 2191.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44; DB 6; Length 6077;
Best Local Similarity 44.8%; Pred. No. 34;
RESULT 1273
ID ABL33823 standard; DNA; 6113 BP.
DE Human immune system associated gene SEQ ID NO: 1796.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44; DB 6; Length 6113;
Best Local Similarity 45.2%; Pred. No. 34;
RESULT 1274
ID ABL33215 standard; DNA; 6249 BP.
DE Human immune system associated gene SEQ ID NO: 1188.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44; DB 6; Length 6249;
Best Local Similarity 47.8%; Pred. No. 34;
RESULT 1275
ID ABK31305 standard; DNA; 6249 BP.
DE Signal transduction associated gene modified complementary DNA #74.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44; DB 6; Length 6249;
Best Local Similarity 47.8%; Pred. No. 34;
RESULT 1276
ID ABL70556 standard; DNA; 6249 BP.
DE Chemically treated cell signalling DNA sequence complementary to#223.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44; DB 6; Length 6249;
Best Local Similarity 47.8%; Pred. No. 34;
RESULT 1277
ID ABN80159 standard; DNA; 6249 BP.
DE Human chemically modified disease associated gene SEQ ID NO 176.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44; DB 6; Length 6249;
Best Local Similarity 47.8%; Pred. No. 34;
RESULT 1278
ID ABL34117 standard; DNA; 7046 BP.
DE Human immune system associated gene SEQ ID NO: 2090.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44; DB 6; Length 7046;
Best Local Similarity 47.8%; Pred. No. 35;
RESULT 1279
ID ABN80289 standard; DNA; 7046 BP.
DE Human chemically modified disease associated gene SEQ ID NO 306.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44; DB 6; Length 7046;
Best Local Similarity 47.8%; Pred. No. 35;
RESULT 1280
ID ABN80224 standard; DNA; 8067 BP.
DE Human chemically modified disease associated gene SEQ ID NO 241.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44; DB 6; Length 8067;
Best Local Similarity 43.9%; Pred. No. 35;
RESULT 1281
ID AAQ62924 standard; cDNA; 8920 BP.
DE Carbamoyl-phosphate-synthetase II.
PN WO9412643-A1.
PD 09-JUN-1994.
PA (UNIX) UNISEARCH LTD.
Query Match 3.3%; Score 44; DB 2; Length 8920;
Best Local Similarity 50.3%; Pred. No. 36;
RESULT 1282
ID AAS45502 standard; DNA; 11812 BP.
DE Chemically pretreated genomic DNA associated with cell cycle #104.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44; DB 4; Length 11812;
Best Local Similarity 47.4%; Pred. No. 37;
RESULT 1283
ID AAS46742 standard; DNA; 11812 BP.
DE Tumour suppressor gene derived chemically modified sequence #466.
PN WO200168912-A2.
PD 20-SEP-2001.

PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44; DB 4; Length 11812;
Best Local Similarity 47.4%; Pred. No. 37;
RESULT 1284
ID ABL34119 standard; DNA; 11812 BP.
DE Human immune system associated gene SEQ ID NO: 2092.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44; DB 6; Length 11812;
Best Local Similarity 47.4%; Pred. No. 37;
RESULT 1285
ID ABK28432 standard; DNA; 11812 BP.
DE DNA transcription associated complementary genomic DNA #153.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44; DB 6; Length 11812;
Best Local Similarity 47.4%; Pred. No. 37;
RESULT 1286
ID AAS45395 standard; DNA; 11836 BP.
DE Chemically pretreated complementary DNA associated with cell cycle #50.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44; DB 4; Length 11836;
Best Local Similarity 44.6%; Pred. No. 37;
RESULT 1287
ID ABK28240 standard; DNA; 11836 BP.
DE DNA transcription associated complementary genomic DNA #57.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44; DB 6; Length 11836;
Best Local Similarity 44.6%; Pred. No. 37;
RESULT 1288
ID AAS46660 standard; DNA; 12578 BP.
DE Tumour suppressor gene derived chemically modified sequence #382.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44; DB 4; Length 12578;
Best Local Similarity 43.8%; Pred. No. 38;
RESULT 1289
ID ABL32487 standard; DNA; 17183 BP.
DE Human immune system associated gene SEQ ID NO: 460.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44; DB 6; Length 17183;
Best Local Similarity 44.5%; Pred. No. 39;
RESULT 1290
ID ABL34608 standard; DNA; 18585 BP.
DE Human metastasis associated gene SEQ ID NO: 161.
PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 44; DB 6; Length 18585;
Best Local Similarity 45.0%; Pred. No. 40;
RESULT 1291
ID ADS99869 standard; DNA; 18585 BP.
DE Bisulphite treated human gene associated with metastasis #81.
PN US2003148327-A1.
PD 07-AUG-2003.
PA (OLEK/) OLEK A.
PA (PIEP/) PIEPENBROCK C.
PA (BERL/) BERLIN K.
Query Match 3.3%; Score 44; DB 7; Length 18585;
Best Local Similarity 45.0%; Pred. No. 40;
RESULT 1292
ID ABD33125 standard; DNA; 58320 BP.
DE Human cancer-associated (CA) gene HD07-013.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.3%; Score 44; DB 13; Length 58320;
Best Local Similarity 50.0%; Pred. No. 47;
RESULT 1293
ID ABV47167 standard; cDNA; 230 BP.
DE Human prostate expression marker cDNA 47158.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.3%; Score 43.8; DB 5; Length 230;
Best Local Similarity 54.7%; Pred. No. 23;
RESULT 1294
ID AAX99162 standard; DNA; 516 BP.
DE DNA encoding N. meningitidis protein ORF82.
PN WO9936544-A2.
PD 22-JUL-1999.
PA (CHIR-) CHIRON SPA.
Query Match 3.3%; Score 43.8; DB 2; Length 516;
Best Local Similarity 47.9%; Pred. No. 26;
RESULT 1295
ID AAA81451 standard; DNA; 516 BP.
DE N. meningitidis MenB polynucleotide sequence ORF number 122.
PN WO200022430-A2.
PD 20-APR-2000.
PA (CHIR) CHIRON CORP.
Query Match 3.3%; Score 43.8; DB 3; Length 516;
Best Local Similarity 47.9%; Pred. No. 26;
RESULT 1296
ID AAX99163 standard; DNA; 729 BP.
DE DNA encoding N. meningitidis protein ORF82-1.
PN WO9936544-A2.
PD 22-JUL-1999.
PA (CHIR-) CHIRON SPA.
Query Match 3.3%; Score 43.8; DB 2; Length 729;
Best Local Similarity 47.9%; Pred. No. 27;
RESULT 1297
ID AAX99164 standard; DNA; 729 BP.
DE DNA encoding N. meningitidis protein ORF82a.
PN WO9936544-A2.
PD 22-JUL-1999.
PA (CHIR-) CHIRON SPA.
Query Match 3.3%; Score 43.8; DB 2; Length 729;
Best Local Similarity 47.9%; Pred. No. 27;
RESULT 1298
ID AAV19304 standard; cDNA; 889 BP.
DE Human p26 cDNA sequence.
PN JP09299092-A.
PD 25-NOV-1997.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 3.3%; Score 43.8; DB 2; Length 889;
Best Local Similarity 81.0%; Pred. No. 28;
RESULT 1299
ID AAC75917 standard; cDNA; 1501 BP.
DE Human ORFX ORF1472 polynucleotide sequence SEQ ID NO:2943.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 3.3%; Score 43.8; DB 3; Length 1501;
Best Local Similarity 60.5%; Pred. No. 30;
RESULT 1300
ID ABL56222 standard; DNA; 2619 BP.
DE AmEPV mRNA capping large subunit (AMV135) encoding sequence.
PN WO200212526-A2.
PD 14-FEB-2002.
PA (UYFL) UNIV FLORIDA.
Query Match 3.3%; Score 43.8; DB 6; Length 2619;
Best Local Similarity 44.2%; Pred. No. 33;
RESULT 1301
ID ABQ67089 standard; DNA; 3873 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 119.
PN WO200246454-A2.
PD 13-JUN-2002.

PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 43.8; DB 6; Length 3873;
Best Local Similarity 41.6%; Pred. No. 35;
RESULT 1302
ID ADS89338 standard; DNA; 4930 BP.
DE Oligonucleotide of the invention SEQ ID NO:354.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 43.8; DB 13; Length 4930;
Best Local Similarity 47.0%; Pred. No. 36;
RESULT 1303
ID AAA70189 standard; DNA; 5454 BP.
DE Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:322.
PN WO200025728-A2.
PD 11-MAY-2000.
PA (HOFF/) HOFFMAN S.
PA (CARU/) CARUCCI D.
PA (GARD/) GARDNER M.
PA (VENT/) VENTER J C.
Query Match 3.3%; Score 43.8; DB 3; Length 5454;
Best Local Similarity 44.7%; Pred. No. 36;
RESULT 1304
ID ABZ10144 standard; DNA; 5660 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #284.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 43.8; DB 8; Length 5660;
Best Local Similarity 47.4%; Pred. No. 37;
RESULT 1305
ID ACF62812 standard; DNA; 5666 BP.
DE Colon cancer analysis related genomic DNA SEQ ID NO:61.
PN WO2003014388-A2.
PD 20-FEB-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 43.8; DB 8; Length 5666;
Best Local Similarity 47.4%; Pred. No. 37;
RESULT 1306
ID ADS89495 standard; DNA; 6001 BP.
DE Oligonucleotide of the invention SEQ ID NO:511.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 43.8; DB 13; Length 6001;
Best Local Similarity 47.0%; Pred. No. 37;
RESULT 1307
ID ABK31361 standard; DNA; 6013 BP.
DE Signal transduction associated gene modified complementary DNA #102.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 43.8; DB 6; Length 6013;
Best Local Similarity 50.2%; Pred. No. 37;
RESULT 1308
ID AAS61265 standard; DNA; 6013 BP.
DE Human gene regulation-associated gene oligonucleotide #220.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 43.8; DB 6; Length 6013;
Best Local Similarity 50.2%; Pred. No. 37;
RESULT 1309
ID AAS45311 standard; DNA; 6046 BP.
DE Chemically pretreated complementary DNA associated with cell cycle #8.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 43.8; DB 4; Length 6046;
Best Local Similarity 76.1%; Pred. No. 37;
RESULT 1310
ID ABK28150 standard; DNA; 6046 BP.
DE DNA transcription associated complementary genomic DNA #12.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 43.8; DB 6; Length 6046;
Best Local Similarity 76.1%; Pred. No. 37;
RESULT 1311
ID ABL54343 standard; DNA; 6059 BP.
DE Chemically treated apoptosis gene #22.
PN WO200177164-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 43.8; DB 6; Length 6059;
Best Local Similarity 46.8%; Pred. No. 37;
RESULT 1312
ID ABL32366 standard; DNA; 6071 BP.
DE Human immune system associated gene SEQ ID NO: 339.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 43.8; DB 6; Length 6071;
Best Local Similarity 45.6%; Pred. No. 37;
RESULT 1313
ID ABL34482 standard; DNA; 6071 BP.
DE Human metastasis associated gene SEQ ID NO: 35.
PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 43.8; DB 6; Length 6071;
Best Local Similarity 45.6%; Pred. No. 37;
RESULT 1314
ID ABL70153 standard; DNA; 6071 BP.
DE Chemically treated cell signalling DNA sequence#22.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 43.8; DB 6; Length 6071;
Best Local Similarity 45.6%; Pred. No. 37;
RESULT 1315
ID ADS99743 standard; DNA; 6071 BP.
DE Bisulphite treated human gene associated with metastasis #18.
PN US2003148327-A1.
PD 07-AUG-2003.
PA (OLEK/) OLEK A.
PA (PIEP/) PIEPENBROCK C.
PA (BERL/) BERLIN K.
Query Match 3.3%; Score 43.8; DB 7; Length 6071;
Best Local Similarity 45.6%; Pred. No. 37;
RESULT 1316
ID AAS45465 standard; DNA; 6078 BP.
DE Chemically pretreated complementary DNA associated with cell cycle #85.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 43.8; DB 4; Length 6078;
Best Local Similarity 69.0%; Pred. No. 37;
RESULT 1317
ID ABL33890 standard; DNA; 6078 BP.
DE Human immune system associated gene SEQ ID NO: 1863.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 43.8; DB 6; Length 6078;
Best Local Similarity 69.0%; Pred. No. 37;
RESULT 1318
ID ABK28321 standard; DNA; 6078 BP.
DE DNA transcription associated genomic DNA #98.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 43.8; DB 6; Length 6078;
Best Local Similarity 69.0%; Pred. No. 37;
RESULT 1319
ID ABL32177 standard; DNA; 6378 BP.

DE Human immune system associated gene SEQ ID NO: 150.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 43.8; DB 6; Length 6378;
Best Local Similarity 44.5%; Pred. No. 37;
RESULT 1320
ID ABQ67028 standard; DNA; 6378 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 58.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 43.8; DB 6; Length 6378;
Best Local Similarity 44.5%; Pred. No. 37;
RESULT 1321
ID ABL33408 standard; DNA; 6948 BP.
DE Human immune system associated gene SEQ ID NO: 1381.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 43.8; DB 6; Length 6948;
Best Local Similarity 76.1%; Pred. No. 38;
RESULT 1322
ID AAS61229 standard; DNA; 6948 BP.
DE Human gene regulation-associated gene oligonucleotide #184.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 43.8; DB 6; Length 6948;
Best Local Similarity 76.1%; Pred. No. 38;
RESULT 1323
ID AAS46335 standard; DNA; 7348 BP.
DE Tumour suppressor gene derived chemically modified sequence #57.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 43.8; DB 4; Length 7348;
Best Local Similarity 54.7%; Pred. No. 38;
RESULT 1324
ID AAS45469 standard; DNA; 8588 BP.
DE Chemically pretreated complementary DNA associated with cell cycle #87.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 43.8; DB 4; Length 8588;
Best Local Similarity 47.0%; Pred. No. 39;
RESULT 1325
ID ABK28325 standard; DNA; 8588 BP.
DE DNA transcription associated genomic DNA #100.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 43.8; DB 6; Length 8588;
Best Local Similarity 47.0%; Pred. No. 39;
RESULT 1326
ID ADB54240 standard; DNA; 8666 BP.
DE Pretreated genomic DNA region 164.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 43.8; DB 10; Length 8666;
Best Local Similarity 47.4%; Pred. No. 39;
RESULT 1327
ID ADE84178 standard; DNA; 8666 BP.
DE Human lymphoid cell proliferative disorder gene derived DNA #114.
PN WO2003044226-A2.
PD 30-MAY-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 43.8; DB 10; Length 8666;
Best Local Similarity 47.4%; Pred. No. 39;
RESULT 1328
ID ADS89542 standard; DNA; 8666 BP.
DE Oligonucleotide of the invention SEQ ID NO:558.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 43.8; DB 13; Length 8666;
Best Local Similarity 47.4%; Pred. No. 39;
RESULT 1329
ID AAS46394 standard; DNA; 9110 BP.
DE Tumour suppressor gene derived chemically modified sequence #116.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 43.8; DB 4; Length 9110;
Best Local Similarity 45.7%; Pred. No. 39;
RESULT 1330
ID AAS46510 standard; DNA; 12356 BP.
DE Tumour suppressor gene derived chemically modified sequence #232.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 43.8; DB 4; Length 12356;
Best Local Similarity 44.9%; Pred. No. 41;
RESULT 1331
ID ABL32298 standard; DNA; 12507 BP.
DE Human immune system associated gene SEQ ID NO: 271.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 43.8; DB 6; Length 12507;
Best Local Similarity 46.6%; Pred. No. 41;
RESULT 1332
ID ABL34026 standard; DNA; 17594 BP.
DE Human immune system associated gene SEQ ID NO: 1999.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 43.8; DB 6; Length 17594;
Best Local Similarity 43.6%; Pred. No. 43;
RESULT 1333
ID AAA81455 standard; DNA; 23532 BP.
DE N. meningitidis partial DNA sequence gnm_3 SEQ ID NO:3.
PN WO200022430-A2.
PD 20-APR-2000.
PA (CHIR) CHIRON CORP.
Query Match 3.3%; Score 43.8; DB 3; Length 23532;
Best Local Similarity 47.9%; Pred. No. 45;
RESULT 1334
ID AAL03263 standard; DNA; 24977 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 5951.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43.8; DB 4; Length 24977;
Best Local Similarity 53.9%; Pred. No. 46;
RESULT 1335
ID AAL05788 standard; DNA; 24977 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8476.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43.8; DB 4; Length 24977;
Best Local Similarity 53.9%; Pred. No. 46;
RESULT 1336
ID ABL98352 standard; DNA; 24977 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 3004.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43.8; DB 4; Length 24977;
Best Local Similarity 53.9%; Pred. No. 46;
RESULT 1337
ID AAL05787 standard; DNA; 24983 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8475.
PN WO200155320-A2.

PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43.8; DB 4; Length 24983;
Best Local Similarity 53.9%; Pred. No. 46;
RESULT 1338
ID AAL03262 standard; DNA; 24983 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 5950.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43.8; DB 4; Length 24983;
Best Local Similarity 53.9%; Pred. No. 46;
RESULT 1339
ID ABL98351 standard; DNA; 24983 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 3003.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43.8; DB 4; Length 24983;
Best Local Similarity 53.9%; Pred. No. 46;
RESULT 1340
ID AAS33462 standard; DNA; 25715 BP.
DE DNA encoding human secreted protein, Seq ID No 745.
PN WO200155326-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43.8; DB 4; Length 25715;
Best Local Similarity 44.4%; Pred. No. 46;
RESULT 1341
Query Match 3.3%; Score 43.8; DB 3; Length 37668;
Best Local Similarity 47.9%; Pred. No. 49;
RESULT 1342
Query Match 3.3%; Score 43.8; DB 3; Length 110000;
Best Local Similarity 47.9%; Pred. No. 57;
RESULT 1343
ID ADQ97397 standard; DNA; 225587 BP.
DE Human cancer associated sequence HD08-043, SEQ ID 374.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.3%; Score 43.8; DB 12; Length 225587;
Best Local Similarity 45.7%; Pred. No. 64;
RESULT 1344
ID ADQ59440 standard; DNA; 347814 BP.
DE Human cancer-associated (CA) gene sequence SEQ ID NO:76.
PN WO2004058288-A1.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.3%; Score 43.8; DB 12; Length 347814;
Best Local Similarity 46.5%; Pred. No. 68;
RESULT 1345
ID AAF21610 standard; DNA; 349980 BP.
DE Neisseria meningitidis B nucleotide sequence SEQ ID NO:111.
PN WO200066791-A1.
PD 09-NOV-2000.
PA (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
Query Match 3.3%; Score 43.8; DB 3; Length 349980;
Best Local Similarity 47.9%; Pred. No. 68;
RESULT 1346
ID ABX45169 standard; cDNA; 228 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #10334.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 3.2%; Score 43.6; DB 8; Length 228;
Best Local Similarity 59.8%; Pred. No. 25;
RESULT 1347
ID ADL36867 standard; DNA; 293 BP.
DE Human ovarian cancer DNA marker #10757.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.2%; Score 43.6; DB 5; Length 293;
Best Local Similarity 50.6%; Pred. No. 26;
RESULT 1348
ID ADI71712 standard; DNA; 293 BP.
DE Human ovarian cancer DNA marker #4454.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.2%; Score 43.6; DB 5; Length 293;
Best Local Similarity 50.6%; Pred. No. 26;
RESULT 1349
ID ACN63020 standard; cDNA; 396 BP.
DE Cotton carpel wall/septum EST Clone ID: LIB3831-002-Q1-N6-A7, SEQ:17801.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 3.2%; Score 43.6; DB 13; Length 396;
Best Local Similarity 46.4%; Pred. No. 27;
RESULT 1350
ID ACN53005 standard; cDNA; 569 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-020-Q1-N6-E7, SEQ:7786.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 3.2%; Score 43.6; DB 13; Length 569;
Best Local Similarity 54.3%; Pred. No. 28;
RESULT 1351
ID AAH33135 standard; cDNA; 858 BP.
DE Human colon cancer antigen encoding cDNA SEQ ID NO:191.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 43.6; DB 4; Length 858;
Best Local Similarity 67.8%; Pred. No. 30;
RESULT 1352
ID ADQ23789 standard; DNA; 2116 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6609.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.2%; Score 43.6; DB 12; Length 2116;
Best Local Similarity 51.0%; Pred. No. 35;
RESULT 1353
ID ABL18982 standard; DNA; 2279 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 8419.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.2%; Score 43.6; DB 4; Length 2279;
Best Local Similarity 46.0%; Pred. No. 35;
RESULT 1354
ID AAS27049 standard; cDNA; 2418 BP.
DE cDNA encoding novel signal transduction pathway protein, Seq ID 84.
PN WO200154733-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 43.6; DB 4; Length 2418;
Best Local Similarity 67.8%; Pred. No. 35;
RESULT 1355
ID ADB93227 standard; cDNA; 2418 BP.
DE Human cDNA encoding a novel protein #74.
PN US2002168711-A1.
PD 14-NOV-2002.
PA (ROSE/) ROSEN C A.

PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 3.2%; Score 43.6; DB 10; Length 2418;
Best Local Similarity 67.8%; Pred. No. 35;
RESULT 1356
ID ADH41462 standard; DNA; 3345 BP.
DE Novel human nucleic acid NOV3a.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 3.2%; Score 43.6; DB 12; Length 3345;
Best Local Similarity 49.1%; Pred. No. 37;
RESULT 1357
ID ADH41498 standard; DNA; 3345 BP.
DE Novel human nucleic acid NOV3s.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 3.2%; Score 43.6; DB 12; Length 3345;
Best Local Similarity 49.1%; Pred. No. 37;
RESULT 1358
ID ADH41494 standard; DNA; 3345 BP.
DE Novel human nucleic acid NOV3q.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 3.2%; Score 43.6; DB 12; Length 3345;
Best Local Similarity 49.1%; Pred. No. 37;
RESULT 1359
ID ADH41496 standard; DNA; 3345 BP.
DE Novel human nucleic acid NOV3r.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 3.2%; Score 43.6; DB 12; Length 3345;
Best Local Similarity 49.1%; Pred. No. 37;
RESULT 1360
ID ADH41492 standard; DNA; 3345 BP.
DE Novel human nucleic acid NOV3p. .
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 3.2%; Score 43.6; DB 12; Length 3345;
Best Local Similarity 49.1%; Pred. No. 37;
RESULT 1361
ID ABL32329 standard; DNA; 5742 BP.
DE Human immune system associated gene SEQ ID NO: 302.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.6; DB 6; Length 5742;
Best Local Similarity 42.8%; Pred. No. 40;
RESULT 1362
ID AAS61080 standard; DNA; 6092 BP.
DE Human gene regulation-associated gene oligonucleotide #35.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.6; DB 6; Length 6092;
Best Local Similarity 45.5%; Pred. No. 41;
RESULT 1363
ID ABL49326 standard; DNA; 6583 BP.
DE Human polynucleotide associated with DNA replication SEQ ID NO 26.
PN WO200177377-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.6; DB 6; Length 6583;
Best Local Similarity 44.1%; Pred. No. 41;
RESULT 1364
ID ABL32791 standard; DNA; 6636 BP.
DE Human immune system associated gene SEQ ID NO: 764.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.6; DB 6; Length 6636;
Best Local Similarity 42.6%; Pred. No. 41;
RESULT 1365
ID ABL32739 standard; DNA; 6759 BP.
DE Human immune system associated gene SEQ ID NO: 712.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.6; DB 6; Length 6759;
Best Local Similarity 50.9%; Pred. No. 41;
RESULT 1366
ID ABL33929 standard; DNA; 6801 BP.
DE Human immune system associated gene SEQ ID NO: 1902.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.6; DB 6; Length 6801;
Best Local Similarity 49.0%; Pred. No. 41;
RESULT 1367
ID ABL92291 standard; DNA; 6801 BP.
DE Chemically treated DNA repair gene fragment complementary to#50.
PN WO200181622-A2.
PD 01-NOV-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.6; DB 6; Length 6801;
Best Local Similarity 49.0%; Pred. No. 41;
RESULT 1368
ID ABL49362 standard; DNA; 6801 BP.
DE Human polynucleotide associated with DNA replication SEQ ID NO 62.
PN WO200177377-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.6; DB 6; Length 6801;
Best Local Similarity 49.0%; Pred. No. 41;
RESULT 1369
ID ABL32979 standard; DNA; 6963 BP.
DE Human immune system associated gene SEQ ID NO: 952.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.6; DB 6; Length 6963;
Best Local Similarity 44.7%; Pred. No. 41;
RESULT 1370
ID ABL32982 standard; DNA; 7143 BP.
DE Human immune system associated gene SEQ ID NO: 955.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.6; DB 6; Length 7143;
Best Local Similarity 61.4%; Pred. No. 42;
RESULT 1371
ID AAQ55138 standard; DNA; 8654 BP.
DE Staphylococcus epidermidis probe SE-22.
PN WO9401583-A1.
PD 20-JAN-1994.
PA (FUSO) FUSO PHARM IND LTD.
Query Match 3.2%; Score 43.6; DB 2; Length 8654;
Best Local Similarity 46.9%; Pred. No. 43;
RESULT 1372
ID ABZ77353 standard; DNA; 8654 BP.
DE Nucleotide sequence designated SE-22.
PN WO2002101037-A1.
PD 19-DEC-2002.
PA (FUSO) FUSO PHARM IND LTD.
Query Match 3.2%; Score 43.6; DB 8; Length 8654;
Best Local Similarity 46.9%; Pred. No. 43;
RESULT 1373
ID AAL51841 standard; DNA; 8654 BP.
DE Staphylococcus epidermidis microbe identification-related DNA sequence 1.
PN WO200299133-A1.
PD 12-DEC-2002.
PA (FUSO) FUSO PHARM IND LTD.

PA (OHNO/) OHNO T.
Query Match 3.2%; Score 43.6; DB 10; Length 8654;
Best Local Similarity 46.9%; Pred. No. 43;
RESULT 1374
ID ABL32910 standard; DNA; 8946 BP.
DE Human immune system associated gene SEQ ID NO: 883.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.6; DB 6; Length 8946;
Best Local Similarity 55.2%; Pred. No. 43;
RESULT 1375
ID ABL32656 standard; DNA; 9832 BP.
DE Human immune system associated gene SEQ ID NO: 629.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.6; DB 6; Length 9832;
Best Local Similarity 45.8%; Pred. No. 44;
RESULT 1376
ID ABL33545 standard; DNA; 10328 BP.
DE Human immune system associated gene SEQ ID NO: 1518.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.6; DB 6; Length 10328;
Best Local Similarity 57.2%; Pred. No. 44;
RESULT 1377
ID ABL32605 standard; DNA; 11155 BP.
DE Human immune system associated gene SEQ ID NO: 578.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.6; DB 6; Length 11155;
Best Local Similarity 44.6%; Pred. No. 45;
RESULT 1378
ID ABL32343 standard; DNA; 11534 BP.
DE Human immune system associated gene SEQ ID NO: 316.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.6; DB 6; Length 11534;
Best Local Similarity 45.4%; Pred. No. 45;
RESULT 1379
ID ABL34071 standard; DNA; 13503 BP.
DE Human immune system associated gene SEQ ID NO: 2044.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.6; DB 6; Length 13503;
Best Local Similarity 46.6%; Pred. No. 46;
RESULT 1380
ID ABL70543 standard; DNA; 15649 BP.
DE Chemically treated cell signalling DNA sequence#217.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.6; DB 6; Length 15649;
Best Local Similarity 45.7%; Pred. No. 47;
RESULT 1381
ID ABN79985 standard; DNA; 16633 BP.
DE Human chemically modified disease associated gene SEQ ID NO 2.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.6; DB 6; Length 16633;
Best Local Similarity 42.2%; Pred. No. 47;
RESULT 1382
ID AAZ30355 standard; DNA; 19966 BP.
DE Nucleotide sequence of the eps operon of S. thermophilus Sfi39.
PN WO9954475-A2.
PD 28-OCT-1999.
PA (NEST) SOC PROD NESTLE SA.
Query Match 3.2%; Score 43.6; DB 3; Length 19966;
Best Local Similarity 44.9%; Pred. No. 49;
RESULT 1383
ID AAZ45258 standard; DNA; 19966 BP.
DE DNA encoding enzymes involved in exopolysaccharide biosynthesis.
PN WO9962316-A2.
PD 09-DEC-1999.
PA (NEST) SOC PROD NESTLE SA.
Query Match 3.2%; Score 43.6; DB 3; Length 19966;
Best Local Similarity 44.9%; Pred. No. 49;
RESULT 1384
ID ABD33520 standard; DNA; 34722 BP.
DE Human cancer-associated (CA) gene HD07-102.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.2%; Score 43.6; DB 13; Length 34722;
Best Local Similarity 44.4%; Pred. No. 53;
RESULT 1385
ID ACC79619 standard; DNA; 71843 BP.
DE Zebrafish protein kinase C lambda related genomic DNA SEQ ID NO:3.
PN WO2003023048-A2.
PD 20-MAR-2003.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 3.2%; Score 43.6; DB 8; Length 71843;
Best Local Similarity 33.7%; Pred. No. 59;
RESULT 1386
ID ABX47508 standard; cDNA; 277 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #12673.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 3.2%; Score 43.4; DB 8; Length 277;
Best Local Similarity 56.7%; Pred. No. 28;
RESULT 1387
ID ABX45291 standard; cDNA; 439 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #10456.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 3.2%; Score 43.4; DB 8; Length 439;
Best Local Similarity 60.7%; Pred. No. 30;
RESULT 1388
ID ADT96917 standard; cDNA; 440 BP.
DE Colon cancer associated human cDNA sequence #2424.
PN US2003087818-A1.
PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match 3.2%; Score 43.4; DB 11; Length 440;
Best Local Similarity 51.7%; Pred. No. 30;
RESULT 1389
ID ADR61743 standard; cDNA; 649 BP.
DE Cotton cDNA sequence, SEQ ID 2524.
PN US2004181830-A1.
PD 16-SEP-2004.
PA (KOVA/) KOVALIC D K.
PA (ZHOU/) ZHOU Y.
PA (CAOY/) CAO Y.
Query Match 3.2%; Score 43.4; DB 13; Length 649;
Best Local Similarity 49.3%; Pred. No. 32;
RESULT 1390
ID AAF72814 standard; DNA; 776 BP.
DE Secreted protein gene #16.
PN WO200107459-A1.
PD 01-FEB-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 43.4; DB 4; Length 776;

Best Local Similarity 62.4%; Pred. No. 33;
RESULT 1391
ID ABL34290 standard; DNA; 1701 BP.
DE Human immune system associated gene SEQ ID NO: 2263.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.4; DB 6; Length 1701;
Best Local Similarity 43.7%; Pred. No. 37;
RESULT 1392
ID AAA16635 standard; cDNA; 1759 BP.
DE Human secreted protein clone rd610_1 nucleotide sequence SEQ ID NO:35.
PN WO200009552-A1.
PD 24-FEB-2000.
PA (GEMY) GENETICS INST INC.
Query Match 3.2%; Score 43.4; DB 3; Length 1759;
Best Local Similarity 51.4%; Pred. No. 37;
RESULT 1393
ID AAC77031 standard; cDNA; 2060 BP.
DE Human ORFX ORF2586 polynucleotide sequence SEQ ID NO:5171.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 3.2%; Score 43.4; DB 3; Length 2060;
Best Local Similarity 47.3%; Pred. No. 38;
RESULT 1394
ID AAH54753 standard; DNA; 3167 BP.
DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:4117.
PN WO200134809-A2.
PD 17-MAY-2001.
PA (GLAX) GLAXO GROUP LTD.
Query Match 3.2%; Score 43.4; DB 4; Length 3167;
Best Local Similarity 46.3%; Pred. No. 40;
RESULT 1395
ID AAH54912 standard; DNA; 3241 BP.
DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:4276.
PN WO200134809-A2.
PD 17-MAY-2001.
PA (GLAX) GLAXO GROUP LTD.
Query Match 3.2%; Score 43.4; DB 4; Length 3241;
Best Local Similarity 46.3%; Pred. No. 41;
RESULT 1396
ID ABX71421 standard; cDNA; 3353 BP.
DE Human testes-derived cDNA from clone DKFZphtes3_7j8.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 3.2%; Score 43.4; DB 5; Length 3353;
Best Local Similarity 55.7%; Pred. No. 41;
RESULT 1397
ID ADQ24431 standard; DNA; 3373 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7251.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.2%; Score 43.4; DB 12; Length 3373;
Best Local Similarity 47.3%; Pred. No. 41;
RESULT 1398
ID AAS46376 standard; DNA; 5278 BP.
DE Tumour suppressor gene derived chemically modified sequence #98.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.4; DB 4; Length 5278;
Best Local Similarity 44.9%; Pred. No. 44;
RESULT 1399
ID ABL32823 standard; DNA; 5278 BP.
DE Human immune system associated gene SEQ ID NO: 796.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.4; DB 6; Length 5278;
Best Local Similarity 44.9%; Pred. No. 44;
RESULT 1400
ID ABL33790 standard; DNA; 5324 BP.
DE Human immune system associated gene SEQ ID NO: 1763.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.4; DB 6; Length 5324;
Best Local Similarity 44.2%; Pred. No. 44;
RESULT 1401
ID AAQ11710 standard; DNA; 5852 BP.
DE Dictyostelium plasmid Ddp2 containing Rep gene.
PN WO9106644-A.
PD 16-MAY-1991.
PA (UYMA-) UNIV MACQUARIE.
Query Match 3.2%; Score 43.4; DB 2; Length 5852;
Best Local Similarity 46.7%; Pred. No. 44;
RESULT 1402
ID ABL33826 standard; DNA; 6204 BP.
DE Human immune system associated gene SEQ ID NO: 1799.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.4; DB 6; Length 6204;
Best Local Similarity 45.5%; Pred. No. 45;
RESULT 1403
ID ABL33873 standard; DNA; 6270 BP.
DE Human immune system associated gene SEQ ID NO: 1846.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.4; DB 6; Length 6270;
Best Local Similarity 48.6%; Pred. No. 45;
RESULT 1404
ID ABL32155 standard; DNA; 6681 BP.
DE Human immune system associated gene SEQ ID NO: 128.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.4; DB 6; Length 6681;
Best Local Similarity 46.8%; Pred. No. 45;
RESULT 1405
ID ABL54304 standard; DNA; 6681 BP.
DE Chemically treated apoptosis gene complementary to gene #2.
PN WO200177164-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.4; DB 6; Length 6681;
Best Local Similarity 46.8%; Pred. No. 45;
RESULT 1406
ID ABL33487 standard; DNA; 6831 BP.
DE Human immune system associated gene SEQ ID NO: 1460.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.4; DB 6; Length 6831;
Best Local Similarity 47.3%; Pred. No. 45;
RESULT 1407
ID AAS45496 standard; DNA; 7038 BP.
DE Chemically pretreated genomic DNA associated with cell cycle #101.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.4; DB 4; Length 7038;
Best Local Similarity 47.0%; Pred. No. 46;
RESULT 1408
ID ABL34097 standard; DNA; 7038 BP.
DE Human immune system associated gene SEQ ID NO: 2070.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.4; DB 6; Length 7038;
Best Local Similarity 47.0%; Pred. No. 46;
RESULT 1409

ID ABK28426 standard; DNA; 7038 BP.
DE DNA transcription associated complementary genomic DNA #150.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.4; DB 6; Length 7038;
Best Local Similarity 47.0%; Pred. No. 46;
RESULT 1410
ID ABL32483 standard; DNA; 7134 BP.
DE Human immune system associated gene SEQ ID NO: 456.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.4; DB 6; Length 7134;
Best Local Similarity 44.0%; Pred. No. 46;
RESULT 1411
ID ABL32746 standard; DNA; 7384 BP.
DE Human immune system associated gene SEQ ID NO: 719.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.4; DB 6; Length 7384;
Best Local Similarity 51.0%; Pred. No. 46;
RESULT 1412
ID ABK39955 standard; DNA; 8076 BP.
DE Human chemically pretreated gene sequence #18 strand 2.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.4; DB 6; Length 8076;
Best Local Similarity 43.8%; Pred. No. 47;
RESULT 1413
ID ABK39957 standard; DNA; 8136 BP.
DE Human chemically pretreated gene sequence #19 strand 2.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.4; DB 6; Length 8136;
Best Local Similarity 43.8%; Pred. No. 47;
RESULT 1414
ID ABL32555 standard; DNA; 8136 BP.
DE Human immune system associated gene SEQ ID NO: 528.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.4; DB 6; Length 8136;
Best Local Similarity 43.8%; Pred. No. 47;
RESULT 1415
ID AAS46801 standard; DNA; 8237 BP.
DE Tumour suppressor gene derived chemically modified sequence #527.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.4; DB 4; Length 8237;
Best Local Similarity 43.5%; Pred. No. 47;
RESULT 1416
ID AAQ55138 standard; DNA; 8654 BP.
DE Staphylococcus epidermidis probe SE-22.
PN WO9401583-A1.
PD 20-JAN-1994.
PA (FUSO) FUSO PHARM IND LTD.
Query Match 3.2%; Score 43.4; DB 2; Length 8654;
Best Local Similarity 44.6%; Pred. No. 47;
RESULT 1417
ID ABZ77353 standard; DNA; 8654 BP.
DE Nucleotide sequence designated SE-22.
PN WO2002101037-A1.
PD 19-DEC-2002.
PA (FUSO) FUSO PHARM IND LTD.
Query Match 3.2%; Score 43.4; DB 8; Length 8654;
Best Local Similarity 44.6%; Pred. No. 47;
RESULT 1418
ID AAL51841 standard; DNA; 8654 BP.
DE Staphylococcus epidermidis microbe identification-related DNA sequence 1.
PN WO200299133-A1.
PD 12-DEC-2002.
PA (FUSO) FUSO PHARM IND LTD.
PA (OHNO/) OHNO T.
Query Match 3.2%; Score 43.4; DB 10; Length 8654;
Best Local Similarity 44.6%; Pred. No. 47;
RESULT 1419
ID ABL33512 standard; DNA; 11092 BP.
DE Human immune system associated gene SEQ ID NO: 1485.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.4; DB 6; Length 11092;
Best Local Similarity 53.9%; Pred. No. 49;
RESULT 1420
ID ABK28331 standard; DNA; 11745 BP.
DE DNA transcription associated genomic DNA #103.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.4; DB 6; Length 11745;
Best Local Similarity 42.0%; Pred. No. 49;
RESULT 1421
ID ABL33749 standard; DNA; 11805 BP.
DE Human immune system associated gene SEQ ID NO: 1722.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.4; DB 6; Length 11805;
Best Local Similarity 47.0%; Pred. No. 49;
RESULT 1422
ID AAL37611 standard; DNA; 12003 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3976.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 43.4; DB 4; Length 12003;
Best Local Similarity 45.1%; Pred. No. 49;
RESULT 1423
ID ABX60599 standard; cDNA; 12003 BP.
DE cDNA encoding novel human musculoskeletal system antigen #2943.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 3.2%; Score 43.4; DB 8; Length 12003;
Best Local Similarity 45.1%; Pred. No. 49;
RESULT 1424
ID ADJ31349 standard; DNA; 12003 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3976.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 43.4; DB 12; Length 12003;
Best Local Similarity 45.1%; Pred. No. 49;
RESULT 1425
ID ADN41630 standard; DNA; 12003 BP.
DE Novel human secreted protein polynucleotide seqid 752.
PN US2004044191-A1.
PD 04-MAR-2004.
PA (FISC/) FISCHER C L.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (RUBE/) RUBEN S M.
PA (KYAW/) KYAW H.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (LAFL/) LAFLEUR D W.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (OLSE/) OLSEN H.

PA (EBNE/) EBNER R.
PA (BIRS/) BIRSE C E.
Query Match 3.2%; Score 43.4; DB 12; Length 12003;
Best Local Similarity 45.1%; Pred. No. 49;
RESULT 1426
ID ABK40062 standard; DNA; 13784 BP.
DE Human chemically pretreated gene sequence #72 strand 2.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.4; DB 6; Length 13784;
Best Local Similarity 45.0%; Pred. No. 50;
RESULT 1427
ID ABL32525 standard; DNA; 15861 BP.
DE Human immune system associated gene SEQ ID NO: 498.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.4; DB 6; Length 15861;
Best Local Similarity 46.6%; Pred. No. 52;
RESULT 1428
ID AAS46771 standard; DNA; 17280 BP.
DE Tumour suppressor gene derived chemically modified sequence #495.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.4; DB 4; Length 17280;
Best Local Similarity 44.2%; Pred. No. 52;
RESULT 1429
ID ABL33365 standard; DNA; 17893 BP.
DE Human immune system associated gene SEQ ID NO: 1338.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.4; DB 6; Length 17893;
Best Local Similarity 43.5%; Pred. No. 52;
RESULT 1430
ID ABV99730 standard; cDNA; 30350 BP.
DE Human Ras-like protein encoding cDNA.
Query Match 3.2%; Score 43.4; DB 8; Length 30350;
Best Local Similarity 45.1%; Pred. No. 57;
RESULT 1431
ID ABQ67005 standard; DNA; 33053 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 35.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.4; DB 6; Length 33053;
Best Local Similarity 43.6%; Pred. No. 58;
RESULT 1432
ID AAL48890 standard; DNA; 53332 BP.
DE Human Pftaire family kinase gene.
PN WO200261060-A2.
PD 08-AUG-2002.
PA (PEKE) PE CORP NY.
Query Match 3.2%; Score 43.4; DB 6; Length 53332;
Best Local Similarity 48.8%; Pred. No. 62;
RESULT 1433
ID ADL13931 standard; DNA; 180385 BP.
DE Osteoarthritis-associated polymorphic nucleotide #463.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 3.2%; Score 43.4; DB 10; Length 180385;
Best Local Similarity 45.9%; Pred. No. 74;
RESULT 1434
ID ABD32548 standard; DNA; 310268 BP.
DE Human cancer-associated genomic DNA HD14-033.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.2%; Score 43.4; DB 13; Length 310268;
Best Local Similarity 49.1%; Pred. No. 81;

RESULT 1435
ID ACN53869 standard; cDNA; 355 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-014-Q1-K6-B10, SEQ:8650.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 3.2%; Score 43.2; DB 13; Length 355;
Best Local Similarity 63.5%; Pred. No. 32;
RESULT 1436
ID ADI69402 standard; DNA; 528 BP.
DE Human ovarian cancer DNA marker #2144.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.2%; Score 43.2; DB 5; Length 528;
Best Local Similarity 56.0%; Pred. No. 34;
RESULT 1437
ID ADI75744 standard; DNA; 528 BP.
DE Human ovarian cancer DNA marker #8486.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.2%; Score 43.2; DB 5; Length 528;
Best Local Similarity 56.0%; Pred. No. 34;
RESULT 1438
ID ACN45220 standard; cDNA; 574 BP.
DE Cotton primed seed EST Clone ID: LIB3825-002-Q1-N6-A11, SEQ:1.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 3.2%; Score 43.2; DB 13; Length 574;
Best Local Similarity 63.5%; Pred. No. 34;
RESULT 1439
ID ACN52180 standard; cDNA; 599 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-012-Q1-N6-E8, SEQ:6961.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 3.2%; Score 43.2; DB 13; Length 599;
Best Local Similarity 63.5%; Pred. No. 35;
RESULT 1440
ID ADR01532 standard; DNA; 782 BP.
DE A. gossypii genomic DNA PAG1208RP.
PN US6239264-B1.
PD 29-MAY-2001.
PA (SYNG-) SYNGENTA PARTICIPATIONS AG.
Query Match 3.2%; Score 43.2; DB 2; Length 782;
Best Local Similarity 47.6%; Pred. No. 36;
RESULT 1441
ID AAF82249 standard; cDNA; 1220 BP.
DE Cyclamen dihydroflavonol-4-reductase nucleotide sequence.
PN JP2001037485-A.
PD 13-FEB-2001.
PA (HOKK) HOKKO CHEM IND CO LTD.
Query Match 3.2%; Score 43.2; DB 4; Length 1220;
Best Local Similarity 68.2%; Pred. No. 38;
RESULT 1442
ID AAN60472 standard; DNA; 4590 BP.
DE Sequence encoding the ring-infected Erythrocyte Surface Antigen (RESA).
PN WO8601802-A.
PD 27-MAR-1986.
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
Query Match 3.2%; Score 43.2; DB 1; Length 4590;
Best Local Similarity 44.7%; Pred. No. 47;

RESULT 1443
ID ADS89551 standard; DNA; 5286 BP.
DE Oligonucleotide of the invention SEQ ID NO:567.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.2; DB 13; Length 5286;
Best Local Similarity 46.2%; Pred. No. 48;
RESULT 1444
ID ADS89277 standard; DNA; 5286 BP.
DE Oligonucleotide of the invention SEQ ID NO:293.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.2; DB 13; Length 5286;
Best Local Similarity 46.2%; Pred. No. 48;
RESULT 1445
ID ABL33676 standard; DNA; 5379 BP.
DE Human immune system associated gene SEQ ID NO: 1649.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.2; DB 6; Length 5379;
Best Local Similarity 50.5%; Pred. No. 48;
RESULT 1446
ID ABL34576 standard; DNA; 5379 BP.
DE Human metastasis associated gene SEQ ID NO: 129.
PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.2; DB 6; Length 5379;
Best Local Similarity 50.5%; Pred. No. 48;
RESULT 1447
ID ABL70369 standard; DNA; 5379 BP.
DE Chemically treated cell signalling DNA sequence#130.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.2; DB 6; Length 5379;
Best Local Similarity 50.5%; Pred. No. 48;
RESULT 1448
ID ADS99837 standard; DNA; 5379 BP.
DE Bisulphite treated human gene associated with metastasis #65.
PN US2003148327-A1.
PD 07-AUG-2003.
PA (OLEK/) OLEK A.
PA (PIEP/) PIEPENBROCK C.
PA (BERL/) BERLIN K.
Query Match 3.2%; Score 43.2; DB 7; Length 5379;
Best Local Similarity 50.5%; Pred. No. 48;
RESULT 1449
ID ABL32101 standard; DNA; 5728 BP.
DE Human immune system associated gene SEQ ID NO: 74.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.2; DB 6; Length 5728;
Best Local Similarity 46.4%; Pred. No. 49;
RESULT 1450
ID ABL32891 standard; DNA; 6131 BP.
DE Human immune system associated gene SEQ ID NO: 864.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.2; DB 6; Length 6131;
Best Local Similarity 43.2%; Pred. No. 49;
RESULT 1451
ID ABL33010 standard; DNA; 6171 BP.
DE Human immune system associated gene SEQ ID NO: 983.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.2; DB 6; Length 6171;
Best Local Similarity 44.3%; Pred. No. 49;
RESULT 1452
ID ABL32960 standard; DNA; 6255 BP.
DE Human immune system associated gene SEQ ID NO: 933.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.2; DB 6; Length 6255;
Best Local Similarity 48.1%; Pred. No. 49;
RESULT 1453
ID ADQ24856 standard; DNA; 6816 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7676.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.2%; Score 43.2; DB 12; Length 6816;
Best Local Similarity 36.4%; Pred. No. 50;
RESULT 1454
ID ABL34145 standard; DNA; 7076 BP.
DE Human immune system associated gene SEQ ID NO: 2118.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.2; DB 6; Length 7076;
Best Local Similarity 45.7%; Pred. No. 50;
RESULT 1455
ID ABL32401 standard; DNA; 7167 BP.
DE Human immune system associated gene SEQ ID NO: 374.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.2; DB 6; Length 7167;
Best Local Similarity 42.3%; Pred. No. 50;
RESULT 1456
ID ABL32028 standard; DNA; 7351 BP.
DE Human immune system associated gene SEQ ID NO: 1.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.2; DB 6; Length 7351;
Best Local Similarity 46.1%; Pred. No. 50;
RESULT 1457
ID ABL34152 standard; DNA; 9255 BP.
DE Human immune system associated gene SEQ ID NO: 2125.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.2; DB 6; Length 9255;
Best Local Similarity 47.6%; Pred. No. 52;
RESULT 1458
ID AAS63354 standard; DNA; 9265 BP.
DE Chemically pretreated metabolism associated gene #49.
PN WO200176451-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.2; DB 6; Length 9265;
Best Local Similarity 47.6%; Pred. No. 52;
RESULT 1459
ID ABL33689 standard; DNA; 9646 BP.
DE Human immune system associated gene SEQ ID NO: 1662.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.2; DB 6; Length 9646;
Best Local Similarity 46.2%; Pred. No. 52;
RESULT 1460
ID ABN80083 standard; DNA; 10250 BP.
DE Human chemically modified disease associated gene SEQ ID NO 100.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.2; DB 6; Length 10250;
Best Local Similarity 45.7%; Pred. No. 53;

RESULT 1461
ID ABL34135 standard; DNA; 10886 BP.
DE Human immune system associated gene SEQ ID NO: 2108.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.2; DB 6; Length 10886;
Best Local Similarity 43.2%; Pred. No. 53;
RESULT 1462
ID AAS46471 standard; DNA; 12269 BP.
DE Tumour suppressor gene derived chemically modified sequence #193.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.2; DB 4; Length 12269;
Best Local Similarity 48.1%; Pred. No. 54;
RESULT 1463
ID ABL33410 standard; DNA; 12269 BP.
DE Human immune system associated gene SEQ ID NO: 1383.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.2; DB 6; Length 12269;
Best Local Similarity 48.1%; Pred. No. 54;
RESULT 1464
ID ABL56202 standard; DNA; 50000 BP.
DE AmEPV genome fragment#4.
PN WO200212526-A2.
PD 14-FEB-2002.
PA (UYFL) UNIV FLORIDA.
Query Match 3.2%; Score 43.2; DB 6; Length 50000;
Best Local Similarity 43.6%; Pred. No. 67;
RESULT 1465
ID AAS46794 standard; DNA; 56153 BP.
DE Tumour suppressor gene derived chemically modified sequence #520.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43.2; DB 4; Length 56153;
Best Local Similarity 44.7%; Pred. No. 68;
RESULT 1466
Query Match 3.2%; Score 43.2; DB 2; Length 110000;
Best Local Similarity 45.8%; Pred. No. 76;
RESULT 1467
ID ACN44998 standard; DNA; 122614 BP.
DE Human genomic sequence hCG29191.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.2%; Score 43.2; DB 11; Length 122614;
Best Local Similarity 46.0%; Pred. No. 77;
RESULT 1468
ID ADO47190 standard; DNA; 200000 BP.
DE DNA sequence of a human immunoglobulin heavy chain variable region.
PN WO2004029249-A1.
PD 08-APR-2004.
PA (CENT-) CENTENARY INST CANCER MEDICINE & CELL BI.
Query Match 3.2%; Score 43.2; DB 12; Length 200000;
Best Local Similarity 58.6%; Pred. No. 83;
RESULT 1469
ID AAI76073 standard; DNA; 51 BP.
DE Human silent SNP containing nucleic acid SEQ:3014.
PN WO200140521-A2.
PD 07-JUN-2001.
PA (CURA-) CURAGEN CORP.
Query Match 3.2%; Score 43; DB 4; Length 51;
Best Local Similarity 90.2%; Pred. No. 26;
RESULT 1470
ID ADI73348 standard; DNA; 291 BP.
DE Human ovarian cancer DNA marker #6090.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.2%; Score 43; DB 5; Length 291;
Best Local Similarity 48.8%; Pred. No. 34;
RESULT 1471
ID ADL38479 standard; DNA; 291 BP.
DE Human ovarian cancer DNA marker #12369.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.2%; Score 43; DB 5; Length 291;
Best Local Similarity 48.8%; Pred. No. 34;
RESULT 1472
ID AAI91325 standard; cDNA; 412 BP.
DE Human polynucleotide SEQ ID NO 11385.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.2%; Score 43; DB 4; Length 412;
Best Local Similarity 69.9%; Pred. No. 36;
RESULT 1473
ID ADL43533 standard; DNA; 492 BP.
DE Human ovarian cancer DNA marker #17423.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.2%; Score 43; DB 5; Length 492;
Best Local Similarity 54.8%; Pred. No. 37;
RESULT 1474
ID ABV46528 standard; cDNA; 563 BP.
DE Human prostate expression marker cDNA 46519.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.2%; Score 43; DB 5; Length 563;
Best Local Similarity 62.0%; Pred. No. 38;
RESULT 1475
ID ADL37093 standard; DNA; 714 BP.
DE Human ovarian cancer DNA marker #10983.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.2%; Score 43; DB 5; Length 714;
Best Local Similarity 50.0%; Pred. No. 39;
RESULT 1476
ID ADI71942 standard; DNA; 714 BP.
DE Human ovarian cancer DNA marker #4684.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.2%; Score 43; DB 5; Length 714;
Best Local Similarity 50.0%; Pred. No. 39;
RESULT 1477
ID AAN93084 standard; cDNA; 857 BP.
DE Lambda gt 11 pl(13T) contg. cDNA encoding Der p I antigen.
PN WO8810297-A.
PD 29-DEC-1988.
PA (PRIN-) PRINCESS MARGARET CHILD.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (HALL-) HALL W & E INST MED RES.
Query Match 3.2%; Score 43; DB 1; Length 857;
Best Local Similarity 60.8%; Pred. No. 40;
RESULT 1478
ID ADQ25281 standard; DNA; 1129 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 8101.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.2%; Score 43; DB 12; Length 1129;
Best Local Similarity 64.6%; Pred. No. 42;
RESULT 1479
ID AAZ99724 standard; cDNA; 4137 BP.
DE cDNA encoding human cardiovascular system associated protein kinase-1.
PN WO200014212-A1.
PD 16-MAR-2000.

PA (MILL-) MILLENNIUM PHARM INC.
Query Match 3.2%; Score 43; DB 3; Length 4137;
Best Local Similarity 45.7%; Pred. No. 51;
RESULT 1480
ID ADC51563 standard; DNA; 4176 BP.
DE Schizosaccharomyces pombe alpha-glucosidase coding sequence.
PN JP2003088365-A.
PD 25-MAR-2003.
PA (NISO) NIPPON SHOKUHIN KAKO KK.
Query Match 3.2%; Score 43; DB 10; Length 4176;
Best Local Similarity 73.3%; Pred. No. 51;
RESULT 1481
ID ABL32636 standard; DNA; 5308 BP.
DE Human immune system associated gene SEQ ID NO: 609.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43; DB 6; Length 5308;
Best Local Similarity 45.1%; Pred. No. 53;
RESULT 1482
ID ABK31164 standard; DNA; 6133 BP.
DE Signal transduction associated gene modified DNA #4.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43; DB 6; Length 6133;
Best Local Similarity 47.3%; Pred. No. 54;
RESULT 1483
ID ABL70503 standard; DNA; 6133 BP.
DE Chemically treated cell signalling DNA sequence#197.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43; DB 6; Length 6133;
Best Local Similarity 47.3%; Pred. No. 54;
RESULT 1484
ID AAS61051 standard; DNA; 6133 BP.
DE Human gene regulation-associated gene oligonucleotide #6.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43; DB 6; Length 6133;
Best Local Similarity 47.3%; Pred. No. 54;
RESULT 1485
ID ABN79986 standard; DNA; 6133 BP.
DE Human chemically modified disease associated gene SEQ ID NO 3.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43; DB 6; Length 6133;
Best Local Similarity 47.3%; Pred. No. 54;
RESULT 1486
ID ABL32485 standard; DNA; 6244 BP.
DE Human immune system associated gene SEQ ID NO: 458.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43; DB 6; Length 6244;
Best Local Similarity 44.7%; Pred. No. 54;
RESULT 1487
ID AAS46644 standard; DNA; 6261 BP.
DE Tumour suppressor gene derived chemically modified sequence #366.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43; DB 4; Length 6261;
Best Local Similarity 45.8%; Pred. No. 54;
RESULT 1488
ID ABK31161 standard; DNA; 6261 BP.
DE Signal transduction associated gene modified complementary DNA #2.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43; DB 6; Length 6261;
Best Local Similarity 45.8%; Pred. No. 54;
RESULT 1489
ID ABL32566 standard; DNA; 6907 BP.
DE Human immune system associated gene SEQ ID NO: 539.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43; DB 6; Length 6907;
Best Local Similarity 46.1%; Pred. No. 55;
RESULT 1490
ID ABK34029 standard; DNA; 8056 BP.
DE Human DNA for staging of Astrocytomas #59.
PN WO200202808-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43; DB 6; Length 8056;
Best Local Similarity 45.2%; Pred. No. 56;
RESULT 1491
ID ABZ09933 standard; DNA; 8056 BP.
DE Human 5' and/or regulatory region of CMYCex3 DNA SEQ ID NO:73.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43; DB 8; Length 8056;
Best Local Similarity 45.2%; Pred. No. 56;
RESULT 1492
ID ABZ10099 standard; DNA; 8056 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #239.
PN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43; DB 8; Length 8056;
Best Local Similarity 45.2%; Pred. No. 56;
RESULT 1493
ID ABL92313 standard; DNA; 8079 BP.
DE Chemically treated DNA repair gene fragment complementary to#61.
PN WO200181622-A2.
PD 01-NOV-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43; DB 6; Length 8079;
Best Local Similarity 73.3%; Pred. No. 56;
RESULT 1494
ID ABL32203 standard; DNA; 8246 BP.
DE Human immune system associated gene SEQ ID NO: 176.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43; DB 6; Length 8246;
Best Local Similarity 46.0%; Pred. No. 56;
RESULT 1495
ID ABL16590 standard; DNA; 8786 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 1243.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.2%; Score 43; DB 4; Length 8786;
Best Local Similarity 46.7%; Pred. No. 57;
RESULT 1496
ID AAS46805 standard; DNA; 10996 BP.
DE Tumour suppressor gene derived chemically modified sequence #531.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43; DB 4; Length 10996;
Best Local Similarity 45.2%; Pred. No. 59;
RESULT 1497
ID ABK28465 standard; DNA; 10996 BP.
DE DNA transcription associated genomic DNA #170.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43; DB 6; Length 10996;

Best Local Similarity 45.2%; Pred. No. 59;
RESULT 1498
ID ABK39930 standard; DNA; 12069 BP.
DE Human chemically pretreated gene sequence #6 strand 1.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43; DB 6; Length 12069;
Best Local Similarity 46.7%; Pred. No. 60;
RESULT 1499
ID ADS89426 standard; DNA; 12610 BP.
DE Oligonucleotide of the invention SEQ ID NO:442.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43; DB 13; Length 12610;
Best Local Similarity 55.8%; Pred. No. 60;
RESULT 1500
ID ABL32583 standard; DNA; 13376 BP.
DE Human immune system associated gene SEQ ID NO: 556.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 43; DB 6; Length 13376;
Best Local Similarity 47.5%; Pred. No. 61;

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OM nucleic - nucleic search, using sw model

Run on: February 24, 2005, 19:27:51 ; Search time 255.638 Seconds
(without alignments)
8615.409 Million cell updates/sec

Title: US-09-989-724-386
Perfect score: 1346
Sequence: 1 gaaagaatgttgtggctgct.....aaaaaaaaaaaaaaaaaaa 1346

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	845.2	62.8	862	3	US-09-289-349-6	Sequence 6, Appli
	2	799.4	59.4	848	3	US-08-905-223-27	Sequence 27, Appl
	3	799.4	59.4	848	3	US-09-247-155-27	Sequence 27, Appl
	4	799.4	59.4	848	4	US-09-663-600A-27	Sequence 27, Appl
	5	799.4	59.4	848	4	US-09-621-976-5	Sequence 5, Appli
	6	799.4	59.4	848	4	US-09-513-999C-5	Sequence 5, Appli
	7	799.4	59.4	848	4	US-09-471-276-5	Sequence 5, Appli
	8	125	9.3	2415	3	US-08-989-299-3	Sequence 3, Appli
	9	125	9.3	2415	4	US-09-407-427-3	Sequence 3, Appli
	10	125	9.3	3388	4	US-09-949-016-5413	Sequence 5413, Ap
	11	125	9.3	3396	3	US-08-989-299-1	Sequence 1, Appli
	12	125	9.3	3396	4	US-10-158-847-141	Sequence 141, App
	13	125	9.3	3396	4	US-09-407-427-1	Sequence 1, Appli
	14	117	8.7	2920	4	US-10-158-847-137	Sequence 137, App
	15	77.4	5.8	43986	4	US-09-949-016-17155	Sequence 17155, A
c	16	69.4	5.2	2350	3	US-09-280-116-40	Sequence 40, Appl
c	17	54	4.0	11288	3	US-08-646-301A-1	Sequence 1, Appli
c	18	54	4.0	11288	3	US-08-481-968A-4	Sequence 4, Appli
c	19	54	4.0	11288	3	US-08-154-712B-4	Sequence 4, Appli
c	20	54	4.0	11288	4	US-09-947-925A-4	Sequence 4, Appli
c	21	54	4.0	15056	4	US-09-474-699-10	Sequence 10, Appl
c	22	54	4.0	15056	4	US-09-814-351-14	Sequence 14, Appl
	23	53.8	4.0	1141	4	US-09-806-708B-22	Sequence 22, Appl
	24	53.4	4.0	147382	4	US-09-949-016-14624	Sequence 14624, A
c	25	52.8	3.9	26000	4	US-09-843-376-10	Sequence 10, Appl
	26	51.8	3.8	50383	4	US-09-949-016-17600	Sequence 17600, A
	27	51.6	3.8	168575	3	US-09-426-290-1	Sequence 1, Appli
	28	51.2	3.8	187169	4	US-09-949-016-12776	Sequence 12776, A
	29	51.2	3.8	191569	4	US-09-949-016-15940	Sequence 15940, A
	30	50.8	3.8	30820	4	US-09-949-016-17145	Sequence 17145, A
c	31	50.6	3.8	29717	4	US-09-949-016-16284	Sequence 16284, A
c	32	50.6	3.8	60376	4	US-09-949-016-12423	Sequence 12423, A
	33	49.6	3.7	601	4	US-09-949-016-30531	Sequence 30531, A
	34	49.6	3.7	601	4	US-09-949-016-37150	Sequence 37150, A
	35	49.6	3.7	601	4	US-09-949-016-37164	Sequence 37164, A
	36	49.6	3.7	601	4	US-09-949-016-145868	Sequence 145868,
	37	49.6	3.7	601	4	US-09-949-016-146136	Sequence 146136,
	38	49.6	3.7	601	4	US-09-949-016-146404	Sequence 146404,
c	39	49.6	3.7	205044	4	US-09-949-016-15851	Sequence 15851, A
c	40	49.6	3.7	205044	4	US-09-949-016-15852	Sequence 15852, A
c	41	49.6	3.7	205044	4	US-09-949-016-15853	Sequence 15853, A
c	42	49.6	3.7	223471	4	US-09-949-016-12387	Sequence 12387, A
c	43	49.6	3.7	223471	4	US-09-949-016-12724	Sequence 12724, A
c	44	49.6	3.7	223471	4	US-09-949-016-12725	Sequence 12725, A
	45	49.4	3.7	133719	4	US-09-949-016-15092	Sequence 15092, A
c	46	49	3.6	636591	4	US-09-949-016-11808	Sequence 11808, A
c	47	49	3.6	636591	4	US-09-949-016-13388	Sequence 13388, A
c	48	48.8	3.6	1141	4	US-09-806-708B-22	Sequence 22, Appl
	49	48.8	3.6	231129	4	US-09-949-016-16110	Sequence 16110, A
	50	48.8	3.6	266293	4	US-09-949-016-11934	Sequence 11934, A
	51	48.6	3.6	18773	4	US-09-949-016-14164	Sequence 14164, A
	52	48.6	3.6	119153	4	US-09-949-016-12378	Sequence 12378, A
c	53	48.4	3.6	601	4	US-09-949-016-156535	Sequence 156535,
	54	48.4	3.6	23501	4	US-09-949-016-17517	Sequence 17517, A
c	55	48	3.6	601	4	US-09-949-016-30532	Sequence 30532, A
c	56	48	3.6	601	4	US-09-949-016-30533	Sequence 30533, A
c	57	48	3.6	601	4	US-09-949-016-30534	Sequence 30534, A
c	58	48	3.6	601	4	US-09-949-016-37151	Sequence 37151, A
c	59	48	3.6	601	4	US-09-949-016-37152	Sequence 37152, A
c	60	48	3.6	601	4	US-09-949-016-37153	Sequence 37153, A
c	61	48	3.6	601	4	US-09-949-016-37165	Sequence 37165, A
c	62	48	3.6	601	4	US-09-949-016-37166	Sequence 37166, A
c	63	48	3.6	601	4	US-09-949-016-37167	Sequence 37167, A
c	64	48	3.6	601	4	US-09-949-016-145869	Sequence 145869,
c	65	48	3.6	601	4	US-09-949-016-145870	Sequence 145870,
c	66	48	3.6	601	4	US-09-949-016-145871	Sequence 145871,
c	67	48	3.6	601	4	US-09-949-016-146137	Sequence 146137,
c	68	48	3.6	601	4	US-09-949-016-146138	Sequence 146138,
c	69	48	3.6	601	4	US-09-949-016-146139	Sequence 146139,
c	70	48	3.6	601	4	US-09-949-016-146405	Sequence 146405,
c	71	48	3.6	601	4	US-09-949-016-146406	Sequence 146406,
c	72	48	3.6	601	4	US-09-949-016-146407	Sequence 146407,
	73	48	3.6	601	4	US-09-949-016-156535	Sequence 156535,
	74	48	3.6	205044	4	US-09-949-016-15851	Sequence 15851, A
	75	48	3.6	205044	4	US-09-949-016-15852	Sequence 15852, A
	76	48	3.6	205044	4	US-09-949-016-15853	Sequence 15853, A
	77	48	3.6	223471	4	US-09-949-016-12387	Sequence 12387, A
	78	48	3.6	223471	4	US-09-949-016-12724	Sequence 12724, A
	79	48	3.6	223471	4	US-09-949-016-12725	Sequence 12725, A
c	80	47.8	3.6	636	3	US-08-998-416-1137	Sequence 1137, Ap
c	81	47.6	3.5	2238	3	US-08-617-860B-28	Sequence 28, Appl
	82	47.6	3.5	15567	3	US-09-627-376-3	Sequence 3, Appli
	83	47.6	3.5	15567	4	US-10-047-676B-3	Sequence 3, Appli
	84	47.4	3.5	96922	4	US-09-949-016-17061	Sequence 17061, A
c	85	47.4	3.5	134987	4	US-09-949-016-15348	Sequence 15348, A
c	86	47.4	3.5	134987	4	US-09-949-016-15349	Sequence 15349, A
c	87	47.4	3.5	134987	4	US-09-949-016-15350	Sequence 15350, A
c	88	47.4	3.5	134987	4	US-09-949-016-15507	Sequence 15507, A
c	89	47.4	3.5	134987	4	US-09-949-016-15508	Sequence 15508, A
c	90	47.4	3.5	134987	4	US-09-949-016-15509	Sequence 15509, A
c	91	47.2	3.5	1055	4	US-09-806-708B-23	Sequence 23, Appl
c	92	47.2	3.5	8797	4	US-09-949-016-16186	Sequence 16186, A
	93	47.2	3.5	95255	4	US-09-949-016-17067	Sequence 17067, A
	94	47.2	3.5	298336	4	US-09-949-016-16600	Sequence 16600, A
	95	46.8	3.5	601	4	US-09-949-016-168053	Sequence 168053,
	96	46.8	3.5	601	4	US-09-949-016-168054	Sequence 168054,
	97	46.8	3.5	601	4	US-09-949-016-168055	Sequence 168055,
	98	46.8	3.5	601	4	US-09-949-016-168056	Sequence 168056,
c	99	46.8	3.5	141560	4	US-09-949-016-16476	Sequence 16476, A
c	100	46.8	3.5	231129	4	US-09-949-016-16110	Sequence 16110, A

c 101	46.8	3.5	263693	4	US-09-949-016-12386	Sequence 12386, A
c 102	46.8	3.5	263694	4	US-09-949-016-16915	Sequence 16915, A
c 103	46.8	3.5	266293	4	US-09-949-016-11934	Sequence 11934, A
104	46.4	3.4	387902	4	US-09-949-016-14543	Sequence 14543, A
105	46.4	3.4	421883	4	US-09-949-016-12557	Sequence 12557, A
106	46.2	3.4	601	4	US-09-949-016-30530	Sequence 30530, A
107	46.2	3.4	601	4	US-09-949-016-37149	Sequence 37149, A
108	46.2	3.4	601	4	US-09-949-016-37163	Sequence 37163, A
109	46.2	3.4	601	4	US-09-949-016-145867	Sequence 145867,
110	46.2	3.4	601	4	US-09-949-016-146135	Sequence 146135,
111	46.2	3.4	601	4	US-09-949-016-146403	Sequence 146403,
c 112	46.2	3.4	55264	4	US-09-949-016-15014	Sequence 15014, A
c 113	46.2	3.4	94755	4	US-09-949-016-11839	Sequence 11839, A
c 114	46	3.4	25992	4	US-09-949-016-17308	Sequence 17308, A
115	45.8	3.4	1559	4	US-09-489-847-42	Sequence 42, Appl
116	45.8	3.4	2500	4	US-09-579-383-5	Sequence 5, Appli
117	45.6	3.4	255	4	US-09-540-236-28	GENERAL INFORMATI
c 118	45.6	3.4	187169	4	US-09-949-016-12776	Sequence 12776, A
c 119	45.6	3.4	191569	4	US-09-949-016-15940	Sequence 15940, A
c 120	45.4	3.4	615	3	US-08-998-416-186	Sequence 186, App
121	45.4	3.4	3744	3	US-08-961-527-263	Sequence 263, App
122	45.4	3.4	55264	4	US-09-949-016-15014	Sequence 15014, A
123	45.4	3.4	94755	4	US-09-949-016-11839	Sequence 11839, A
c 124	45.2	3.4	147382	4	US-09-949-016-14624	Sequence 14624, A
c 125	45.2	3.4	462589	4	US-09-949-016-12900	Sequence 12900, A
c 126	45.2	3.4	476044	4	US-09-949-016-12412	Sequence 12412, A
c 127	45	3.3	18773	4	US-09-949-016-14164	Sequence 14164, A
128	45	3.3	139049	4	US-09-949-016-17030	Sequence 17030, A
129	45	3.3	251672	4	US-09-949-016-17296	Sequence 17296, A
130	45	3.3	251682	4	US-09-949-016-11973	Sequence 11973, A
c 131	44.8	3.3	837	3	US-08-998-416-288	Sequence 288, App
132	44.6	3.3	19124	2	US-08-487-826B-13	Sequence 13, Appl
133	44.6	3.3	29717	4	US-09-949-016-16284	Sequence 16284, A
134	44.6	3.3	60376	4	US-09-949-016-12423	Sequence 12423, A
135	44.6	3.3	129415	4	US-09-949-016-16997	Sequence 16997, A
c 136	44.6	3.3	200663	4	US-09-949-016-12569	Sequence 12569, A
c 137	44.6	3.3	203093	4	US-09-949-016-14445	Sequence 14445, A
c 138	44.4	3.3	19438	4	US-09-949-016-12699	Sequence 12699, A
c 139	44.4	3.3	451924	4	US-09-949-016-12896	Sequence 12896, A
c 140	44.4	3.3	451925	4	US-09-949-016-17305	Sequence 17305, A
c 141	44.2	3.3	601	4	US-09-949-016-30530	Sequence 30530, A
c 142	44.2	3.3	601	4	US-09-949-016-30531	Sequence 30531, A
143	44.2	3.3	601	4	US-09-949-016-30532	Sequence 30532, A
c 144	44.2	3.3	601	4	US-09-949-016-37149	Sequence 37149, A
c 145	44.2	3.3	601	4	US-09-949-016-37150	Sequence 37150, A
146	44.2	3.3	601	4	US-09-949-016-37151	Sequence 37151, A
c 147	44.2	3.3	601	4	US-09-949-016-37163	Sequence 37163, A
c 148	44.2	3.3	601	4	US-09-949-016-37164	Sequence 37164, A
149	44.2	3.3	601	4	US-09-949-016-37165	Sequence 37165, A
c 150	44.2	3.3	601	4	US-09-949-016-145867	Sequence 145867,
c 151	44.2	3.3	601	4	US-09-949-016-145868	Sequence 145868,
152	44.2	3.3	601	4	US-09-949-016-145869	Sequence 145869,
c 153	44.2	3.3	601	4	US-09-949-016-146135	Sequence 146135,
c 154	44.2	3.3	601	4	US-09-949-016-146136	Sequence 146136,
155	44.2	3.3	601	4	US-09-949-016-146137	Sequence 146137,
c 156	44.2	3.3	601	4	US-09-949-016-146403	Sequence 146403,
c 157	44.2	3.3	601	4	US-09-949-016-146404	Sequence 146404,
158	44.2	3.3	601	4	US-09-949-016-146405	Sequence 146405,
c 159	44.2	3.3	601	4	US-09-949-016-186365	Sequence 186365,
160	44.2	3.3	1584	3	US-08-745-995A-1	Sequence 1, Appli
c 161	44.2	3.3	1584	3	US-08-745-995A-3	Sequence 3, Appli
162	44.2	3.3	1584	4	US-09-005-352-1	Sequence 1, Appli
c 163	44.2	3.3	1584	4	US-09-005-352-3	Sequence 3, Appli
164	44.2	3.3	134987	4	US-09-949-016-15348	Sequence 15348, A
165	44.2	3.3	134987	4	US-09-949-016-15349	Sequence 15349, A
166	44.2	3.3	134987	4	US-09-949-016-15350	Sequence 15350, A
167	44.2	3.3	134987	4	US-09-949-016-15507	Sequence 15507, A
168	44.2	3.3	134987	4	US-09-949-016-15508	Sequence 15508, A
169	44.2	3.3	134987	4	US-09-949-016-15509	Sequence 15509, A
170	44.2	3.3	260247	4	US-09-949-016-13358	Sequence 13358, A
171	44.2	3.3	786431	4	US-09-751-389-3	Sequence 3, Appli
172	44	3.3	1111	4	US-08-956-171E-756	Sequence 756, App
173	44	3.3	1111	4	US-08-781-986A-756	Sequence 756, App
174	44	3.3	8920	2	US-08-446-855A-1	Sequence 1, Appli
175	44	3.3	8920	3	US-09-150-741-1	Sequence 1, Appli
176	43.8	3.3	516	4	US-09-302-626B-79	Sequence 79, Appl
c 177	43.8	3.3	601	4	US-09-949-016-18855	Sequence 18855, A
c 178	43.8	3.3	601	4	US-09-949-016-56720	Sequence 56720, A
179	43.8	3.3	729	4	US-09-302-626B-81	Sequence 81, Appl
180	43.8	3.3	729	4	US-09-302-626B-83	Sequence 83, Appl
181	43.8	3.3	18989	4	US-09-949-016-13435	Sequence 13435, A
182	43.8	3.3	21885	4	US-09-949-016-12600	Sequence 12600, A
c 183	43.8	3.3	331814	4	US-09-949-016-12008	Sequence 12008, A
c 184	43.8	3.3	331814	4	US-09-949-016-17056	Sequence 17056, A
185	43.6	3.2	582	4	US-09-949-016-61868	Sequence 61868, A
c 186	43.6	3.2	8654	1	US-08-920-812-6	Sequence 6, Appli
c 187	43.6	3.2	8654	1	US-08-920-827-6	Sequence 6, Appli
c 188	43.6	3.2	8654	1	US-08-921-177-6	Sequence 6, Appli
c 189	43.6	3.2	8654	1	US-08-362-577C-6	Sequence 6, Appli
c 190	43.6	3.2	8654	2	US-08-920-828-6	Sequence 6, Appli
c 191	43.6	3.2	119153	4	US-09-949-016-12378	Sequence 12378, A
192	43.6	3.2	314798	4	US-09-949-016-13539	Sequence 13539, A
c 193	43.4	3.2	601	4	US-09-949-016-86304	Sequence 86304, A
c 194	43.4	3.2	3167	4	US-09-710-279-4117	Sequence 4117, Ap
c 195	43.4	3.2	3241	4	US-09-710-279-4276	Sequence 4276, Ap
c 196	43.4	3.2	5852	1	US-07-867-106-2	Sequence 2, Appli
197	43.4	3.2	8654	1	US-08-920-812-6	Sequence 6, Appli
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200	43.4	3.2	8654	1	US-08-362-577C-6	Sequence 6, Appli
201	43.4	3.2	8654	2	US-08-920-828-6	Sequence 6, Appli
202	43.4	3.2	30350	4	US-10-118-328-3	Sequence 3, Appli
c 203	43.4	3.2	30820	4	US-09-949-016-17145	Sequence 17145, A
c 204	43.4	3.2	34011	4	US-09-949-016-12485	Sequence 12485, A
205	43.4	3.2	43463	4	US-09-949-016-16341	Sequence 16341, A
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207	43.4	3.2	53332	4	US-09-801-861-3	Sequence 3, Appli
208	43.4	3.2	53332	4	US-10-224-562-3	Sequence 3, Appli
209	43.4	3.2	422592	4	US-09-949-016-14182	Sequence 14182, A
c 210	43.2	3.2	782	3	US-08-998-416-224	Sequence 224, App
c 211	43.2	3.2	20229	4	US-09-949-016-16649	Sequence 16649, A
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214	43.2	3.2	1664976	4	US-09-692-570-1	Sequence 1, Appli
c 215	43	3.2	601	4	US-09-949-016-86305	Sequence 86305, A
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217	43	3.2	4137	3	US-09-221-928-1	Sequence 1, Appli
218	43	3.2	4137	3	US-09-221-527-1	Sequence 1, Appli
219	43	3.2	4137	3	US-09-221-236-1	Sequence 1, Appli
220	43	3.2	4137	3	US-09-221-416-1	Sequence 1, Appli
221	43	3.2	4137	3	US-09-221-245-1	Sequence 1, Appli
222	43	3.2	4137	3	US-09-163-115-1	Sequence 1, Appli
223	43	3.2	4137	3	US-09-221-528-1	Sequence 1, Appli
224	43	3.2	4137	3	US-09-593-553-1	Sequence 1, Appli
225	43	3.2	4137	3	US-09-221-237-1	Sequence 1, Appli
226	43	3.2	4137	4	US-09-757-982-1	Sequence 1, Appli
227	43	3.2	91062	4	US-09-949-016-13019	Sequence 13019, A
c 228	43	3.2	91062	4	US-09-949-016-13019	Sequence 13019, A
229	43	3.2	165841	4	US-09-949-016-16192	Sequence 16192, A
c 230	43	3.2	256171	4	US-09-949-016-12822	Sequence 12822, A
c 231	43	3.2	256176	4	US-09-949-016-15524	Sequence 15524, A
232	43	3.2	451924	4	US-09-949-016-12896	Sequence 12896, A
233	43	3.2	451925	4	US-09-949-016-17305	Sequence 17305, A
234	42.8	3.2	317366	4	US-09-949-016-16001	Sequence 16001, A
c 235	42.8	3.2	387902	4	US-09-949-016-14543	Sequence 14543, A
c 236	42.8	3.2	421883	4	US-09-949-016-12557	Sequence 12557, A
237	42.8	3.2	640681	4	US-09-790-988-1	Sequence 1, Appli
238	42.6	3.2	857	3	US-08-460-040-1	Sequence 1, Appli
239	42.6	3.2	1172	1	US-07-945-288-9	Sequence 9, Appli
240	42.6	3.2	1172	1	US-08-462-831-9	Sequence 9, Appli
241	42.6	3.2	1172	1	US-08-461-809-9	Sequence 9, Appli
242	42.6	3.2	1172	1	US-08-461-441-9	Sequence 9, Appli
243	42.6	3.2	1172	5	PCT-US93-08518-9	Sequence 9, Appli
c 244	42.6	3.2	1785	4	US-09-601-198-156	Sequence 156, App
c 245	42.6	3.2	19124	2	US-08-487-826B-13	Sequence 13, Appl
246	42.6	3.2	256287	4	US-09-949-016-14608	Sequence 14608, A

	247	42.4	3.2	961	6	5194596-16	Patent No. 5194596
	248	42.4	3.2	961	6	5219739-16	Patent No. 5219739
	249	42.4	3.2	961	6	5194596-16	Patent No. 5194596
	250	42.4	3.2	961	6	5219739-16	Patent No. 5219739
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c	252	42.4	3.2	23790	4	US-09-949-016-14212	Sequence 14212, A
c	253	42.4	3.2	57507	4	US-09-949-016-15019	Sequence 15019, A
c	254	42.4	3.2	304533	4	US-09-949-016-15371	Sequence 15371, A
c	255	42.4	3.2	304533	4	US-09-949-016-15372	Sequence 15372, A
c	256	42.2	3.1	597	4	US-09-248-796A-7629	Sequence 7629, Ap
c	257	42.2	3.1	601	4	US-09-949-016-18854	Sequence 18854, A
c	258	42.2	3.1	601	4	US-09-949-016-56719	Sequence 56719, A
	259	42.2	3.1	612	4	US-09-902-540-1357	Sequence 1357, Ap
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	261	42	3.1	2058	3	US-09-390-200-1	Sequence 1, Appli
	262	42	3.1	360470	4	US-09-949-016-13173	Sequence 13173, A
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	265	41.8	3.1	601	4	US-09-949-016-191305	Sequence 191305,
	266	41.8	3.1	881	4	US-08-956-171E-518	Sequence 518, App
	267	41.8	3.1	881	4	US-08-781-986A-518	Sequence 518, App
	268	41.8	3.1	2038	4	US-09-885-723-6	Sequence 6, Appli
	269	41.8	3.1	19438	4	US-09-949-016-12699	Sequence 12699, A
c	270	41.8	3.1	121970	4	US-09-949-016-17216	Sequence 17216, A
c	271	41.8	3.1	124110	4	US-09-949-016-13353	Sequence 13353, A
	272	41.6	3.1	406	4	US-09-829-481-3	Sequence 3, Appli
	273	41.6	3.1	561	4	US-09-601-198-172	Sequence 172, App
c	274	41.6	3.1	601	4	US-09-949-016-179398	Sequence 179398,
c	275	41.6	3.1	601	4	US-09-949-016-179399	Sequence 179399,
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c	279	41.6	3.1	29927	4	US-09-949-016-17475	Sequence 17475, A
c	280	41.6	3.1	37802	4	US-09-949-016-12639	Sequence 12639, A
	281	41.6	3.1	136917	4	US-09-949-016-16369	Sequence 16369, A
c	282	41.4	3.1	601	4	US-09-949-016-168196	Sequence 168196,
	283	41.4	3.1	1039	4	US-09-902-540-1280	Sequence 1280, Ap
	284	41.4	3.1	1779	3	US-09-323-427-1	Sequence 1, Appli
c	285	41.4	3.1	1779	3	US-09-323-427-2	Sequence 2, Appli
	286	41.4	3.1	1779	3	US-09-812-642-1	Sequence 1, Appli
c	287	41.4	3.1	1779	3	US-09-812-642-2	Sequence 2, Appli
	288	41.4	3.1	1779	4	US-10-054-562A-1	Sequence 1, Appli
c	289	41.4	3.1	1779	4	US-10-054-562A-2	Sequence 2, Appli
	290	41.4	3.1	2276	4	US-09-090-672B-6	Sequence 6, Appli
	291	41.4	3.1	124110	4	US-09-949-016-13353	Sequence 13353, A
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	293	41.4	3.1	304533	4	US-09-949-016-15371	Sequence 15371, A
	294	41.4	3.1	304533	4	US-09-949-016-15372	Sequence 15372, A
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	296	41.2	3.1	1897	1	US-08-184-632-1	Sequence 1, Appli
	297	41.2	3.1	97376	4	US-09-949-016-16093	Sequence 16093, A
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	299	41	3.0	601	4	US-09-949-016-37135	Sequence 37135, A
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	301	41	3.0	601	4	US-09-949-016-161112	Sequence 161112,
	302	41	3.0	41798	4	US-09-949-016-16058	Sequence 16058, A
	303	41	3.0	107800	4	US-09-949-016-13118	Sequence 13118, A
	304	41	3.0	116425	4	US-09-949-016-11809	Sequence 11809, A
c	305	41	3.0	139049	4	US-09-949-016-17030	Sequence 17030, A
	306	41	3.0	211049	4	US-09-949-016-15770	Sequence 15770, A
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	308	41	3.0	319608	4	US-09-679-409-1	Sequence 1, Appli
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	310	40.8	3.0	601	4	US-09-949-016-54022	Sequence 54022, A
	311	40.8	3.0	601	4	US-09-949-016-54023	Sequence 54023, A
	312	40.8	3.0	601	4	US-09-949-016-54024	Sequence 54024, A
	313	40.8	3.0	601	4	US-09-949-016-108655	Sequence 108655,
	314	40.8	3.0	601	4	US-09-949-016-108656	Sequence 108656,
	315	40.8	3.0	601	4	US-09-949-016-108657	Sequence 108657,
	316	40.8	3.0	601	4	US-09-949-016-108658	Sequence 108658,
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	318	40.8	3.0	789	6	5219739-8	Patent No. 5219739
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	320	40.8	3.0	1461	5	PCT-US95-04258-4	Sequence 4, Appli
	321	40.8	3.0	3993	3	US-09-167-109-5	Sequence 5, Appli
c	322	40.8	3.0	4529	4	US-09-949-016-14004	Sequence 14004, A
	323	40.8	3.0	25992	4	US-09-949-016-17308	Sequence 17308, A
	324	40.8	3.0	104520	4	US-09-949-016-13303	Sequence 13303, A
	325	40.8	3.0	126029	4	US-09-949-016-14731	Sequence 14731, A
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	327	40.6	3.0	370	3	US-09-376-113-1	Sequence 1, Appli
	328	40.6	3.0	958	2	US-08-757-046A-5	Sequence 5, Appli
	329	40.6	3.0	958	3	US-09-447-208-5	Sequence 5, Appli
	330	40.6	3.0	958	3	US-09-135-988-5	Sequence 5, Appli
	331	40.6	3.0	958	3	US-09-277-716-5	Sequence 5, Appli
	332	40.6	3.0	958	3	US-08-597-274A-5	Sequence 5, Appli
	333	40.6	3.0	958	3	US-08-908-909-5	Sequence 5, Appli
	334	40.6	3.0	958	3	US-09-609-161B-5	Sequence 5, Appli
	335	40.6	3.0	958	3	US-08-990-103-5	Sequence 5, Appli
	336	40.6	3.0	958	4	US-09-746-485A-5	Sequence 5, Appli
	337	40.6	3.0	958	4	US-10-126-139-5	Sequence 5, Appli
	338	40.6	3.0	958	4	US-10-126-798-5	Sequence 5, Appli
	339	40.6	3.0	958	4	US-10-126-777-5	Sequence 5, Appli
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	341	40.6	3.0	2304	4	US-08-781-986A-432	Sequence 432, App
	342	40.6	3.0	2360	3	US-08-836-567-9	Sequence 9, Appli
	343	40.6	3.0	2360	4	US-09-606-304-9	Sequence 9, Appli
c	344	40.6	3.0	12313	4	US-09-949-016-13248	Sequence 13248, A
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c	347	40.4	3.0	601	4	US-09-949-016-196366	Sequence 196366,
c	348	40.4	3.0	601	4	US-09-949-016-196367	Sequence 196367,
	349	40.4	3.0	17612	4	US-09-949-016-15061	Sequence 15061, A
	350	40.4	3.0	42381	4	US-09-949-016-12012	Sequence 12012, A
	351	40.4	3.0	134890	4	US-09-949-016-15602	Sequence 15602, A
c	352	40.4	3.0	258775	4	US-09-949-016-16435	Sequence 16435, A
c	353	40.2	3.0	601	4	US-09-949-016-109751	Sequence 109751,
	354	40.2	3.0	601	4	US-09-949-016-153149	Sequence 153149,
	355	40.2	3.0	616	2	US-08-630-822A-93	Sequence 93, Appl
	356	40.2	3.0	616	2	US-09-005-069-93	Sequence 93, Appl
	357	40.2	3.0	616	3	US-09-171-156A-42	Sequence 42, Appl
	358	40.2	3.0	616	4	US-09-004-730A-42	Sequence 42, Appl
	359	40.2	3.0	616	4	US-08-981-799A-42	Sequence 42, Appl
	360	40.2	3.0	1518	4	US-09-614-912-191	Sequence 191, App
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c	362	40.2	3.0	36242	4	US-09-949-016-12997	Sequence 12997, A
c	363	40.2	3.0	36242	4	US-09-949-016-12998	Sequence 12998, A
c	364	40.2	3.0	36242	4	US-09-949-016-12999	Sequence 12999, A
c	365	40.2	3.0	36242	4	US-09-949-016-13000	Sequence 13000, A
c	366	40.2	3.0	44353	4	US-09-949-016-15302	Sequence 15302, A
c	367	40.2	3.0	101128	4	US-09-949-016-14293	Sequence 14293, A
c	368	40.2	3.0	134434	4	US-09-949-016-17362	Sequence 17362, A
c	369	40.2	3.0	145320	4	US-09-949-016-15858	Sequence 15858, A
c	370	40	3.0	436	3	US-09-439-313-353	Sequence 353, App
c	371	40	3.0	436	3	US-09-352-616A-353	Sequence 353, App
c	372	40	3.0	436	4	US-09-636-215-353	Sequence 353, App
c	373	40	3.0	436	4	US-09-685-166A-353	Sequence 353, App
c	374	40	3.0	436	4	US-09-679-426-353	Sequence 353, App
c	375	40	3.0	436	4	US-09-759-143-353	Sequence 353, App
c	376	40	3.0	436	4	US-09-651-236-353	Sequence 353, App
c	377	40	3.0	601	4	US-09-949-016-75657	Sequence 75657, A
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c	379	40	3.0	2112	4	US-09-248-796A-5361	Sequence 5361, Ap
c	380	40	3.0	14871	4	US-09-949-016-13013	Sequence 13013, A
	381	40	3.0	51259	3	US-08-781-891-209	Sequence 209, App
	382	40	3.0	51259	4	US-09-618-166-209	Sequence 209, App
	383	40	3.0	65415	4	US-09-949-016-16699	Sequence 16699, A
c	384	40	3.0	95255	4	US-09-949-016-17067	Sequence 17067, A
c	385	40	3.0	120213	4	US-09-949-016-13304	Sequence 13304, A
c	386	40	3.0	120217	4	US-09-949-016-12260	Sequence 12260, A
c	387	40	3.0	129415	4	US-09-949-016-16997	Sequence 16997, A
c	388	40	3.0	155617	4	US-09-949-016-16191	Sequence 16191, A
	389	40	3.0	263693	4	US-09-949-016-12386	Sequence 12386, A
	390	40	3.0	263694	4	US-09-949-016-16915	Sequence 16915, A
c	391	39.8	3.0	601	4	US-09-949-016-77299	Sequence 77299, A
c	392	39.8	3.0	601	4	US-09-949-016-199095	Sequence 199095,

	393	39.8	3.0	1719	4	US-09-949-016-667	Sequence 667, App
	394	39.8	3.0	2527	4	US-09-244-805-29	Sequence 29, Appl
	395	39.8	3.0	2751	4	US-09-270-767-14784	Sequence 14784, A
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	397	39.8	3.0	6124	3	US-08-213-419B-3	Sequence 3, Appli
	398	39.8	3.0	6265	3	US-09-129-112-3	Sequence 3, Appli
c	399	39.8	3.0	46823	4	US-09-949-016-12723	Sequence 12723, A
c	400	39.8	3.0	46940	4	US-09-949-016-16252	Sequence 16252, A
c	401	39.8	3.0	78649	4	US-09-949-016-14619	Sequence 14619, A
c	402	39.8	3.0	78649	4	US-09-949-016-14620	Sequence 14620, A
c	403	39.8	3.0	78649	4	US-09-949-016-16227	Sequence 16227, A
c	404	39.8	3.0	78649	4	US-09-949-016-16228	Sequence 16228, A
	405	39.8	3.0	157644	4	US-09-949-016-16179	Sequence 16179, A
	406	39.8	3.0	157644	4	US-09-949-016-16180	Sequence 16180, A
	407	39.8	3.0	225127	4	US-09-949-016-16480	Sequence 16480, A
c	408	39.8	3.0	360470	4	US-09-949-016-13173	Sequence 13173, A
	409	39.6	2.9	601	4	US-09-949-016-36969	Sequence 36969, A
c	410	39.6	2.9	601	4	US-09-949-016-93907	Sequence 93907, A
c	411	39.6	2.9	601	4	US-09-949-016-138144	Sequence 138144,
c	412	39.6	2.9	601	4	US-09-949-016-138145	Sequence 138145,
	413	39.6	2.9	682	4	US-09-614-912-17	Sequence 17, Appl
c	414	39.6	2.9	7050	4	US-09-976-594-683	Sequence 683, App
c	415	39.6	2.9	20674	3	US-09-641-638-651	Sequence 651, App
c	416	39.6	2.9	20674	4	US-10-170-097-651	Sequence 651, App
c	417	39.6	2.9	27783	4	US-09-949-016-16736	Sequence 16736, A
	418	39.6	2.9	54576	4	US-09-949-016-15954	Sequence 15954, A
	419	39.6	2.9	54576	4	US-09-949-016-15955	Sequence 15955, A
c	420	39.6	2.9	112705	4	US-09-949-016-15630	Sequence 15630, A
	421	39.6	2.9	164061	4	US-09-949-016-17422	Sequence 17422, A
	422	39.6	2.9	393753	4	US-09-949-016-14573	Sequence 14573, A
	423	39.6	2.9	393753	4	US-09-949-016-14574	Sequence 14574, A
	424	39.6	2.9	818128	4	US-09-949-016-14546	Sequence 14546, A
	425	39.6	2.9	818128	4	US-09-949-016-14547	Sequence 14547, A
	426	39.6	2.9	818128	4	US-09-949-016-14548	Sequence 14548, A
	427	39.6	2.9	818128	4	US-09-949-016-14549	Sequence 14549, A
	428	39.6	2.9	818128	4	US-09-949-016-14550	Sequence 14550, A
	429	39.6	2.9	818128	4	US-09-949-016-14551	Sequence 14551, A
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	432	39.6	2.9	818128	4	US-09-949-016-14554	Sequence 14554, A
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	434	39.6	2.9	818128	4	US-09-949-016-14556	Sequence 14556, A
	435	39.6	2.9	818128	4	US-09-949-016-14557	Sequence 14557, A
	436	39.6	2.9	818128	4	US-09-949-016-14558	Sequence 14558, A
	437	39.6	2.9	818128	4	US-09-949-016-14559	Sequence 14559, A
	438	39.6	2.9	818128	4	US-09-949-016-14560	Sequence 14560, A
	439	39.6	2.9	818128	4	US-09-949-016-14561	Sequence 14561, A
	440	39.6	2.9	818128	4	US-09-949-016-14562	Sequence 14562, A
	441	39.6	2.9	818128	4	US-09-949-016-14564	Sequence 14564, A
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	444	39.6	2.9	818128	4	US-09-949-016-14567	Sequence 14567, A
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c	448	39.4	2.9	396	4	US-09-970-966-10	Sequence 10, Appl
	449	39.4	2.9	601	4	US-09-949-016-168196	Sequence 168196,
c	450	39.4	2.9	660	1	US-07-991-867B-32	Sequence 32, Appl
c	451	39.4	2.9	660	1	US-08-107-755A-32	Sequence 32, Appl
c	452	39.4	2.9	660	2	US-08-544-332-32	Sequence 32, Appl
c	453	39.4	2.9	660	3	US-09-370-861A-32	Sequence 32, Appl
	454	39.4	2.9	946	3	US-08-916-443A-15	Sequence 15, Appl
	455	39.4	2.9	1319	2	US-08-504-459-7	Sequence 7, Appli
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c	457	39.4	2.9	1511	1	US-08-107-755A-8	Sequence 8, Appli
c	458	39.4	2.9	1511	2	US-08-544-332-8	Sequence 8, Appli
c	459	39.4	2.9	1511	3	US-09-370-861A-8	Sequence 8, Appli
c	460	39.4	2.9	1853	4	US-09-220-132-120	Sequence 120, App
	461	39.4	2.9	2193	3	US-09-427-261-2	Sequence 2, Appli
	462	39.4	2.9	2193	3	US-09-427-261-3	Sequence 3, Appli
c	463	39.4	2.9	4810	3	US-08-852-629-11	Sequence 11, Appl
c	464	39.4	2.9	4838	3	US-08-852-629-15	Sequence 15, Appl
c	465	39.4	2.9	29291	4	US-09-949-016-16263	Sequence 16263, A
	466	39.4	2.9	29927	4	US-09-949-016-11814	Sequence 11814, A
	467	39.4	2.9	29927	4	US-09-949-016-17474	Sequence 17474, A
	468	39.4	2.9	29927	4	US-09-949-016-17475	Sequence 17475, A
	469	39.4	2.9	37802	4	US-09-949-016-12639	Sequence 12639, A
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c	471	39.4	2.9	57402	4	US-09-949-016-13293	Sequence 13293, A
	472	39.4	2.9	60465	4	US-09-949-016-15995	Sequence 15995, A
c	473	39.4	2.9	124480	4	US-09-949-016-15921	Sequence 15921, A
c	474	39.4	2.9	314798	4	US-09-949-016-13539	Sequence 13539, A
c	475	39.4	2.9	580073	4	US-08-545-528D-1	Sequence 1, Appli
	476	39.2	2.9	458	1	US-08-524-757-1	Sequence 1, Appli
	477	39.2	2.9	601	4	US-09-949-016-54020	Sequence 54020, A
	478	39.2	2.9	601	4	US-09-949-016-108654	Sequence 108654,
	479	39.2	2.9	1146	3	US-09-452-239-3	Sequence 3, Appli
	480	39.2	2.9	1286	4	US-09-489-847-124	Sequence 124, App
	481	39.2	2.9	1342	4	US-09-489-847-89	Sequence 89, Appl
	482	39.2	2.9	1622	4	US-08-956-171E-732	Sequence 732, App
	483	39.2	2.9	1622	4	US-08-781-986A-732	Sequence 732, App
	484	39.2	2.9	2020	4	US-09-716-129-29	Sequence 29, Appl
c	485	39.2	2.9	2614	4	US-09-004-056-1	Sequence 1, Appli
c	486	39.2	2.9	6124	3	US-08-213-419B-3	Sequence 3, Appli
c	487	39.2	2.9	53722	4	US-09-949-016-12077	Sequence 12077, A
c	488	39.2	2.9	96922	4	US-09-949-016-17061	Sequence 17061, A
	489	39.2	2.9	114139	4	US-09-949-016-16536	Sequence 16536, A
	490	39.2	2.9	227750	4	US-09-949-016-17175	Sequence 17175, A
	491	39	2.9	239	4	US-09-621-976-16632	Sequence 16632, A
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	493	39	2.9	536	2	US-08-472-604-1	Sequence 1, Appli
	494	39	2.9	536	2	US-08-486-117-1	Sequence 1, Appli
	495	39	2.9	536	3	US-08-477-537-1	Sequence 1, Appli
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	497	39	2.9	601	4	US-09-949-016-37133	Sequence 37133, A
	498	39	2.9	601	4	US-09-949-016-37134	Sequence 37134, A
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c	500	39	2.9	601	4	US-09-949-016-86306	Sequence 86306, A
c	501	39	2.9	601	4	US-09-949-016-86307	Sequence 86307, A
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	504	39	2.9	601	4	US-09-949-016-144794	Sequence 144794,
	505	39	2.9	601	4	US-09-949-016-161110	Sequence 161110,
	506	39	2.9	601	4	US-09-949-016-161111	Sequence 161111,
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	513	39	2.9	1478	3	US-09-020-818-3	Sequence 3, Appli
	514	39	2.9	1478	3	US-08-907-740-3	Sequence 3, Appli
	515	39	2.9	1478	4	US-09-797-467-3	Sequence 3, Appli
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	517	39	2.9	1478	5	PCT-US94-07072-1	Sequence 1, Appli
	518	39	2.9	1579	4	US-09-311-021-93	Sequence 93, Appl
	519	39	2.9	1651	3	US-09-465-558-49	Sequence 49, Appl
	520	39	2.9	3781	3	US-08-688-988-5	Sequence 5, Appli
	521	39	2.9	5021	4	US-09-949-016-786	Sequence 786, App
c	522	39	2.9	14176	1	US-08-307-499-1	Sequence 1, Appli
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c	524	39	2.9	14176	3	US-09-299-268-1	Sequence 1, Appli
	525	39	2.9	14176	3	US-09-299-268-14	Sequence 14, Appl
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c	527	39	2.9	23574	4	US-09-949-016-15351	Sequence 15351, A
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c	529	39	2.9	47781	4	US-09-949-016-16492	Sequence 16492, A
c	530	39	2.9	47781	4	US-09-949-016-16493	Sequence 16493, A
c	531	39	2.9	47781	4	US-09-949-016-16494	Sequence 16494, A
	532	39	2.9	83697	4	US-09-949-016-16040	Sequence 16040, A
c	533	39	2.9	86116	4	US-09-949-016-14766	Sequence 14766, A
c	534	39	2.9	140224	4	US-09-949-016-17002	Sequence 17002, A
	535	39	2.9	140844	4	US-09-949-016-14199	Sequence 14199, A
c	536	39	2.9	154626	4	US-09-949-016-14000	Sequence 14000, A
	537	39	2.9	285478	4	US-09-949-016-13362	Sequence 13362, A
c	538	38.8	2.9	601	4	US-09-949-016-45739	Sequence 45739, A

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541	38.8	2.9	660	1	US-08-107-755A-32	Sequence 32, Appl
542	38.8	2.9	660	2	US-08-544-332-32	Sequence 32, Appl
543	38.8	2.9	660	3	US-09-370-861A-32	Sequence 32, Appl
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545	38.8	2.9	1004	4	US-09-071-252-3	Sequence 3, Appli
c 546	38.8	2.9	1230	3	US-09-140-466-1	Sequence 1, Appli
547	38.8	2.9	1511	1	US-07-991-867B-8	Sequence 8, Appli
548	38.8	2.9	1511	1	US-08-107-755A-8	Sequence 8, Appli
549	38.8	2.9	1511	2	US-08-544-332-8	Sequence 8, Appli
550	38.8	2.9	1511	3	US-09-370-861A-8	Sequence 8, Appli
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553	38.8	2.9	4838	3	US-08-852-629-15	Sequence 15, Appl
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c 555	38.8	2.9	23501	4	US-09-949-016-17517	Sequence 17517, A
c 556	38.8	2.9	37580	4	US-09-949-016-16658	Sequence 16658, A
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558	38.8	2.9	45300	4	US-09-949-016-13045	Sequence 13045, A
559	38.8	2.9	94142	4	US-09-949-016-16553	Sequence 16553, A
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c 561	38.8	2.9	285478	4	US-09-949-016-13362	Sequence 13362, A
c 562	38.8	2.9	678533	4	US-09-949-016-14577	Sequence 14577, A
c 563	38.8	2.9	678533	4	US-09-949-016-14578	Sequence 14578, A
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566	38.6	2.9	601	4	US-09-949-016-161109	Sequence 161109,
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569	38.6	2.9	601	4	US-09-949-016-207004	Sequence 207004,
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573	38.6	2.9	1420	2	US-08-909-965C-3	Sequence 3, Appli
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575	38.6	2.9	1641	4	US-08-988-197-8	Sequence 8, Appli
576	38.6	2.9	1641	4	US-10-385-072-8	Sequence 8, Appli
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580	38.6	2.9	33044	4	US-09-949-016-17613	Sequence 17613, A
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583	38.6	2.9	46323	4	US-09-949-016-13267	Sequence 13267, A
c 584	38.6	2.9	88758	4	US-09-949-016-13502	Sequence 13502, A
c 585	38.6	2.9	95318	4	US-09-949-016-11784	Sequence 11784, A
c 586	38.6	2.9	95318	4	US-09-949-016-13998	Sequence 13998, A
c 587	38.6	2.9	114139	4	US-09-949-016-16536	Sequence 16536, A
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589	38.4	2.9	277	1	US-08-244-113-18	Sequence 18, Appl
c 590	38.4	2.9	340	1	US-08-171-385-27	Sequence 27, Appl
c 591	38.4	2.9	340	3	US-08-361-441B-27	Sequence 27, Appl
c 592	38.4	2.9	601	4	US-09-949-016-62108	Sequence 62108, A
c 593	38.4	2.9	601	4	US-09-949-016-75658	Sequence 75658, A
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599	38.4	2.9	57507	4	US-09-949-016-15019	Sequence 15019, A
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c 601	38.4	2.9	152070	4	US-09-949-016-15402	Sequence 15402, A
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603	38.4	2.9	476044	4	US-09-949-016-12412	Sequence 12412, A
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605	38.2	2.8	173	4	US-09-621-976-15319	Sequence 15319, A
606	38.2	2.8	178	4	US-09-621-976-15322	Sequence 15322, A
607	38.2	2.8	180	4	US-09-621-976-15320	Sequence 15320, A
608	38.2	2.8	194	4	US-09-621-976-15317	Sequence 15317, A
609	38.2	2.8	675	4	US-09-621-976-2461	Sequence 2461, Ap
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c 611	38.2	2.8	865	4	US-09-557-170A-12	Sequence 12, Appl
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614	38.2	2.8	1330	4	US-09-557-170A-26	Sequence 26, Appl
615	38.2	2.8	1337	4	US-09-557-170A-24	Sequence 24, Appl
616	38.2	2.8	1441	3	US-08-821-994-63	Sequence 63, Appl
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618	38.2	2.8	1941	3	US-09-368-240-2	Sequence 2, Appli
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622	38.2	2.8	2964	4	US-09-578-063-25	Sequence 25, Appl
623	38.2	2.8	3001	4	US-09-539-333D-187	Sequence 187, App
624	38.2	2.8	3999	3	US-09-351-224E-9	Sequence 9, Appli
625	38.2	2.8	3999	4	US-09-677-488A-9	Sequence 9, Appli
626	38.2	2.8	3999	4	US-09-677-682B-9	Sequence 9, Appli
627	38.2	2.8	3999	4	US-09-882-694B-9	Sequence 9, Appli
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632	38.2	2.8	4905	2	US-08-475-352-3	Sequence 3, Appli
633	38.2	2.8	4905	4	US-09-170-699-3	Sequence 3, Appli
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635	38.2	2.8	12513	4	US-09-949-016-14989	Sequence 14989, A
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c 642	38.2	2.8	116425	4	US-09-949-016-11809	Sequence 11809, A
c 643	38.2	2.8	151295	4	US-09-949-016-14568	Sequence 14568, A
c 644	38.2	2.8	151295	4	US-09-949-016-14569	Sequence 14569, A
c 645	38.2	2.8	151295	4	US-09-949-016-14570	Sequence 14570, A
c 646	38.2	2.8	151295	4	US-09-949-016-14571	Sequence 14571, A
c 647	38.2	2.8	151295	4	US-09-949-016-14572	Sequence 14572, A
c 648	38.2	2.8	393753	4	US-09-949-016-14573	Sequence 14573, A
c 649	38.2	2.8	393753	4	US-09-949-016-14574	Sequence 14574, A
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c 653	38.2	2.8	818128	4	US-09-949-016-14548	Sequence 14548, A
c 654	38.2	2.8	818128	4	US-09-949-016-14549	Sequence 14549, A
c 655	38.2	2.8	818128	4	US-09-949-016-14550	Sequence 14550, A
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c 657	38.2	2.8	818128	4	US-09-949-016-14552	Sequence 14552, A
c 658	38.2	2.8	818128	4	US-09-949-016-14553	Sequence 14553, A
c 659	38.2	2.8	818128	4	US-09-949-016-14554	Sequence 14554, A
c 660	38.2	2.8	818128	4	US-09-949-016-14555	Sequence 14555, A
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c 663	38.2	2.8	818128	4	US-09-949-016-14558	Sequence 14558, A
c 664	38.2	2.8	818128	4	US-09-949-016-14559	Sequence 14559, A
c 665	38.2	2.8	818128	4	US-09-949-016-14560	Sequence 14560, A
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c 667	38.2	2.8	818128	4	US-09-949-016-14562	Sequence 14562, A
c 668	38.2	2.8	818128	4	US-09-949-016-14564	Sequence 14564, A
c 669	38.2	2.8	818128	4	US-09-949-016-14565	Sequence 14565, A
c 670	38.2	2.8	818128	4	US-09-949-016-14566	Sequence 14566, A
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677	38	2.8	601	4	US-09-949-016-113637	Sequence 113637,
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679	38	2.8	1096	4	US-09-270-767-20872	Sequence 20872, A
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681	38	2.8	1477	4	US-09-585-173B-7	Sequence 7, Appli
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683	38	2.8	1910	3	US-09-517-467B-7	Sequence 7, Appli
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	685	38	2.8	1964	4	US-09-963-908-2 Sequence 2, Appli
	686	38	2.8	2090	2	US-08-439-814-1 Sequence 1, Appli
	687	38	2.8	3812	1	US-08-188-582-19 Sequence 19, Appl
	688	38	2.8	3812	1	US-08-646-715-19 Sequence 19, Appl
	689	38	2.8	6243	2	US-09-056-075-1 Sequence 1, Appli
	690	38	2.8	17013	4	US-09-949-016-16229 Sequence 16229, A
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	696	38	2.8	49309	4	US-09-949-016-13084 Sequence 13084, A
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	699	38	2.8	111235	4	US-09-949-016-15328 Sequence 15328, A
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	702	38	2.8	193689	4	US-09-949-016-13088 Sequence 13088, A
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	707	37.8	2.8	601	4	US-09-949-016-46041 Sequence 46041, A
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	709	37.8	2.8	601	4	US-09-949-016-196366 Sequence 196366,
	710	37.8	2.8	711	4	US-09-621-976-17854 Sequence 17854, A
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	712	37.8	2.8	891	4	US-09-535-909-13 Sequence 13, Appl
	713	37.8	2.8	997	4	US-09-523-686-1 Sequence 1, Appli
	714	37.8	2.8	1494	4	US-09-535-909-2 Sequence 2, Appli
	715	37.8	2.8	1512	2	US-08-909-965C-8 Sequence 8, Appli
	716	37.8	2.8	1895	3	US-09-444-336-7 Sequence 7, Appli
	717	37.8	2.8	1908	3	US-09-149-476-39 Sequence 39, Appl
	718	37.8	2.8	2091	3	US-09-813-818-1 Sequence 1, Appli
	719	37.8	2.8	2091	4	US-10-199-333-1 Sequence 1, Appli
	720	37.8	2.8	2422	1	US-07-867-106-5 Sequence 5, Appli
	721	37.8	2.8	2447	2	US-09-014-969-14 Sequence 14, Appl
	722	37.8	2.8	2628	2	US-08-696-944-1 Sequence 1, Appli
	723	37.8	2.8	5828	4	US-09-023-655-1386 Sequence 1386, Ap
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	725	37.8	2.8	5828	4	US-09-903-199-6 Sequence 6, Appli
	726	37.8	2.8	5828	4	US-09-903-216-6 Sequence 6, Appli
	727	37.8	2.8	5828	4	US-09-903-063-6 Sequence 6, Appli
	728	37.8	2.8	5828	4	US-09-859-604-6 Sequence 6, Appli
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c	730	37.8	2.8	15418	4	US-09-994-427A-1 Sequence 1, Appli
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	742	37.6	2.8	601	4	US-09-949-016-57772 Sequence 57772, A
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	749	37.6	2.8	1181	3	US-09-149-476-310 Sequence 310, App
	750	37.6	2.8	1212	3	US-09-149-476-186 Sequence 186, App
	751	37.6	2.8	1474	3	US-08-821-994-64 Sequence 64, Appl
	752	37.6	2.8	2434	4	US-09-489-847-67 Sequence 67, Appl
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c	754	37.6	2.8	2555	3	US-09-265-731-3 Sequence 3, Appli
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	761	37.6	2.8	103894	4	US-09-949-016-14450 Sequence 14450, A
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	769	37.4	2.8	396	4	US-09-004-730A-33 Sequence 33, Appl
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	776	37.4	2.8	601	4	US-09-949-016-37153 Sequence 37153, A
	777	37.4	2.8	601	4	US-09-949-016-37166 Sequence 37166, A
	778	37.4	2.8	601	4	US-09-949-016-37167 Sequence 37167, A
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	788	37.4	2.8	601	4	US-09-949-016-146407 Sequence 146407,
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	794	37.4	2.8	857	1	US-08-308-883-1 Sequence 1, Appli
	795	37.4	2.8	857	1	US-08-730-163-1 Sequence 1, Appli
	796	37.4	2.8	857	3	US-08-256-799-1 Sequence 1, Appli
	797	37.4	2.8	857	3	US-08-462-437-1 Sequence 1, Appli
	798	37.4	2.8	1007	4	US-09-640-211A-197 Sequence 197, App
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	801	37.4	2.8	1347	4	US-09-248-796A-3017 Sequence 3017, Ap
	802	37.4	2.8	1408	4	US-10-000-489-111 Sequence 111, App
	803	37.4	2.8	1443	4	US-09-904-615-21 Sequence 21, Appl
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	806	37.4	2.8	2711	4	US-09-765-111A-24 Sequence 24, Appl
	807	37.4	2.8	2915	4	US-09-578-063-72 Sequence 72, Appl
	808	37.4	2.8	3299	4	US-09-800-729-68 Sequence 68, Appl
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	814	37.4	2.8	54452	4	US-09-949-016-13003 Sequence 13003, A
	815	37.4	2.8	85665	4	US-09-949-016-17345 Sequence 17345, A
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c	817	37.4	2.8	101982	4	US-09-949-016-12590 Sequence 12590, A
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	820	37.4	2.8	201529	4	US-09-949-016-12740 Sequence 12740, A
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c	822	37.4	2.8	254964	4	US-09-949-016-12583 Sequence 12583, A
c	823	37.4	2.8	254964	4	US-09-949-016-17392 Sequence 17392, A
	824	37.4	2.8	767677	4	US-09-949-016-12147 Sequence 12147, A
	825	37.4	2.8	767677	4	US-09-949-016-17361 Sequence 17361, A
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c	828	37.2	2.8	396	4	US-09-713-550-16 Sequence 16, Appl
	829	37.2	2.8	396	4	US-09-621-976-19065 Sequence 19065, A
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835	37.2	2.8	757	4	US-09-270-767-5589	Sequence 5589, Ap
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838	37.2	2.8	817	3	US-09-625-918-1	Sequence 1, Appli
839	37.2	2.8	923	3	US-08-906-769-144	Sequence 144, App
840	37.2	2.8	923	3	US-08-906-616-144	Sequence 144, App
841	37.2	2.8	923	3	US-08-639-075A-144	Sequence 144, App
842	37.2	2.8	923	3	US-09-012-431-144	Sequence 144, App
843	37.2	2.8	923	3	US-09-012-692-144	Sequence 144, App
844	37.2	2.8	923	3	US-08-906-613-144	Sequence 144, App
845	37.2	2.8	1159	3	US-09-410-464-14	Sequence 14, Appl
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847	37.2	2.8	1279	3	US-09-609-161B-31	Sequence 31, Appl
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c 849	37.2	2.8	1289	4	US-09-270-767-21901	Sequence 21901, A
850	37.2	2.8	1712	4	US-09-148-545-106	Sequence 106, App
851	37.2	2.8	1753	3	US-09-149-476-56	Sequence 56, Appl
852	37.2	2.8	1822	4	US-09-148-545-105	Sequence 105, App
853	37.2	2.8	1939	1	US-07-715-751B-2	Sequence 2, Appli
854	37.2	2.8	2202	3	US-09-388-743-1	Sequence 1, Appli
855	37.2	2.8	2202	4	US-10-044-543-1	Sequence 1, Appli
c 856	37.2	2.8	2680	4	US-09-614-408-7	Sequence 7, Appli
857	37.2	2.8	2798	3	US-09-318-448-34	Sequence 34, Appl
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859	37.2	2.8	3437	3	US-08-860-339-17	Sequence 17, Appl
860	37.2	2.8	3437	4	US-09-573-629-17	Sequence 17, Appl
861	37.2	2.8	3437	4	US-10-208-349-17	Sequence 17, Appl
862	37.2	2.8	3527	2	US-08-909-965C-7	Sequence 7, Appli
863	37.2	2.8	4239	4	US-09-815-048-1	Sequence 1, Appli
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866	37.2	2.8	10136	5	PCT-US95-16216-2	Sequence 2, Appli
867	37.2	2.8	47555	4	US-09-949-016-16549	Sequence 16549, A
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871	37.2	2.8	108310	4	US-09-949-016-16366	Sequence 16366, A
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873	37	2.7	257	4	US-09-621-976-10203	Sequence 10203, A
874	37	2.7	259	4	US-09-621-976-10297	Sequence 10297, A
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876	37	2.7	271	4	US-09-621-976-10193	Sequence 10193, A
877	37	2.7	279	4	US-09-621-976-10220	Sequence 10220, A
878	37	2.7	299	4	US-09-621-976-10211	Sequence 10211, A
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c 880	37	2.7	601	4	US-09-949-016-144793	Sequence 144793,
c 881	37	2.7	601	4	US-09-949-016-144794	Sequence 144794,
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883	37	2.7	832	4	US-09-621-976-2813	Sequence 2813, Ap
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885	37	2.7	991	3	US-09-247-373B-25	Sequence 25, Appl
886	37	2.7	991	3	US-09-296-715-25	Sequence 25, Appl
887	37	2.7	1042	3	US-08-978-289-7	Sequence 7, Appli
888	37	2.7	1151	4	US-09-270-767-12633	Sequence 12633, A
889	37	2.7	1190	4	US-09-390-207-1	Sequence 1, Appli
c 890	37	2.7	1374	4	US-09-601-198-158	Sequence 158, App
891	37	2.7	1465	4	US-09-573-906-1	Sequence 1, Appli
892	37	2.7	1486	4	US-09-461-325-73	Sequence 73, Appl
893	37	2.7	1486	4	US-10-012-542-73	Sequence 73, Appl
894	37	2.7	1486	4	US-10-115-123-73	Sequence 73, Appl
895	37	2.7	1872	3	US-09-801-052-1	Sequence 1, Appli
896	37	2.7	1872	4	US-10-020-121-1	Sequence 1, Appli
897	37	2.7	1927	4	US-09-187-999-12	Sequence 12, Appl
898	37	2.7	1982	3	US-08-747-221B-13	Sequence 13, Appl
c 899	37	2.7	1982	3	US-08-747-221B-15	Sequence 15, Appl
900	37	2.7	1982	3	US-09-005-051-13	Sequence 13, Appl
c 901	37	2.7	1982	3	US-09-005-051-15	Sequence 15, Appl
902	37	2.7	1982	4	US-09-403-942F-13	Sequence 13, Appl
c 903	37	2.7	1982	4	US-09-403-942F-15	Sequence 15, Appl
904	37	2.7	2007	4	US-09-328-352-2460	Sequence 2460, Ap
905	37	2.7	2144	3	US-08-747-221B-57	Sequence 57, Appl
c 906	37	2.7	2144	3	US-08-747-221B-59	Sequence 59, Appl
907	37	2.7	2144	3	US-09-005-051-57	Sequence 57, Appl
c 908	37	2.7	2144	3	US-09-005-051-59	Sequence 59, Appl
909	37	2.7	2144	4	US-09-403-942F-57	Sequence 57, Appl
c 910	37	2.7	2144	4	US-09-403-942F-59	Sequence 59, Appl
911	37	2.7	2287	4	US-09-949-016-134	Sequence 134, App
c 912	37	2.7	3130	2	US-08-474-379C-62	Sequence 62, Appl
c 913	37	2.7	3130	3	US-09-146-249A-62	Sequence 62, Appl
c 914	37	2.7	3130	3	US-08-206-188B-62	Sequence 62, Appl
915	37	2.7	4595	4	US-09-023-905A-9	Sequence 9, Appli
916	37	2.7	5798	4	US-09-377-285B-33	Sequence 33, Appl
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919	37	2.7	25199	4	US-09-949-016-13361	Sequence 13361, A
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924	37	2.7	66933	4	US-09-543-771B-11	Sequence 11, Appl
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926	37	2.7	72049	4	US-09-543-771B-9	Sequence 9, Appli
927	37	2.7	76281	4	US-09-949-016-12708	Sequence 12708, A
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929	37	2.7	192302	4	US-09-949-016-15270	Sequence 15270, A
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c 936	36.8	2.7	396	4	US-09-713-550-33	Sequence 33, Appl
c 937	36.8	2.7	396	4	US-09-825-294-25	Sequence 25, Appl
c 938	36.8	2.7	396	4	US-09-825-294-33	Sequence 33, Appl
c 939	36.8	2.7	396	4	US-09-970-966-25	Sequence 25, Appl
c 940	36.8	2.7	396	4	US-09-970-966-33	Sequence 33, Appl
941	36.8	2.7	531	3	US-09-399-913-37	Sequence 37, Appl
942	36.8	2.7	531	4	US-09-350-614-37	Sequence 37, Appl
943	36.8	2.7	601	4	US-09-949-016-37136	Sequence 37136, A
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945	36.8	2.7	601	4	US-09-949-016-161113	Sequence 161113,
946	36.8	2.7	601	4	US-09-949-016-185995	Sequence 185995,
947	36.8	2.7	601	4	US-09-949-016-185996	Sequence 185996,
948	36.8	2.7	979	4	US-09-770-916-3	Sequence 3, Appli
949	36.8	2.7	1016	4	US-09-716-129-42	Sequence 42, Appl
950	36.8	2.7	1100	3	US-07-861-458C-4	Sequence 4, Appli
951	36.8	2.7	1230	3	US-09-387-574-5	Sequence 5, Appli
952	36.8	2.7	1230	3	US-09-668-096-5	Sequence 5, Appli
953	36.8	2.7	1440	2	US-08-743-637B-174	Sequence 174, App
954	36.8	2.7	1440	3	US-08-526-840B-174	Sequence 174, App
955	36.8	2.7	1440	4	US-09-107-532A-3398	Sequence 3398, Ap
956	36.8	2.7	1440	4	US-09-134-000C-1302	Sequence 1302, Ap
957	36.8	2.7	1466	3	US-08-984-919A-10	Sequence 10, Appl
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959	36.8	2.7	1472	3	US-08-781-420-10	Sequence 10, Appl
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961	36.8	2.7	1472	3	US-08-874-102-10	Sequence 10, Appl
c 962	36.8	2.7	1472	3	US-08-874-102-12	Sequence 12, Appl
963	36.8	2.7	1472	3	US-09-006-595A-10	Sequence 10, Appl
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974	36.8	2.7	2369	4	US-09-057-996-13	Sequence 13, Appl
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c1203	36.2	2.7	601	4	US-09-949-016-28998	Sequence 28998, A
c1204	36.2	2.7	601	4	US-09-949-016-62109	Sequence 62109, A
c1205	36.2	2.7	601	4	US-09-949-016-66698	Sequence 66698, A
c1206	36.2	2.7	601	4	US-09-949-016-74456	Sequence 74456, A
1207	36.2	2.7	601	4	US-09-949-016-111546	Sequence 111546,
1208	36.2	2.7	601	4	US-09-949-016-111694	Sequence 111694,
1209	36.2	2.7	601	4	US-09-949-016-111840	Sequence 111840,
1210	36.2	2.7	601	4	US-09-949-016-111985	Sequence 111985,
c1211	36.2	2.7	601	4	US-09-949-016-148284	Sequence 148284,
c1212	36.2	2.7	601	4	US-09-949-016-148285	Sequence 148285,
c1213	36.2	2.7	601	4	US-09-949-016-148286	Sequence 148286,
1214	36.2	2.7	663	3	US-08-998-416-191	Sequence 191, App
1215	36.2	2.7	803	4	US-09-800-729-60	Sequence 60, Appl
1216	36.2	2.7	1034	4	US-09-311-021-105	Sequence 105, App
1217	36.2	2.7	1114	3	US-09-152-060-41	Sequence 41, Appl
1218	36.2	2.7	1116	3	US-08-916-443A-16	Sequence 16, Appl
1219	36.2	2.7	1240	1	US-08-388-756-1	Sequence 1, Appli
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1222	36.2	2.7	1323	3	US-09-413-068-3	Sequence 3, Appli
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1224	36.2	2.7	1378	4	US-09-935-038A-4	Sequence 4, Appli
1225	36.2	2.7	1411	3	US-08-964-127-5	Sequence 5, Appli
1226	36.2	2.7	1411	3	US-09-496-692-5	Sequence 5, Appli
1227	36.2	2.7	1411	4	US-10-000-273-5	Sequence 5, Appli
1228	36.2	2.7	1459	4	US-09-537-654-3	Sequence 3, Appli
1229	36.2	2.7	1582	3	US-08-545-196B-10	Sequence 10, Appl
1230	36.2	2.7	1582	3	US-08-545-196B-12	Sequence 12, Appl
1231	36.2	2.7	1821	4	US-09-800-729-59	Sequence 59, Appl
1232	36.2	2.7	1851	3	US-09-149-476-62	Sequence 62, Appl
1233	36.2	2.7	1866	4	US-09-673-395A-24	Sequence 24, Appl
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1236	36.2	2.7	2288	4	US-09-800-729-24	Sequence 24, Appl
1237	36.2	2.7	2422	4	US-09-369-247-53	Sequence 53, Appl
1238	36.2	2.7	2634	3	US-09-463-238-3	Sequence 3, Appli
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1243	36.2	2.7	4895	3	US-09-053-866-1	Sequence 1, Appli
1244	36.2	2.7	4895	3	US-09-479-130-1	Sequence 1, Appli
1245	36.2	2.7	4895	4	US-09-472-130A-1	Sequence 1, Appli
1246	36.2	2.7	5796	4	US-09-366-715-4	Sequence 4, Appli
1247	36.2	2.7	6768	1	US-08-107-755A-1	Sequence 1, Appli
1248	36.2	2.7	8457	1	US-07-991-867B-1	Sequence 1, Appli
1249	36.2	2.7	8457	2	US-08-544-332-1	Sequence 1, Appli
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1265	36.2	2.7	78649	4	US-09-949-016-14620	Sequence 14620, A
1266	36.2	2.7	78649	4	US-09-949-016-16227	Sequence 16227, A
1267	36.2	2.7	78649	4	US-09-949-016-16228	Sequence 16228, A
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c1271	36.2	2.7	112507	4	US-09-949-016-12420	Sequence 12420, A
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c1274	36.2	2.7	112508	4	US-09-949-016-16590	Sequence 16590, A
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1276	36.2	2.7	129658	4	US-09-949-016-17195	Sequence 17195, A
1277	36.2	2.7	222452	4	US-09-949-016-12968	Sequence 12968, A
1278	36.2	2.7	255679	4	US-09-949-016-17189	Sequence 17189, A
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1293	36	2.7	601	4	US-09-949-016-162707	Sequence 162707,
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c1296	36	2.7	601	4	US-09-949-016-170211	Sequence 170211,
1297	36	2.7	601	4	US-09-949-016-196367	Sequence 196367,
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1309	36	2.7	1215	3	US-09-149-976-1	Sequence 1, Appli
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1311	36	2.7	1652	3	US-09-436-063C-2	Sequence 2, Appli
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1313	36	2.7	1740	3	US-08-964-939-3	Sequence 3, Appli
1314	36	2.7	1740	4	US-09-854-774-3	Sequence 3, Appli
1315	36	2.7	1810	4	US-09-800-729-73	Sequence 73, Appl
1316	36	2.7	1811	4	US-09-800-729-77	Sequence 77, Appl
1317	36	2.7	1856	1	US-08-706-214-1	Sequence 1, Appli
1318	36	2.7	1856	4	US-09-949-016-475	Sequence 475, App
1319	36	2.7	2132	3	US-09-552-322-1	Sequence 1, Appli
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1321	36	2.7	2525	3	US-09-234-393-39	Sequence 39, Appl
1322	36	2.7	2525	3	US-09-865-171-39	Sequence 39, Appl
1323	36	2.7	2862	1	US-08-148-209A-1	Sequence 1, Appli
1324	36	2.7	3001	4	US-09-539-333D-204	Sequence 204, App
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1329	36	2.7	3453	1	US-07-906-397A-1	Sequence 1, Appli
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1334	36	2.7	3453	5	PCT-US92-05401-1	Sequence 1, Appli
1335	36	2.7	3453	5	PCT-US92-09893-1	Sequence 1, Appli
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1342	36	2.7	47781	4	US-09-949-016-16492	Sequence 16492, A
1343	36	2.7	47781	4	US-09-949-016-16493	Sequence 16493, A
1344	36	2.7	47781	4	US-09-949-016-16494	Sequence 16494, A
1345	36	2.7	51049	4	US-09-949-016-15571	Sequence 15571, A
1346	36	2.7	51161	4	US-09-949-016-17416	Sequence 17416, A
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c1348	36	2.7	55130	4	US-09-949-016-11850	Sequence 11850, A
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1351	36	2.7	77663	4	US-09-949-016-13751	Sequence 13751, A
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1354	36	2.7	90050	4	US-09-358-055B-5	Sequence 5, Appli
1355	36	2.7	90050	4	US-09-893-238-5	Sequence 5, Appli
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1358	36	2.7	112507	4	US-09-949-016-12794	Sequence 12794, A
1359	36	2.7	112508	4	US-09-949-016-16589	Sequence 16589, A
1360	36	2.7	112508	4	US-09-949-016-16590	Sequence 16590, A
1361	36	2.7	136264	4	US-09-949-016-12756	Sequence 12756, A
1362	36	2.7	136265	4	US-09-949-016-13001	Sequence 13001, A
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1364	36	2.7	202111	4	US-09-949-016-13877	Sequence 13877, A
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c1366	36	2.7	248968	4	US-09-949-016-12614	Sequence 12614, A
1367	36	2.7	346112	4	US-09-949-016-13165	Sequence 13165, A
1368	36	2.7	670689	4	US-09-949-016-12505	Sequence 12505, A
1369	36	2.7	670690	4	US-09-949-016-14207	Sequence 14207, A
1370	35.8	2.7	147	4	US-09-621-976-10383	Sequence 10383, A
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1372	35.8	2.7	596	4	US-09-311-021-163	Sequence 163, App
c1373	35.8	2.7	601	4	US-09-949-016-28999	Sequence 28999, A
1374	35.8	2.7	601	4	US-09-949-016-54238	Sequence 54238, A
1375	35.8	2.7	601	4	US-09-949-016-54239	Sequence 54239, A
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c1377	35.8	2.7	601	4	US-09-949-016-76700	Sequence 76700, A
c1378	35.8	2.7	601	4	US-09-949-016-86309	Sequence 86309, A
c1379	35.8	2.7	601	4	US-09-949-016-127232	Sequence 127232,
c1380	35.8	2.7	601	4	US-09-949-016-148287	Sequence 148287,
c1381	35.8	2.7	601	4	US-09-949-016-165815	Sequence 165815,
1382	35.8	2.7	664	4	US-09-904-615-66	Sequence 66, Appl
1383	35.8	2.7	763	4	US-09-743-207-3	Sequence 3, Appli
c1384	35.8	2.7	863	3	US-08-998-416-498	Sequence 498, App
c1385	35.8	2.7	1215	4	US-09-710-279-1129	Sequence 1129, Ap
1386	35.8	2.7	1516	4	US-09-244-805-7	Sequence 7, Appli
1387	35.8	2.7	1530	4	US-09-344-882-7	Sequence 7, Appli
1388	35.8	2.7	1539	3	US-09-364-230-29	Sequence 29, Appl
1389	35.8	2.7	1810	4	US-09-369-247-11	Sequence 11, Appl
1390	35.8	2.7	1848	4	US-09-323-998E-46	Sequence 46, Appl
1391	35.8	2.7	2196	3	US-09-149-476-163	Sequence 163, App
1392	35.8	2.7	2239	3	US-09-196-390-1	Sequence 1, Appli
1393	35.8	2.7	2239	4	US-09-952-677-1	Sequence 1, Appli
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1395	35.8	2.7	2625	1	US-08-188-228-57	Sequence 57, Appl
1396	35.8	2.7	2625	1	US-08-332-643-51	Sequence 51, Appl
1397	35.8	2.7	2625	1	US-08-332-638-57	Sequence 57, Appl
1398	35.8	2.7	2625	4	US-09-654-328-1	Sequence 1, Appli
1399	35.8	2.7	3252	3	US-09-118-442-1	Sequence 1, Appli
1400	35.8	2.7	3252	3	US-09-677-064-1	Sequence 1, Appli
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1403	35.8	2.7	3862	4	US-10-164-595-5	Sequence 5, Appli
1404	35.8	2.7	3937	4	US-10-164-595-7	Sequence 7, Appli
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1409	35.8	2.7	7430	4	US-08-781-986A-260	Sequence 260, App
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c1412	35.8	2.7	17056	4	US-09-358-055B-3	Sequence 3, Appli
c1413	35.8	2.7	17056	4	US-09-893-238-3	Sequence 3, Appli
c1414	35.8	2.7	22973	4	US-09-949-016-13644	Sequence 13644, A

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c1417	35.8	2.7	68452	4	US-09-949-016-13305	Sequence 13305, A
1418	35.8	2.7	72604	3	US-09-268-992-7	Sequence 7, Appli
1419	35.8	2.7	72604	3	US-09-657-474-7	Sequence 7, Appli
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c1423	35.8	2.7	113967	4	US-09-949-016-17051	Sequence 17051, A
1424	35.8	2.7	155617	4	US-09-949-016-16191	Sequence 16191, A
c1425	35.8	2.7	235452	4	US-09-949-016-13675	Sequence 13675, A
1426	35.8	2.7	253345	4	US-09-949-016-12656	Sequence 12656, A
1427	35.8	2.7	253364	4	US-09-949-016-13639	Sequence 13639, A
1428	35.8	2.7	301828	4	US-09-949-016-13969	Sequence 13969, A
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1432	35.6	2.6	198	5	PCT-US92-10087-16	Sequence 16, Appl
1433	35.6	2.6	261	4	US-09-621-976-18330	Sequence 18330, A
1434	35.6	2.6	276	4	US-09-621-976-18329	Sequence 18329, A
1435	35.6	2.6	326	3	US-09-629-645A-17	Sequence 17, Appl
1436	35.6	2.6	348	4	US-09-621-976-13740	Sequence 13740, A
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c1438	35.6	2.6	393	3	US-09-352-616A-357	Sequence 357, App
c1439	35.6	2.6	393	4	US-09-636-215-357	Sequence 357, App
c1440	35.6	2.6	393	4	US-09-685-166A-357	Sequence 357, App
c1441	35.6	2.6	393	4	US-09-679-426-357	Sequence 357, App
c1442	35.6	2.6	393	4	US-09-759-143-357	Sequence 357, App
c1443	35.6	2.6	393	4	US-09-651-236-357	Sequence 357, App
1444	35.6	2.6	397	4	US-09-270-767-5289	Sequence 5289, Ap
1445	35.6	2.6	397	4	US-09-270-767-20571	Sequence 20571, A
c1446	35.6	2.6	593	3	US-09-385-982-262	Sequence 262, App
c1447	35.6	2.6	601	4	US-09-949-016-24313	Sequence 24313, A
c1448	35.6	2.6	601	4	US-09-949-016-28051	Sequence 28051, A
c1449	35.6	2.6	601	4	US-09-949-016-28052	Sequence 28052, A
c1450	35.6	2.6	601	4	US-09-949-016-28757	Sequence 28757, A
c1451	35.6	2.6	601	4	US-09-949-016-44053	Sequence 44053, A
c1452	35.6	2.6	601	4	US-09-949-016-48187	Sequence 48187, A
c1453	35.6	2.6	601	4	US-09-949-016-53733	Sequence 53733, A
c1454	35.6	2.6	601	4	US-09-949-016-77751	Sequence 77751, A
1455	35.6	2.6	601	4	US-09-949-016-84010	Sequence 84010, A
c1456	35.6	2.6	601	4	US-09-949-016-84403	Sequence 84403, A
c1457	35.6	2.6	601	4	US-09-949-016-84404	Sequence 84404, A
c1458	35.6	2.6	601	4	US-09-949-016-84405	Sequence 84405, A
1459	35.6	2.6	601	4	US-09-949-016-135470	Sequence 135470,
1460	35.6	2.6	601	4	US-09-949-016-135471	Sequence 135471,
1461	35.6	2.6	601	4	US-09-949-016-135472	Sequence 135472,
1462	35.6	2.6	601	4	US-09-949-016-145317	Sequence 145317,
c1463	35.6	2.6	601	4	US-09-949-016-162153	Sequence 162153,
c1464	35.6	2.6	601	4	US-09-949-016-162154	Sequence 162154,
c1465	35.6	2.6	601	4	US-09-949-016-172330	Sequence 172330,
c1466	35.6	2.6	601	4	US-09-949-016-174857	Sequence 174857,
1467	35.6	2.6	601	4	US-09-949-016-175905	Sequence 175905,
1468	35.6	2.6	601	4	US-09-949-016-179399	Sequence 179399,
1469	35.6	2.6	642	3	US-08-946-026-33	Sequence 33, Appl
c1470	35.6	2.6	723	4	US-09-270-767-4630	Sequence 4630, Ap
c1471	35.6	2.6	723	4	US-09-270-767-19912	Sequence 19912, A
1472	35.6	2.6	731	1	US-08-451-405A-2	Sequence 2, Appli
1473	35.6	2.6	810	4	US-09-543-681A-1137	Sequence 1137, Ap
1474	35.6	2.6	859	1	US-08-345-756-8	Sequence 8, Appli
1475	35.6	2.6	859	1	US-08-625-198-8	Sequence 8, Appli
1476	35.6	2.6	980	3	US-09-452-239-21	Sequence 21, Appl
1477	35.6	2.6	997	4	US-09-907-794A-376	Sequence 376, App
1478	35.6	2.6	997	4	US-09-905-125A-376	Sequence 376, App
1479	35.6	2.6	997	4	US-09-902-775A-376	Sequence 376, App
1480	35.6	2.6	997	4	US-09-906-700-376	Sequence 376, App
1481	35.6	2.6	997	4	US-09-903-603A-376	Sequence 376, App
1482	35.6	2.6	997	4	US-09-904-920A-376	Sequence 376, App
1483	35.6	2.6	997	4	US-09-909-064-376	Sequence 376, App
1484	35.6	2.6	997	4	US-09-905-381A-376	Sequence 376, App
1485	35.6	2.6	997	4	US-09-906-618-376	Sequence 376, App
1486	35.6	2.6	1149	3	US-09-227-357-84	Sequence 84, Appl
1487	35.6	2.6	1215	4	US-09-220-132-184	Sequence 184, App
1488	35.6	2.6	1236	4	US-09-328-352-2298	Sequence 2298, Ap
1489	35.6	2.6	1621	3	US-09-020-956-107	Sequence 107, App
1490	35.6	2.6	1621	3	US-09-030-607-107	Sequence 107, App
1491	35.6	2.6	1621	3	US-09-439-313-107	Sequence 107, App
1492	35.6	2.6	1621	3	US-09-352-616A-107	Sequence 107, App
1493	35.6	2.6	1621	3	US-09-232-149A-107	Sequence 107, App
1494	35.6	2.6	1621	4	US-09-159-812-107	Sequence 107, App
1495	35.6	2.6	1621	4	US-09-636-215-107	Sequence 107, App
1496	35.6	2.6	1621	4	US-09-685-166A-107	Sequence 107, App
1497	35.6	2.6	1621	4	US-09-115-453-107	Sequence 107, App
1498	35.6	2.6	1621	4	US-09-688-489-107	Sequence 107, App
1499	35.6	2.6	1621	4	US-09-679-426-107	Sequence 107, App
1500	35.6	2.6	1621	4	US-09-759-143-107	Sequence 107, App

ALIGNMENTS

RESULT 1
US-09-289-349-6
; Sequence 6, Application US/09289349
; Patent No. 6277574
; GENERAL INFORMATION:
; APPLICANT: Walker, Michael, G.
; APPLICANT: Volkmuth, Wayne
; APPLICANT: Klinger, Tod, M.
; APPLICANT: Azimzai, Yalda
; APPLICANT: Yue, Henry
; TITLE OF INVENTION: GENES ASSOCIATED WITH DISEASES OF THE KIDNEY
; FILE REFERENCE: PB-0010 US
; CURRENT APPLICATION NUMBER: US/09/289,349
; CURRENT FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PERL Program
; SEQ ID NO 6
; LENGTH: 862
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 2580580CT1
US-09-289-349-6

Query Match 62.8%; Score 845.2; DB 3; Length 862;
Best Local Similarity 99.5%; Pred. No. 2.3e-200;
Matches 858; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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Qy      472 GTTGCAATTGCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAA 531
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Db        1 GTTGCAATTGCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAA 60

Qy      532 CCATCTGAAGTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGC 591
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Qy      592 ATCCCCTCTGATCCCCTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGACAGAG 650
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Db      121 ATCCCCTCTGATCCCCTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGACAGAG 180

Qy      651 GATGAGAGGCTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACAT 710
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Db      181 GATGAGAGGCTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACAT 240

Qy      711 TTGTTTCTGTGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTT 770
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Db      241 TTGTTTCTGTGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTT 300

Qy      771 CACCATTCTTCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTAT 830
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 CACCATTCTTCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTAT 360

Qy      831 ACCCACCAACACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTT 890
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 ACCCACCAACACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTT 420
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Qy        891 TCTGACAGTATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATT 950
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Db        421 TCTGACAGTATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATT 480

Qy        951 TTTAGAAATAAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAAT 1010
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTTAGAAATAAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAAT 540

Qy       1011 AAATTTTCCAGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTT 1070
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AAATTTTCCAGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTT 600

Qy       1071 TTGACGATCACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTAT 1130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TTGACGATCACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTAT 660

Qy       1131 TGTAAATGGATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTAT 1190
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Db        661 TGTAAATGGATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCCTGTTAT 720

Qy       1191 CACACCAACAGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTT 1250
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Db        721 CACACCAACAGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTT 780

Qy       1251 GTTGACCATTTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATC 1310
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GTTGACCATTTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATC 840

Qy       1311 ATCTCTTTTTAAAAAAAAAAAA 1332
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RESULT 2
US-08-905-223-27
; Sequence 27, Application US/08905223
; Patent No. 6222029
;  GENERAL INFORMATION:
;    APPLICANT:  Edwards, Jean-Baptiste D.
;    APPLICANT:  Duelert, Aymeric
;    APPLICANT:  Lacroix, Bruno
;    TITLE OF INVENTION:  5' ESTs FOR SECRETED PROTEINS
;    NUMBER OF SEQUENCES:  503
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson & Bear
;      STREET:  501 West Broadway
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92101-3505
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Win95
;      SOFTWARE:  Word
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/905,223
;      FILING DATE:
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Israelsen, Ned A.
;      REGISTRATION NUMBER:  29,655
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 235-8550
;      TELEFAX:  (619) 235-0176
;  INFORMATION FOR SEQ ID NO:  27:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  848 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  DOUBLE
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  CDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo Sapiens
;      DEVELOPMENTAL STAGE:  Fetal
;      TISSUE TYPE:  kidney
;    FEATURE:
;      NAME/KEY:  sig_peptide
;      LOCATION:  32..73
;      IDENTIFICATION METHOD:  Von Heijne matrix
;      OTHER INFORMATION:  score 10.7
;      OTHER INFORMATION:  seq LWLLFFLVTAIHA/EL
US-08-905-223-27

  Query Match             59.4%;  Score 799.4;  DB 3;  Length 848;
  Best Local Similarity   98.8%;  Pred. No. 5.5e-189;
  Matches  809;  Conservative    6;  Mismatches    3;  Indels    1;  Gaps    1;

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Db         26 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 85

Qy         61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
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Db         86 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 145

Qy        121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        146 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 205

Qy        181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
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Db        206 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 265

Qy        241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300
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Db        266 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 325

Qy        301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360
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Db        326 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 385

Qy        361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
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Db        386 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 445

Qy        421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
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Db        446 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 505

Qy        481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540
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Db        506 GCACTACTGATTTTATCAGGGATCTGGCAACGTADAARAAAGAACAAAGAACCATCTGAA 565

Qy        541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 600
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Db        566 GTGGATGACGCTGAAARATAAKTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 625

Qy        601 GATCCCCTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 659
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        626 GATCCCCTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 685

Qy        660 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 719
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RESULT 3
US-09-247-155-27
; Sequence 27, Application US/09247155A
; Patent No. 6312922
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, Jean-Baptiste
;  APPLICANT: Duclert, Aymeric
;  APPLICANT: Bougueleret, Lydie
;  TITLE OF INVENTION: Complementary DNAs
;  FILE REFERENCE: GENSET.021A
;  CURRENT APPLICATION NUMBER: US/09/247,155A
;  CURRENT FILING DATE: 1999-02-09
;  EARLIER APPLICATION NUMBER: 60/074,121
;  EARLIER FILING DATE: 1998-02-09
;  EARLIER APPLICATION NUMBER: 60/081,563
;  EARLIER FILING DATE: 1998-04-13
;  EARLIER APPLICATION NUMBER: 60/096,116
;  EARLIER FILING DATE: 1998-08-10
;  EARLIER APPLICATION NUMBER: 60/099,273
;  EARLIER FILING DATE: 1998-10-04
;  NUMBER OF SEQ ID NOS: 182
;  SOFTWARE: Patent.pm
; SEQ ID NO 27
;   LENGTH: 848
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: sig_peptide
;   LOCATION: 32..73
;   OTHER INFORMATION: Von Heijne matrix
US-09-247-155-27

  Query Match           59.4%;  Score 799.4;  DB 3;  Length 848;
  Best Local Similarity  98.8%;  Pred. No. 5.5e-189;
  Matches  809;  Conservative    6;  Mismatches    3;  Indels    1;  Gaps    1;

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Db         86 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 145

Qy        121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        146 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 205

Qy        181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        206 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 265

Qy        241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        266 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 325

Qy        301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        326 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 385

Qy        361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        386 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 445

Qy        421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        446 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 505

Qy        481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540
              ||||||||||||||||||||||||||||||:||:||||||||||||||||||||||||||
Db        506 GCACTACTGATTTTATCAGGGATCTGGCAACGTADAARAAAGAACAAAGAACCATCTGAA 565

Qy        541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 600
              ||||||||||||||||:||||:||||||||||||||||||||||||||||||||||||||
Db        566 GTGGATGACGCTGAARATAAKTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 625

Qy        601 GATCCCCTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 659
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        626 GATCCCCTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 685

Qy        660 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 719
              ||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db        686 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAARAAATTAAACATTTGTTTCTG 745

Qy        720 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 779
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Db        746 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATWTTTTGTTTCACCATTCT 805

Qy        780 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAA 818
              |||||||||||||||||||||||||||||||||    ||||
Db        806 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAAAAAAAA 844


RESULT 4
US-09-663-600A-27
; Sequence 27, Application US/09663600A
; Patent No. 6573068
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, Jean-Baptiste
;  APPLICANT:  Duclert, Aymeric
;  APPLICANT:  Bougueleret, Lydie
;  TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
;  FILE REFERENCE: 31.US3.CIP
;  CURRENT APPLICATION NUMBER: US/09/663,600A
;  CURRENT FILING DATE:  2000-09-15
;  PRIOR APPLICATION NUMBER: 09/191,997
;  PRIOR FILING DATE: 1998-11-13
;  PRIOR APPLICATION NUMBER: 60/066,677
;  PRIOR FILING DATE: 1997-11-13
;  PRIOR APPLICATION NUMBER: 60/069,957
;  PRIOR FILING DATE: 1997-12-17
;  PRIOR APPLICATION NUMBER: 60/074,121
;  PRIOR FILING DATE: 1998-02-09
;  PRIOR APPLICATION NUMBER: 60/081,563
;  PRIOR FILING DATE: 1998-04-13
;  PRIOR APPLICATION NUMBER: 60/096,116
;  PRIOR FILING DATE: 1998-08-10
;  PRIOR APPLICATION NUMBER: 60/099,273
;  PRIOR FILING DATE: 1998-09-04
;  NUMBER OF SEQ ID NOS: 229
;  SOFTWARE: Patent.pm
; SEQ ID NO 27
;   LENGTH: 848
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: sig_peptide
;   LOCATION: 32..73
;   OTHER INFORMATION: Von Heijne matrix
US-09-663-600A-27

  Query Match           59.4%;  Score 799.4;  DB 4;  Length 848;
  Best Local Similarity  98.8%;  Pred. No. 5.5e-189;
  Matches  809;  Conservative    6;  Mismatches    3;  Indels    1;  Gaps    1;

Qy          1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60
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Db         26 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 85

Qy         61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
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Db         86 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 145

Qy        121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
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Db        146 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 205

Qy        181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
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Db        206 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 265

Qy        241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        266 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 325

Qy        301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360
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Db        326 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 385

Qy        361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
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Db        386 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 445

Qy        421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        446 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 505

Qy        481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540
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Db        506 GCACTACTGATTTTATCAGGGATCTGGCAACGTADAARAAAGAACAAAGAACCATCTGAA 565

Qy        541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 600
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Qy        660 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 719
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Qy        720 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 779
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Db        746 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATWTTTTGTTTCACCATTCT 805

Qy        780 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAA 818
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Db        806 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAAAAAAAA 844
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RESULT 5
US-09-621-976-5
; Sequence 5, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Jobert, S.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;  FILE REFERENCE: GENSET.054PR2
;  CURRENT APPLICATION NUMBER: US/09/621,976
;  CURRENT FILING DATE:  2000-07-21
;  NUMBER OF SEQ ID NOS: 19335
;  SOFTWARE: Patent.pm
; SEQ ID NO 5
;   LENGTH: 848
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 32..697
;   NAME/KEY: sig_peptide
;   LOCATION: 32..73
;   OTHER INFORMATION: Von Heijne matrix
US-09-621-976-5
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  Query Match           59.4%;  Score 799.4;  DB 4;  Length 848;
  Best Local Similarity   98.8%;  Pred. No. 5.5e-189;
  Matches  809;  Conservative    6;  Mismatches    3;  Indels    1;  Gaps    1;

Qy          1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         26 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 85

Qy         61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
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Db         86 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 145

Qy        121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
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Db        146 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 205

Qy        181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
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Db        326 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 385

Qy        361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
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Db        386 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 445

Qy        421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        446 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 505

Qy        481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540
              ||||||||||||||||||||||||||||||||||:||:||||||||||||||||||||||
Db        506 GCACTACTGATTTTATCAGGGATCTGGCAACGTADAARAAAGAACAAAGAACCATCTGAA 565

Qy        541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 600
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Qy        660 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 719
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Db        686 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAARAAATTAAACATTTGTTTCTG 745

Qy        720 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 779
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Qy        780 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAA 818
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Db        806 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAAAAAAAA 844
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RESULT 6
US-09-513-999C-5
; Sequence 5, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Duclert, A.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
;  FILE REFERENCE: 59.US2.REG
;  CURRENT APPLICATION NUMBER: US/09/513,999C
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;  CURRENT FILING DATE:  2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/122,487
;  PRIOR FILING DATE: 1999-02-26
;  NUMBER OF SEQ ID NOS: 36681
;  SOFTWARE: Patent.pm
; SEQ ID NO 5
;   LENGTH: 848
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 32..697
;   FEATURE:
;   NAME/KEY: sig_peptide
;   LOCATION: 32..73
;   OTHER INFORMATION: Von Heijne matrix
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 540
;   OTHER INFORMATION: d=a or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
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;   LOCATION: 581
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;   NAME/KEY: misc_feature
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;   NAME/KEY: UNSURE
;   LOCATION: 171
;   OTHER INFORMATION: Xaa=Lys or Asn
US-09-513-999C-5

  Query Match             59.4%;  Score 799.4;  DB 4;  Length 848;
  Best Local Similarity   98.8%;  Pred. No. 5.5e-189;
  Matches  809;  Conservative    6;  Mismatches    3;  Indels    1;  Gaps    1;

Qy          1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60
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Db        326 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 385

Qy        361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
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Db        386 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 445

Qy        421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        446 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 505

Qy        481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540
              ||||||||||||||||||||||||||||||||||:||:||||||||||||||||||||||
Db        506 GCACTACTGATTTTATCAGGGATCTGGCAACGTADAARAAAGAACAAAGAACCATCTGAA 565

Qy        541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 600
              ||||||||||||||:||||:||||||||||||||||||||||||||||||||||||||||
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Db        626 GATCCCCTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 685

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Qy        720 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 779
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Qy        780 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAA 818
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RESULT 7
US-09-471-276-5
; Sequence 5, Application US/09471276
; Patent No. 6822072
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT: Duclert A.
;  APPLICANT: Giordano, J.Y.
;  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6822072
;  FILE REFERENCE: GENSET.025CP1
;  CURRENT APPLICATION NUMBER: US/09/471,276
;  CURRENT FILING DATE: 1999-12-21
;  EARLIER APPLICATION NUMBER: 09/057,719
;  EARLIER FILING DATE: 1998-04-09
;  EARLIER APPLICATION NUMBER: 09/069,047
;  EARLIER FILING DATE: 1998-04-28
;  EARLIER APPLICATION NUMBER: PCT/IB99/00712
;  EARLIER FILING DATE: 1999-04-09
;  NUMBER OF SEQ ID NOS: 1622
;  SOFTWARE: Patent.pm
; SEQ ID NO 5
;   LENGTH: 848
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: CDS
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;   LOCATION: 32..697
;   NAME/KEY: sig_peptide
;   LOCATION: 32..73
;   OTHER INFORMATION: Von Heijne matrix
US-09-471-276-5

  Query Match             59.4%;  Score 799.4;  DB 4;  Length 848;
  Best Local Similarity   98.8%;  Pred. No. 5.5e-189;
  Matches  809;  Conservative    6;  Mismatches    3;  Indels    1;  Gaps    1;

Qy          1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60
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Db         26 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 85

Qy         61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
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Db         86 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 145

Qy        121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
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Db        146 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 205

Qy        181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
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Qy        241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300
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Qy        301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360
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Db        326 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 385

Qy        361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        386 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 445

Qy        421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        446 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 505

Qy        481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540
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Qy        541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 600
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Qy        601 GATCCCCTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 659
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Qy        660 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTG 719
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Qy        720 TGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCT 779
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Qy        780 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAA 818
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Db        806 TCTTTTGTAATAAATTTTGAATGTGCTTGAAAAAAAAAA 844


RESULT 8
US-08-989-299-3
; Sequence 3, Application US/08989299
; Patent No. 6194556
;  GENERAL INFORMATION:
;    APPLICANT:  Acton, Susan L.
;    APPLICANT:  Robinson, Keith E.
;    TITLE OF INVENTION:  ANGIOTENSIN CONVERTING ENZYME HOMOLOG
;    TITLE OF INVENTION:  AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FOLEY, HOAG & ELIOT LLP
;      STREET:  One Post Office Square
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109-2170
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/989,299
;      FILING DATE:  11-DEC-1997
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Arnold E., Beth
;      REGISTRATION NUMBER:  35,430
;      REFERENCE/DOCKET NUMBER:  MIA-025.01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-832-1000
;      TELEFAX:  617-832-7000
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2415 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-989-299-3

  Query Match             9.3%;  Score 125;  DB 3;  Length 2415;
  Best Local Similarity   57.3%;  Pred. No. 3.3e-21;
  Matches  293;  Conservative    0;  Mismatches  200;  Indels   18;  Gaps    3;

Qy         54 CTGTCAACCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGG 113
              |||   |||  ||||||  |   | ||||||||  | ||  | | | |||||| ||
Db       1827 CTGGAGTCCATATGCAGACCAAAGCATCAAAGTGAGGATAAGCCTAAAATCAGCTCTTGG 1886

Qy        114 AGATAAAGCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTT 173
              ||||||||||||||  ||| |   |||||||   ||||| |||  | |    || || |
Db       1887 AGATAAAGCATATGAATGGAACGACAATGAAATGTACCTGTTCCGATCATCTGTTGCATA 1946

Qy        174 CTCCATGAG--AAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCC------------A 218
              | |||||  |  | ||   || ||  ||  | ||||   |||              |
Db       1947 TGCTATGAGGCAGTACTTTTTAAAAGTAAAAAATCAGATGATTCTTTTTGGGGAGGAGGA 2006

Qy        219 TGTCCTACTTTGCAATGTAACCCAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTC 278
              ||| | | |   ||| | |  |  ||  | || ||    ||  | || || |  |||
Db       2007 TGTGCGAGTGGCTAATTTGAAACCAAGAATCTCCTTTAATTTCTTTGTCACTGCACCTAA 2066

Qy        279 AAAAAA---TCACACCCTTCCTGCTGTTGAGGTGCAATCAGCCATAAGAATGAACAAGAA 335
              |||      | | | | |||||     ||| ||  ||   |||| || |||  |  ||
Db       2067 AAATGTGTCTGATATCATTCCTAGAACTGAAGTTGAAAAGGCCATCAGGATGTCCCGGAG 2126

Qy        336 CCGGATCAACAATGCCTTCTTTCTAAATGACCAAACTCTGGAATTTTTAAAAATCCCTTC 395
              ||| |||||  |||| |||  ||| |||||| | |  || || ||| |    || | |
Db       2127 CCGTATCAATGATGCTTTCCGTCTGAATGACAACAGCCTAGAGTTTCTGGGGATACAGCC 2186

Qy        396 CACACTTGCACCACCCATGGACCCATCTGTGCCCATCTGGATTATTATATTTGGTGTGAT 455
              |||||||  ||| || |   | ||  ||||  |||| ||| | ||| | |||||| ||  |
Db       2187 AACACTTGGACCTCCTAACCAGCCCCCTGTTTCCATATGGCTGATTGTTTTTGGAGTTGT 2246

Qy        456 ATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTATCAGGGATCTGGCAACGTAG 515
              |  |  | ||  | ||||  ||||   | ||||| ||  | |||||| |  | || |
Db       2247 GATGGGAGTGATAGTGGTTGGCATTGTCATCCTGATCTTCACTGGGATCAGAGATCGGAA 2306

Qy        516 AAGAAAGAACAAAGAACCATCTGAAGTGGAT 546
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                |  || || |||| |  |  || ||   ||
Db       2307 GAAGAAAAATAAAGCAAGAAGTGGAGAAAAT 2337


RESULT 9
US-09-407-427-3
; Sequence 3, Application US/09407427
; Patent No. 6610497
; GENERAL INFORMATION:
;  APPLICANT:  Acton, Susan L.
;  APPLICANT:  Robison, Keith E.
;  TITLE OF INVENTION:  ANGIOTENSIN CONVERTING ENZYME HOMOLOG  AND THERAPEUTIC
;  TITLE OF INVENTION:  AND DIAGNOSTIC USES THEREFOR
;  FILE REFERENCE:  MNI-132CP2
;  CURRENT APPLICATION NUMBER: US/09/407,427
;  CURRENT FILING DATE:  1999-09-29
;  PRIOR APPLICATION NUMBER:  09/163,648
;  PRIOR FILING DATE:  1998-09-30
;  PRIOR APPLICATION NUMBER:  08/989,299
;  PRIOR FILING DATE:  1997-12-11
;  NUMBER OF SEQ ID NOS:  14
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 2415
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-407-427-3

  Query Match             9.3%;  Score 125;  DB 4;  Length 2415;
  Best Local Similarity   57.3%;  Pred. No. 3.3e-21;
  Matches  293;  Conservative    0;  Mismatches  200;  Indels   18;  Gaps    3;

Qy         54 CTGTCAACCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGG 113
              |||    |||  ||||||  |      | ||||||||  | ||  | | | ||||||| ||
Db       1827 CTGGAGTCCATATGCAGACCAAAGCATCAAAGTGAGGATAAGCCTAAAATCAGCTCTTGG 1886

Qy        114 AGATAAAGCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTT 173
              ||||||||||||||  ||| |   |||||||   ||||| |||  | |    || || |
Db       1887 AGATAAAGCATATGAATGGAACGACAATGAAATGTACCTGTTCCGATCATCTGTTGCATA 1946

Qy        174 CTCCATGAG--AAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCC------------A 218
                | |||||  |  | ||   || ||  ||  | ||||   |||              |
Db       1947 TGCTATGAGGCAGTACTTTTTAAAAGTAAAAAATCAGATGATTCTTTTTGGGGAGGAGGA 2006

Qy        219 TGTCCTACTTTGCAATGTAACCCAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTC 278
              ||| | | |    ||| | |  |  ||  | || ||    ||  | || || |  |||
Db       2007 TGTGCGAGTGGCTAATTTGAAACCAAGAATCTCCTTTAATTTCTTTGTCACTGCACCTAA 2066

Qy        279 AAAAAA---TCACACCCTTCCTGCTGTTGAGGTGCAATCAGCCATAAGAATGAACAAGAA 335
              |||      | | | |||||     ||| ||  ||   |||| || ||| |  ||
Db       2067 AAATGTGTCTGATATCATTCCTAGAACTGAAGTTGAAAAGGCCATCAGGATGTCCCGGAG 2126

Qy        336 CCGGATCAACAATGCCTTCTTTCTAAATGACCAAACTCTGGAATTTTTAAAAATCCCTTC 395
              ||| |||||  |||| |||  ||| |||||| | |  || || ||| |    || |   |
Db       2127 CCGTATCAATGATGCTTTCCGTCTGAATGACAACAGCCTAGAGTTTCTGGGGATACAGCC 2186

Qy        396 CACACTTGCACCACCCATGGACCCATCTGTGCCCATCTGGATTATTATATTTGGTGTGAT 455
              |||||||  ||| || |   | ||  ||||  |||| ||| | ||| | ||||| ||  |
Db       2187 AACACTTGGACCTCCTAACCAGCCCCCTGTTTCCATATGGCTGATTGTTTTTGGAGTTGT 2246

Qy        456 ATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTATCAGGGATCTGGCAACGTAG 515
                |   | | ||  | ||||  ||||    | ||||| ||  | ||||||  |  | || |
Db       2247 GATGGGAGTGATAGTGGTTGGCATTGTCATCCTGATCTTCACTGGGATCAGAGATCGGAA 2306

Qy        516 AAGAAAGAACAAAGAACCATCTGAAGTGGAT 546
                |  || || |||| |  |  || ||   ||
Db       2307 GAAGAAAAATAAAGCAAGAAGTGGAGAAAAT 2337


RESULT 10
US-09-949-016-5413
; Sequence 5413, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5413
;   LENGTH: 3388
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-5413

  Query Match             9.3%;  Score 125;  DB 4;  Length 3388;
  Best Local Similarity   57.3%;  Pred. No. 3.8e-21;
  Matches  293;  Conservative    0;  Mismatches  200;  Indels   18;  Gaps    3;

Qy         54 CTGTCAACCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGG 113
              |||    |||  ||||||  |      | ||||||||  | ||  | | | ||||||| ||
Db       1930 CTGGAGTCCATATGCAGACCAAAGCATCAAAGTGAGGATAAGCCTAAAATCAGCTCTTGG 1989

Qy        114 AGATAAAGCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTT 173
              ||||||||||||||  ||| |   |||||||   ||||| |||  | |    || || |
Db       1990 AGATAAAGCATATGAATGGAACGACAATGAAATGTACCTGTTCCGATCATCTGTTGCATA 2049

Qy        174 CTCCATGAG--AAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCC------------A 218
                | |||||  |  | ||   || ||  ||  | ||||   |||              |
Db       2050 TGCTATGAGGCAGTACTTTTTAAAAGTAAAAAATCAGATGATTCTTTTTGGGGAGGAGGA 2109

Qy        219 TGTCCTACTTTGCAATGTAACCCAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTC 278
              ||| | | |    ||| | |  |  ||  | || ||    ||  | || || |  |||
Db       2110 TGTGCGAGTGGCTAATTTGAAACCAAGAATCTCCTTTAATTTCTTTGTCACTGCACCTAA 2169

Qy        279 AAAAAA---TCACACCCTTCCTGCTGTTGAGGTGCAATCAGCCATAAGAATGAACAAGAA 335
              |||      | | | |||||     ||| ||  ||   |||| || ||| |  ||
Db       2170 AAATGTGTCTGATATCATTCCTAGAACTGAAGTTGAAAAGGCCATCAGGATGTCCCGGAG 2229

Qy        336 CCGGATCAACAATGCCTTCTTTCTAAATGACCAAACTCTGGAATTTTTAAAAATCCCTTC 395
              ||| |||||  |||| |||  ||| |||||| | |  || || ||| |    || |   |
Db       2230 CCGTATCAATGATGCTTTCCGTCTGAATGACAACAGCCTAGAGTTTCTGGGGATACAGCC 2289

Qy        396 CACACTTGCACCACCCATGGACCCATCTGTGCCCATCTGGATTATTATATTTGGTGTGAT 455
              |||||||  ||| || |   | ||  ||||  |||| ||| | ||| | ||||| ||  |
Db       2290 AACACTTGGACCTCCTAACCAGCCCCCTGTTTCCATATGGCTGATTGTTTTTGGAGTTGT 2349

Qy        456 ATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTATCAGGGATCTGGCAACGTAG 515
                |   | | ||  | ||||  ||||    | ||||| ||  | ||||||  |  | || |
Db       2350 GATGGGAGTGATAGTGGTTGGCATTGTCATCCTGATCTTCACTGGGATCAGAGATCGGAA 2409

Qy        516 AAGAAAGAACAAAGAACCATCTGAAGTGGAT 546
                |  || || |||| |  |  || ||   ||
Db       2410 GAAGAAAAATAAAGCAAGAAGTGGAGAAAAT 2440


RESULT 11
US-08-989-299-1
; Sequence 1, Application US/08989299
; Patent No. 6194556
;  GENERAL INFORMATION:
;    APPLICANT:  Acton, Susan L.
;    APPLICANT:  Robinson, Keith E.
;    TITLE OF INVENTION:  ANGIOTENSIN CONVERTING ENZYME HOMOLOG
;    TITLE OF INVENTION:  AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
```

```
;      ADDRESSEE:  FOLEY, HOAG & ELIOT LLP
;      STREET:  One Post Office Square
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109-2170
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/989,299
;      FILING DATE:  11-DEC-1997
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Arnold E., Beth
;      REGISTRATION NUMBER:  35,430
;      REFERENCE/DOCKET NUMBER:  MIA-025.01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-832-1000
;      TELEFAX:  617-832-7000
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3396 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  82..2496
US-08-989-299-1

  Query Match             9.3%;  Score 125;  DB 3;  Length 3396;
  Best Local Similarity   57.3%;  Pred. No. 3.8e-21;
  Matches  293;  Conservative    0;  Mismatches  200;  Indels   18;  Gaps    3;

Qy         54 CTGTCAACCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGG 113
Db       1908 CTGGAGTCCATATGCAGACCAAAGCATCAAAGTGAGGATAAGCCTAAAATCAGCTCTTGG 1967

Qy        114 AGATAAAGCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTT 173
Db       1968 AGATAAAGCATATGAATGGAACGACAATGAAATGTACCTGTTCCGATCATCTGTTGCATA 2027

Qy        174 CTCCATGAG--AAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCC------------A 218
Db       2028 TGCTATGAGGCAGTACTTTTTAAAAGTAAAAAATCAGATGATTCTTTTTGGGGAGGAGGA 2087

Qy        219 TGTCCTACTTTGCAATGTAACCCAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTC 278
Db       2088 TGTGCGAGTGGCTAATTTGAAACCAAGAATCTCCTTTAATTTCTTTGTCACTGCACCTAA 2147

Qy        279 AAAAAA---TCACACCCTTCCTGCTGTTGAGGTGCAATCAGCCATAAGAATGAACAAGAA 335
Db       2148 AAATGTGTCTGATATCATTCCTAGAACTGAAGTTGAAAAGGCCATCAGGATGTCCCGGAG 2207

Qy        336 CCGGATCAACAATGCCTTCTTTCTAAATGACCAAACTCTGGAATTTTTAAAAATCCCTTC 395
Db       2208 CCGTATCAATGATGCTTTCCGTCTGAATGACAACAGCCTAGAGTTTCTGGGGATACAGCC 2267

Qy        396 CACACTTGCACCACCCATGGACCCATCTGTGCCCATCTGGATTATTATATTTGGTGTGAT 455
Db       2268 AACACTTGGACCTCCTAACCAGCCCCCTGTTTCCATATGGCTGATTGTTTTTGGAGTTGT 2327

Qy        456 ATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTATCAGGGATCTGGCAACGTAG 515
Db       2328 GATGGGAGTGATAGTGGTTGGCATTGTCATCCTGATCTTCACTGGGATCAGAGATCGGAA 2387

Qy        516 AAGAAAGAACAAAGAACCATCTGAAGTGGAT 546
Db       2388 GAAGAAAAATAAAGCAAGAAGTGGAGAAAAT 2418
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RESULT 12
US-10-158-847-141
; Sequence 141, Application US/10158847
; Patent No. 6592865
; GENERAL INFORMATION:
;  APPLICANT: Tom Parry et al.
;  TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
;  FILE REFERENCE: PF557
;  CURRENT APPLICATION NUMBER: US/10/158,847
;  CURRENT FILING DATE:  2002-06-03
;  PRIOR APPLICATION NUMBER: 60/295,004
;  PRIOR FILING DATE: 2001-06-04
;  NUMBER OF SEQ ID NOS: 158
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 141
;   LENGTH: 3396
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-158-847-141

  Query Match             9.3%;  Score 125;  DB 4;  Length 3396;
  Best Local Similarity   57.3%;  Pred. No. 3.8e-21;
  Matches  293;  Conservative    0;  Mismatches  200;  Indels   18;  Gaps    3;

Qy         54 CTGTCAACCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGG 113
Db       1908 CTGGAGTCCATATGCAGACCAAAGCATCAAAGTGAGGATAAGCCTAAAATCAGCTCTTGG 1967

Qy        114 AGATAAAGCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTT 173
Db       1968 AGATAAAGCATATGAATGGAACGACAATGAAATGTACCTGTTCCGATCATCTGTTGCATA 2027

Qy        174 CTCCATGAG--AAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCC------------A 218
Db       2028 TGCTATGAGGCAGTACTTTTTAAAAGTAAAAAATCAGATGATTCTTTTTGGGGAGGAGGA 2087

Qy        219 TGTCCTACTTTGCAATGTAACCCAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTC 278
Db       2088 TGTGCGAGTGGCTAATTTGAAACCAAGAATCTCCTTTAATTTCTTTGTCACTGCACCTAA 2147

Qy        279 AAAAAA---TCACACCCTTCCTGCTGTTGAGGTGCAATCAGCCATAAGAATGAACAAGAA 335
Db       2148 AAATGTGTCTGATATCATTCCTAGAACTGAAGTTGAAAAGGCCATCAGGATGTCCCGGAG 2207

Qy        336 CCGGATCAACAATGCCTTCTTTCTAAATGACCAAACTCTGGAATTTTTAAAAATCCCTTC 395
Db       2208 CCGTATCAATGATGCTTTCCGTCTGAATGACAACAGCCTAGAGTTTCTGGGGATACAGCC 2267

Qy        396 CACACTTGCACCACCCATGGACCCATCTGTGCCCATCTGGATTATTATATTTGGTGTGAT 455
Db       2268 AACACTTGGACCTCCTAACCAGCCCCCTGTTTCCATATGGCTGATTGTTTTTGGAGTTGT 2327

Qy        456 ATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTATCAGGGATCTGGCAACGTAG 515
Db       2328 GATGGGAGTGATAGTGGTTGGCATTGTCATCCTGATCTTCACTGGGATCAGAGATCGGAA 2387

Qy        516 AAGAAAGAACAAAGAACCATCTGAAGTGGAT 546
Db       2388 GAAGAAAAATAAAGCAAGAAGTGGAGAAAAT 2418
```

```
RESULT 13
US-09-407-427-1
; Sequence 1, Application US/09407427
; Patent No. 6610497
; GENERAL INFORMATION:
;  APPLICANT:  Acton, Susan L.
;  APPLICANT:  Robison, Keith E.
;  TITLE OF INVENTION:  ANGIOTENSIN CONVERTING ENZYME HOMOLOG  AND THERAPEUTIC
;  TITLE OF INVENTION:  AND DIAGNOSTIC USES THEREFOR
;  FILE REFERENCE:  MNI-132CP2
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;  CURRENT APPLICATION NUMBER: US/09/407,427
;  CURRENT FILING DATE:  1999-09-29
;  PRIOR APPLICATION NUMBER:  09/163,648
;  PRIOR FILING DATE:  1998-09-30
;  PRIOR APPLICATION NUMBER:  08/989,299
;  PRIOR FILING DATE:  1997-12-11
;  NUMBER OF SEQ ID NOS:  14
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 3396
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (82)..(2496)
US-09-407-427-1

  Query Match             9.3%;  Score 125;  DB 4;  Length 3396;
  Best Local Similarity   57.3%;  Pred. No. 3.8e-21;
  Matches  293;  Conservative    0;  Mismatches  200;  Indels   18;  Gaps    3;

Qy         54 CTGTCAACCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGG 113
              |||    |||  ||||||  |     | ||||||||  | ||  | | | |||||| ||
Db       1908 CTGGAGTCCATATGCAGACCAAAGCATCAAAGTGAGGATAAGCCTAAAATCAGCTCTTGG 1967

Qy        114 AGATAAAGCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTT 173
              ||||||||||||||  ||| |   |||||||   |||||  |||  | |    || || |
Db       1968 AGATAAAGCATATGAATGGAACGACAATGAAATGTACCTGTTCCGATCATCTGTTGCATA 2027

Qy        174 CTCCATGAG--AAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCC------------A 218
                | |||||  |  | ||   || ||  ||  | ||||   |||                |
Db       2028 TGCTATGAGGCAGTACTTTTTAAAAGTAAAAAATCAGATGATTCTTTTTGGGGAGGAGGA 2087

Qy        219 TGTCCTACTTTGCAATGTAACCCAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTC 278
              ||| | | |    ||| | |  |  ||  | || ||    ||  | || || |  |||
Db       2088 TGTGCGAGTGGCTAATTTGAAACCAAGAATCTCCTTTAATTTCTTTGTCACTGCACCTAA 2147

Qy        279 AAAAAA---TCACACCCTTCCTGCTGTTGAGGTGCAATCAGCCATAAGAATGAACAAGAA 335
              |||      | | | | |||||     ||| ||  ||   |||||| || |||  |  ||
Db       2148 AAATGTGTCTGATATCATTCCTAGAACTGAAGTTGAAAAGGCCATCAGGATGTCCCGGAG 2207

Qy        336 CCGGATCAACAATGCCTTCTTTCTAAATGACCAAACTCTGGAATTTTTAAAAATCCCTTC 395
              ||| |||||  |||| |||  ||| |||||| | |  || || ||| |     || |   |
Db       2208 CCGTATCAATGATGCTTTCCGTCTGAATGACAACAGCCTAGAGTTTCTGGGGATACAGCC 2267

Qy        396 CACACTTGCACCACCCATGGACCCATCTGTGCCCATCTGGATTATTATATTTGGTGTGAT 455
              |||||||  ||| || |   | ||  ||||  |||| ||| | ||| | ||||| || |
Db       2268 AACACTTGGACCTCCTAACCAGCCCCCTGTTTCCATATGGCTGATTGTTTTTGGAGTTGT 2327

Qy        456 ATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTATCAGGGATCTGGCAACGTAG 515
              |  |  | ||  | ||||  ||||   | |||||  ||  | |||||| |  | ||| |
Db       2328 GATGGGAGTGATAGTGGTTGGCATTGTCATCCTGATCTTCACTGGGATCAGAGATCGGAA 2387

Qy        516 AAGAAAGAACAAAGAACCATCTGAAGTGGAT 546
              |  || || |||| | |  || ||   ||
Db       2388 GAAGAAAAATAAAGCAAGAAGTGGAGAAAAT 2418


RESULT 14
US-10-158-847-137
; Sequence 137, Application US/10158847
; Patent No. 6592865
; GENERAL INFORMATION:
;  APPLICANT: Tom Parry et al.
;  TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
;  FILE REFERENCE: PF557
;  CURRENT APPLICATION NUMBER: US/10/158,847
;  CURRENT FILING DATE:  2002-06-03
;  PRIOR APPLICATION NUMBER: 60/295,004
;  PRIOR FILING DATE: 2001-06-04
;  NUMBER OF SEQ ID NOS: 158
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 137
;   LENGTH: 2920
;   TYPE: DNA
;   ORGANISM: homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1707)..(1707)
;   OTHER INFORMATION: n equals any amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (2702)..(2702)
;   OTHER INFORMATION: n equals any amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (2749)..(2749)
;   OTHER INFORMATION: n equals any amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (2757)..(2757)
;   OTHER INFORMATION: n equals any amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (2788)..(2789)
;   OTHER INFORMATION: n equals any amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (2819)..(2819)
;   OTHER INFORMATION: n equals any amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (2835)..(2835)
;   OTHER INFORMATION: n equals any amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (2856)..(2856)
;   OTHER INFORMATION: n equals any amino acid
US-10-158-847-137

  Query Match             8.7%;  Score 117;  DB 4;  Length 2920;
  Best Local Similarity   57.6%;  Pred. No. 3.5e-19;
  Matches  276;  Conservative    0;  Mismatches  185;  Indels   18;  Gaps    3;

Qy         54 CTGTCAACCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGG 113
              |||    |||  ||||||  |     | ||||||||  | ||  | | | |||||| ||
Db       1856 CTGGAGTCCATATGCAGACCAAAGCATCAAAGTGAGGATAAGCCTAAAATCAGCTCTTGG 1915

Qy        114 AGATAAAGCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTT 173
              ||||||||||||||  ||| |   |||||||   |||||  |||  | |    || || |
Db       1916 AGATAAAGCATATGAATGGAACGACAATGAAATGTACCTGTTCCGATCATCTGTTGCATA 1975

Qy        174 CTCCATGAG--AAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCC------------A 218
                | |||||  |  | ||   || ||  ||  | ||||   |||                |
Db       1976 TGCTATGAGGCAGTACTTTTTAAAAGTAAAAAATCAGATGATTCTTTTTGGGGAGGAGGA 2035

Qy        219 TGTCCTACTTTGCAATGTAACCCAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTC 278
              ||| | | |    ||| | |  |  ||  | || ||    ||  | || || |  |||
Db       2036 TGTGCGAGTGGCTAATTTGAAACCAAGAATCTCCTTTAATTTCTTTGTCACTGCACCTAA 2095

Qy        279 AAAAAA---TCACACCCTTCCTGCTGTTGAGGTGCAATCAGCCATAAGAATGAACAAGAA 335
              |||      | | | | |||||     ||| ||  ||   |||||| || |||  |  ||
Db       2096 AAATGTGTCTGATATCATTCCTAGAACTGAAGTTGAAAAGGCCATCAGGATGTCCCGGAG 2155

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Qy        456 ATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTATCAGGGATCTGGCAACGTA 514
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RESULT 15
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; Sequence 17155, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17155
; LENGTH: 43986
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17155

Query Match 5.8%; Score 77.4; DB 4; Length 43986;
Best Local Similarity 61.8%; Pred. No. 6.5e-09;
Matches 123; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

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Qy        376 GAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCATCTGG 435
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Job time : 323.638 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 24, 2005, 19:08:56 ; Search time 772.34 Seconds
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Searched: 5384158 seqs, 2955248155 residues

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Maximum Match 100%
Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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519	1325.4	98.5	1432	14	US-10-097-065-17	Sequence 17, Appl
520	1325.4	98.5	1432	17	US-10-372-876-17	Sequence 17, Appl
521	1324.6	98.4	1447	10	US-09-892-877-22	Sequence 22, Appl
522	1324.6	98.4	1447	10	US-09-948-783-22	Sequence 22, Appl
523	1305	97.0	1356	14	US-10-097-065-122	Sequence 122, App
524	1305	97.0	1356	17	US-10-372-876-122	Sequence 122, App
525	1297	96.4	1312	16	US-10-133-013-205	Sequence 205, App
526	799.4	59.4	848	10	US-09-903-190-27	Sequence 27, Appl
527	799.4	59.4	848	15	US-10-319-763-27	Sequence 27, Appl
528	539.6	40.1	1181	17	US-10-152-319A-1744	Sequence 1744, Ap
529	316.6	23.5	532	9	US-09-728-445-570	Sequence 570, App
530	232.6	17.3	355	9	US-09-867-701-1636	Sequence 1636, Ap
c 531	197.4	14.7	213	9	US-09-864-761-23160	Sequence 23160, A
c 532	188.2	14.0	464	9	US-09-864-761-6445	Sequence 6445, Ap
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534	138.4	10.3	620	13	US-10-027-632-228334	Sequence 228334,
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537	125	9.3	3324	14	US-10-116-802-172	Sequence 172, App
538	125	9.3	3325	13	US-10-114-893-85	Sequence 85, Appl
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540	125	9.3	3396	11	US-09-999-781-1	Sequence 1, Appli
541	125	9.3	3396	14	US-10-158-847-141	Sequence 141, App
542	125	9.3	3396	15	US-10-158-825-141	Sequence 141, App
543	125	9.3	3396	18	US-10-158-825-141	Sequence 141, App
544	125	9.3	3405	15	US-10-005-956-569	Sequence 569, App
545	125	9.3	3405	15	US-10-005-956-842	Sequence 842, App
992	119.8	8.9	3732	19	US-10-931-886-71	Sequence 71, Appl
993	117	8.7	2911	9	US-09-969-384-12	Sequence 12, Appl
994	117	8.7	2920	9	US-09-969-384-2	Sequence 2, Appli
995	117	8.7	2920	14	US-10-158-847-137	Sequence 137, App
996	117	8.7	2920	15	US-10-158-825-137	Sequence 137, App
997	117	8.7	2920	18	US-10-158-825-137	Sequence 137, App
c 998	111.4	8.3	435	9	US-09-867-701-1637	Sequence 1637, Ap
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c1004	62.4	4.6	9810	15	US-10-311-455-399	Sequence 399, App
1005	62.2	4.6	8056	18	US-10-473-126-240	Sequence 240, App
1006	61.8	4.6	158001	17	US-10-211-179-11	GENERAL INFORMATI
c1007	60.6	4.5	83391	18	US-10-433-793-123	Sequence 123, App
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c1009	58.8	4.4	9997	15	US-10-311-455-342	Sequence 342, App
c1010	58.8	4.4	9997	15	US-10-240-485-38	Sequence 38, Appl
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c1032	54	4.0	6106	15	US-10-311-455-1446	Sequence 1446, Ap
c1033	54	4.0	6106	17	US-10-257-166-114	Sequence 114, App
c1034	54	4.0	6106	17	US-10-221-714A-152	Sequence 152, App
c1035	54	4.0	11288	9	US-09-947-925A-4	Sequence 4, Appli
c1036	54	4.0	11288	9	US-09-822-634-1	Sequence 1, Appli
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c1054	52.4	3.9	11836	15	US-10-240-453-114	Sequence 114, App
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c1057	52	3.9	7597	15	US-10-311-455-986	Sequence 986, App
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c1079	50.8	3.8	6109	17	US-10-221-613-33	Sequence 33, Appl
1080	50.8	3.8	6631	15	US-10-240-453-214	Sequence 214, App
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1083	50.4	3.7	337344	18	US-10-388-838-58	Sequence 58, Appl
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c1109	49.2	3.7	17183	15	US-10-311-455-459	Sequence 459, App
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c1113	49	3.6	198522	13	US-10-087-192-244	Sequence 244, App
c1114	48.8	3.6	5398	15	US-10-311-455-115	Sequence 115, App
c1115	48.8	3.6	5611	18	US-10-433-793-100	Sequence 100, App
c1116	48.8	3.6	6222	15	US-10-311-455-666	Sequence 666, App
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c1125	48.6	3.6	5033	18	US-10-473-126-139	Sequence 139, App
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c1128	48.6	3.6	7001	18	US-10-480-846-60	Sequence 60, Appl
c1129	48.6	3.6	8033	17	US-10-221-613-73	Sequence 73, Appl
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1147	48.2	3.6	40178	17	US-10-282-174-467	Sequence 467, App
1148	48.2	3.6	40178	17	US-10-282-174-468	Sequence 468, App
1149	48.2	3.6	40178	19	US-10-600-009-467	Sequence 467, App
1150	48.2	3.6	40178	19	US-10-600-009-468	Sequence 468, App
c1151	48.2	3.6	40862	15	US-10-311-455-2046	Sequence 2046, Ap
1152	48.2	3.6	141158	18	US-10-719-993-6837	Sequence 6837, Ap
1153	48.2	3.6	3673778	16	US-10-312-841-2	Sequence 2, Appli
1154	48	3.6	65	10	US-09-908-975-25999	Sequence 25999, A
1155	48	3.6	834	18	US-10-726-699-20	Sequence 20, Appl
1156	48	3.6	3076	9	US-09-745-763-71	Sequence 71, Appl
1157	48	3.6	7167	15	US-10-311-455-373	Sequence 373, App
c1158	48	3.6	14023	15	US-10-311-455-2078	Sequence 2078, Ap
c1159	48	3.6	19576	17	US-10-221-613-220	Sequence 220, App
c1160	48	3.6	37515	18	US-10-433-793-28	Sequence 28, Appl
c1161	48	3.6	83391	18	US-10-433-793-124	Sequence 124, App
c1162	48	3.6	91697	18	US-10-417-375-36	Sequence 36, Appl
c1163	47.8	3.6	614	18	US-10-437-963-57702	Sequence 57702, A
c1164	47.8	3.6	3586	17	US-10-240-454-61	Sequence 61, Appl
c1165	47.8	3.6	7131	17	US-10-221-613-324	Sequence 324, App
1166	47.8	3.6	8238	15	US-10-311-455-1962	Sequence 1962, Ap
1167	47.8	3.6	8238	17	US-10-240-454-44	Sequence 44, Appl
c1168	47.8	3.6	10020	15	US-10-311-455-2266	Sequence 2266, Ap
c1169	47.8	3.6	40324	18	US-10-433-793-179	Sequence 179, App
1170	47.8	3.6	109730	19	US-10-741-600-17809	Sequence 17809, A
1171	47.6	3.5	1830	19	US-10-706-635-67	Sequence 67, Appl
c1172	47.6	3.5	4152	19	US-10-706-635-9	Sequence 9, Appli
c1173	47.6	3.5	6106	15	US-10-311-455-1445	Sequence 1445, Ap
c1174	47.6	3.5	6106	17	US-10-257-166-113	Sequence 113, App
c1175	47.6	3.5	6106	17	US-10-221-714A-151	Sequence 151, App
c1176	47.6	3.5	12237	15	US-10-311-455-2331	Sequence 2331, Ap
c1177	47.6	3.5	13712	15	US-10-311-455-1504	Sequence 1504, Ap
1178	47.6	3.5	15567	13	US-10-047-676A-3	Sequence 3, Appli
1179	47.6	3.5	15567	18	US-10-790-914-3	Sequence 3, Appli
c1180	47.6	3.5	21537	15	US-10-311-455-1972	Sequence 1972, Ap
c1181	47.6	3.5	32392	19	US-10-706-635-27	Sequence 27, Appl
1182	47.6	3.5	335913	10	US-09-754-853A-2	Sequence 2, Appli
1183	47.6	3.5	335913	10	US-09-754-853A-3	Sequence 3, Appli
1184	47.4	3.5	954	18	US-10-425-115-16752	Sequence 16752, A
1185	47.4	3.5	5768	17	US-10-221-613-62	Sequence 62, Appl
1186	47.4	3.5	7657	14	US-10-239-676-185	Sequence 185, App
1187	47.4	3.5	7657	15	US-10-311-455-1995	Sequence 1995, Ap
c1188	47.4	3.5	15161	17	US-10-221-613-386	Sequence 386, App
1189	47.4	3.5	15373	15	US-10-311-455-440	Sequence 440, App
c1190	47.4	3.5	337344	18	US-10-388-838-58	Sequence 58, Appl
c1191	47.2	3.5	6123	15	US-10-311-455-794	Sequence 794, App
1192	47.2	3.5	6641	15	US-10-311-455-288	Sequence 288, App
1193	47.2	3.5	6641	16	US-10-240-452-36	Sequence 36, Appl

1194	47.2	3.5	7445	15	US-10-311-455-824	Sequence 824, App
1195	47.2	3.5	7445	17	US-10-257-166-92	Sequence 92, Appl
c1196	47.2	3.5	11049	15	US-10-311-455-642	Sequence 642, App
c1197	47.2	3.5	11049	17	US-10-240-589C-28	Sequence 28, Appl
c1198	47.2	3.5	16217	15	US-10-311-455-597	Sequence 597, App
c1199	47.2	3.5	18434	15	US-10-311-455-1979	Sequence 1979, Ap
c1200	47	3.5	594	18	US-10-425-115-4325	Sequence 4325, Ap
c1201	47	3.5	5273	15	US-10-311-455-848	Sequence 848, App
1202	47	3.5	11787	17	US-10-240-589C-52	Sequence 52, Appl
c1203	47	3.5	13427	15	US-10-311-455-1900	Sequence 1900, Ap
c1204	47	3.5	98716	19	US-10-741-600-17754	Sequence 17754, A
1205	46.8	3.5	472	17	US-10-424-599-116828	Sequence 116828,
c1206	46.8	3.5	577	18	US-10-437-963-34329	Sequence 34329, A
c1207	46.8	3.5	858	14	US-10-198-846-7035	Sequence 7035, Ap
1208	46.8	3.5	2911	17	US-10-264-049-283	Sequence 283, App
c1209	46.8	3.5	6127	15	US-10-311-455-1587	Sequence 1587, Ap
c1210	46.8	3.5	6609	15	US-10-311-455-1276	Sequence 1276, Ap
1211	46.8	3.5	8310	19	US-10-861-875-9	Sequence 9, Appli
1212	46.8	3.5	9810	15	US-10-311-455-399	Sequence 399, App
c1213	46.8	3.5	15479	17	US-10-257-166-45	Sequence 45, Appl
c1214	46.8	3.5	17721	15	US-10-311-455-1701	Sequence 1701, Ap
c1215	46.6	3.5	474	18	US-10-425-115-64122	Sequence 64122, A
c1216	46.6	3.5	960	14	US-10-198-846-6381	Sequence 6381, Ap
1217	46.6	3.5	3148	17	US-10-424-599-30088	Sequence 30088, A
c1218	46.6	3.5	11787	17	US-10-240-589C-52	Sequence 52, Appl
c1219	46.6	3.5	12507	15	US-10-311-455-271	Sequence 271, App
1220	46.6	3.5	14307	15	US-10-311-455-702	Sequence 702, App
c1221	46.6	3.5	18060	17	US-10-240-589C-21	Sequence 21, Appl
c1222	46.4	3.4	504	18	US-10-437-963-90499	Sequence 90499, A
c1223	46.4	3.4	794	18	US-10-739-930-3501	Sequence 3501, Ap
c1224	46.4	3.4	5518	15	US-10-240-453-180	Sequence 180, App
c1225	46.4	3.4	5551	17	US-10-221-613-55	Sequence 55, Appl
1226	46.4	3.4	5647	15	US-10-311-455-1540	Sequence 1540, Ap
1227	46.4	3.4	5647	17	US-10-221-613-282	Sequence 282, App
c1228	46.4	3.4	5696	15	US-10-311-455-1079	Sequence 1079, Ap
c1229	46.4	3.4	5917	14	US-10-087-464-9	Sequence 9, Appli
c1230	46.4	3.4	6283	15	US-10-311-455-61	Sequence 61, Appl
c1231	46.4	3.4	7503	15	US-10-311-455-1522	Sequence 1522, Ap
c1232	46.4	3.4	7503	18	US-10-433-793-40	Sequence 40, Appl
c1233	46.4	3.4	11745	15	US-10-240-453-206	Sequence 206, App
c1234	46.4	3.4	11996	15	US-10-240-485-46	Sequence 46, Appl
1235	46.4	3.4	32392	19	US-10-706-635-27	Sequence 27, Appl
c1236	46.4	3.4	46951	16	US-10-091-281-2	Sequence 2, Appli
c1237	46.4	3.4	50000	19	US-10-706-635-23	Sequence 23, Appl
c1238	46.2	3.4	469	10	US-09-814-353-17965	Sequence 17965, A
c1239	46.2	3.4	5689	14	US-10-239-676-90	Sequence 90, Appl
c1240	46.2	3.4	5689	15	US-10-240-453-100	Sequence 100, App
c1241	46.2	3.4	5689	17	US-10-221-714A-148	Sequence 148, App
c1242	46.2	3.4	5706	17	US-10-221-613-280	Sequence 280, App
c1243	46.2	3.4	6223	17	US-10-221-613-135	Sequence 135, App
c1244	46.2	3.4	13511	15	US-10-311-455-254	Sequence 254, App
c1245	46.2	3.4	13627	18	US-10-433-793-5	Sequence 5, Appli
c1246	46.2	3.4	105550	18	US-10-741-601-5630	Sequence 5630, Ap
c1247	46.2	3.4	105550	19	US-10-741-600-17620	Sequence 17620, A
c1248	46	3.4	298	9	US-09-960-352-1004	Sequence 1004, Ap
1249	46	3.4	1461	18	US-10-767-701-13778	Sequence 13778, A
c1250	46	3.4	5807	15	US-10-311-455-1128	Sequence 1128, Ap
c1251	46	3.4	6191	15	US-10-311-455-1189	Sequence 1189, Ap
c1252	46	3.4	6881	15	US-10-311-455-1353	Sequence 1353, Ap
c1253	46	3.4	6881	15	US-10-240-453-123	Sequence 123, App
c1254	46	3.4	7814	17	US-10-221-714A-252	Sequence 252, App
1255	46	3.4	8170	15	US-10-240-453-131	Sequence 131, App
c1256	46	3.4	19087	15	US-10-311-455-766	Sequence 766, App
c1257	46	3.4	42027	18	US-10-417-375-58	Sequence 58, Appl
c1258	46	3.4	71553	18	US-10-719-993-7039	Sequence 7039, Ap
c1259	46	3.4	71553	19	US-10-741-600-17960	Sequence 17960, A
1260	46	3.4	1980090	18	US-10-719-993-6815	Sequence 6815, Ap
1261	46	3.4	1980090	19	US-10-741-600-17676	Sequence 17676, A
c1262	45.8	3.4	457	9	US-09-770-444-508	Sequence 508, App
1263	45.8	3.4	531	10	US-09-814-353-18996	Sequence 18996, A
c1264	45.8	3.4	921	18	US-10-425-115-38710	Sequence 38710, A
1265	45.8	3.4	1559	17	US-10-351-334-42	Sequence 42, Appl
1266	45.8	3.4	2056	15	US-10-106-698-2027	Sequence 2027, Ap
1267	45.8	3.4	5795	15	US-10-311-455-1741	Sequence 1741, Ap
c1268	45.8	3.4	6419	15	US-10-311-455-240	Sequence 240, App
c1269	45.8	3.4	9155	15	US-10-311-455-436	Sequence 436, App
c1270	45.8	3.4	9707	15	US-10-311-455-1394	Sequence 1394, Ap
c1271	45.8	3.4	11178	17	US-10-221-613-16	Sequence 16, Appl
c1272	45.8	3.4	15592	15	US-10-311-455-1299	Sequence 1299, Ap
c1273	45.8	3.4	15592	17	US-10-221-714A-175	Sequence 175, App
1274	45.6	3.4	507	18	US-10-437-963-73825	Sequence 73825, A
c1275	45.6	3.4	599	18	US-10-425-115-163442	Sequence 163442,
c1276	45.6	3.4	950	14	US-10-198-846-6625	Sequence 6625, Ap
c1277	45.6	3.4	1730	17	US-10-369-493-29357	Sequence 29357, A
c1278	45.6	3.4	4654	15	US-10-311-455-2196	Sequence 2196, Ap
c1279	45.6	3.4	4654	17	US-10-221-714A-508	Sequence 508, App
1280	45.6	3.4	4985	14	US-10-094-240-10	Sequence 10, Appl
1281	45.6	3.4	4985	16	US-10-056-405-10	Sequence 10, Appl
c1282	45.6	3.4	5388	17	US-10-221-613-199	Sequence 199, App
1283	45.6	3.4	5427	15	US-10-311-455-685	Sequence 685, App
c1284	45.6	3.4	6015	15	US-10-311-455-649	Sequence 649, App
c1285	45.6	3.4	7040	15	US-10-172-086-13	Sequence 13, Appl
c1286	45.6	3.4	7040	17	US-10-221-714A-161	Sequence 161, App
c1287	45.6	3.4	7040	18	US-10-311-507-47	Sequence 47, Appl
c1288	45.6	3.4	7040	18	US-10-480-846-13	Sequence 13, Appl
c1289	45.6	3.4	7040	18	US-10-473-126-173	Sequence 173, App
c1290	45.6	3.4	7040	18	US-10-473-126-319	Sequence 319, App
c1291	45.6	3.4	7990	15	US-10-311-455-131	Sequence 131, App
c1292	45.6	3.4	7990	16	US-10-240-452-7	Sequence 7, Appli
1293	45.6	3.4	8305	15	US-10-311-455-1541	Sequence 1541, Ap
c1294	45.6	3.4	11260	14	US-10-239-676-19	Sequence 19, Appl
c1295	45.6	3.4	11260	15	US-10-240-453-27	Sequence 27, Appl
c1296	45.6	3.4	12393	15	US-10-311-455-1235	Sequence 1235, Ap
c1297	45.6	3.4	14032	15	US-10-311-455-1426	Sequence 1426, Ap
c1298	45.6	3.4	14919	17	US-10-221-714A-228	Sequence 228, App
c1299	45.6	3.4	17421	14	US-10-239-676-53	Sequence 53, Appl
c1300	45.6	3.4	17421	15	US-10-240-453-55	Sequence 55, Appl
1301	45.6	3.4	567564	18	US-10-699-156-3	Sequence 3, Appli
c1302	45.4	3.4	294	10	US-09-814-353-5106	Sequence 5106, Ap
c1303	45.4	3.4	294	10	US-09-814-353-11398	Sequence 11398, A
c1304	45.4	3.4	445	18	US-10-357-930-5422	Sequence 5422, Ap
c1305	45.4	3.4	614	10	US-09-814-353-5117	Sequence 5117, Ap
c1306	45.4	3.4	614	10	US-09-814-353-11409	Sequence 11409, A
1307	45.4	3.4	622	10	US-09-764-891-1673	Sequence 1673, Ap
1308	45.4	3.4	622	15	US-10-205-428-148	Sequence 148, App
1309	45.4	3.4	1014	15	US-10-195-730-34	Sequence 34, Appl
1310	45.4	3.4	1014	18	US-10-799-747-34	Sequence 34, Appl
1311	45.4	3.4	3744	8	US-08-961-527-263	Sequence 263, App
1312	45.4	3.4	3744	17	US-10-158-844-263	Sequence 263, App
c1313	45.4	3.4	4985	14	US-10-094-240-10	Sequence 10, Appl
c1314	45.4	3.4	4985	16	US-10-056-405-10	Sequence 10, Appl
c1315	45.4	3.4	5033	18	US-10-473-126-285	Sequence 285, App
c1316	45.4	3.4	5218	15	US-10-311-455-1239	Sequence 1239, Ap
1317	45.4	3.4	5376	15	US-10-311-455-2123	Sequence 2123, Ap
c1318	45.4	3.4	5427	15	US-10-311-455-686	Sequence 686, App
c1319	45.4	3.4	5675	15	US-10-311-455-1249	Sequence 1249, Ap
c1320	45.4	3.4	5909	15	US-10-311-455-1132	Sequence 1132, Ap
1321	45.4	3.4	6621	15	US-10-311-455-886	Sequence 886, App
c1322	45.4	3.4	7906	14	US-10-239-676-98	Sequence 98, Appl
c1323	45.4	3.4	7906	15	US-10-240-453-110	Sequence 110, App
c1324	45.4	3.4	8227	18	US-10-433-793-155	Sequence 155, App
c1325	45.4	3.4	8524	15	US-10-311-455-1814	Sequence 1814, Ap
c1326	45.4	3.4	8524	17	US-10-221-714A-310	Sequence 310, App
c1327	45.4	3.4	13574	15	US-10-311-455-1290	Sequence 1290, Ap
1328	45.4	3.4	15853	17	US-10-221-613-422	Sequence 422, App
c1329	45.4	3.4	18218	15	US-10-311-455-1922	Sequence 1922, Ap
c1330	45.4	3.4	18855	15	US-10-311-455-583	Sequence 583, App
1331	45.4	3.4	105550	18	US-10-741-601-5630	Sequence 5630, Ap
1332	45.4	3.4	105550	19	US-10-741-600-17620	Sequence 17620, A
c1333	45.4	3.4	158001	17	US-10-211-179-11	GENERAL INFORMATI
c1334	45.4	3.4	2162598	19	US-10-472-928-4979	Sequence 4979, Ap
c1335	45.2	3.4	420	10	US-09-814-353-12772	Sequence 12772, A
c1336	45.2	3.4	421	10	US-09-814-353-5169	Sequence 5169, Ap
c1337	45.2	3.4	453	18	US-10-425-115-28792	Sequence 28792, A
c1338	45.2	3.4	505	14	US-10-060-036-2607	Sequence 2607, Ap
c1339	45.2	3.4	5001	15	US-10-172-086-69	Sequence 69, Appl

c1340	45.2	3.4	5001	16	US-10-240-452-73	Sequence 73, Appl
c1341	45.2	3.4	5001	18	US-10-311-507-33	Sequence 33, Appl
c1342	45.2	3.4	5001	18	US-10-480-846-69	Sequence 69, Appl
c1343	45.2	3.4	5328	15	US-10-311-455-533	Sequence 533, App
c1344	45.2	3.4	5519	17	US-10-257-166-51	Sequence 51, Appl
c1345	45.2	3.4	5930	15	US-10-311-455-490	Sequence 490, App
1346	45.2	3.4	6171	15	US-10-311-455-761	Sequence 761, App
c1347	45.2	3.4	6200	15	US-10-311-455-2188	Sequence 2188, Ap
c1348	45.2	3.4	7346	15	US-10-311-455-318	Sequence 318, App
c1349	45.2	3.4	7892	17	US-10-257-166-138	Sequence 138, App
1350	45.2	3.4	9265	15	US-10-311-455-2125	Sequence 2125, Ap
1351	45.2	3.4	9265	17	US-10-240-454-49	Sequence 49, Appl
c1352	45.2	3.4	12592	17	US-10-221-613-58	Sequence 58, Appl
c1353	45.2	3.4	19380	17	US-10-221-613-390	Sequence 390, App
c1354	45.2	3.4	40324	18	US-10-433-793-180	Sequence 180, App
c1355	45.2	3.4	163382	18	US-10-367-094-179	Sequence 179, App
1356	45.2	3.4	325446	18	US-10-719-993-6824	Sequence 6824, Ap
c1357	45	3.3	411	14	US-10-198-846-4590	Sequence 4590, Ap
c1358	45	3.3	465	18	US-10-425-115-170017	Sequence 170017,
1359	45	3.3	600	13	US-10-027-632-218174	Sequence 218174,
1360	45	3.3	600	13	US-10-027-632-218175	Sequence 218175,
1361	45	3.3	600	17	US-10-027-632-218174	Sequence 218174,
1362	45	3.3	600	17	US-10-027-632-218175	Sequence 218175,
1363	45	3.3	1501	18	US-10-473-126-328	Sequence 328, App
1364	45	3.3	1758	18	US-10-723-860-5011	Sequence 5011, Ap
c1365	45	3.3	2000	9	US-09-938-842A-4184	Sequence 4184, Ap
c1366	45	3.3	2000	11	US-09-938-842A-4184	Sequence 4184, Ap
c1367	45	3.3	5338	17	US-10-221-613-242	Sequence 242, App
c1368	45	3.3	6208	15	US-10-311-455-167	Sequence 167, App
1369	45	3.3	8178	15	US-10-311-455-60	Sequence 60, Appl
c1370	45	3.3	13321	17	US-10-221-714A-143	Sequence 143, App
c1371	45	3.3	18154	15	US-10-311-455-227	Sequence 227, App
1372	44.8	3.3	549	10	US-09-991-936-1290	Sequence 1290, Ap
1373	44.8	3.3	551	10	US-09-986-480-60	Sequence 60, Appl
1374	44.8	3.3	755	13	US-10-027-632-128109	Sequence 128109,
1375	44.8	3.3	755	17	US-10-027-632-128109	Sequence 128109,
1376	44.8	3.3	3095	18	US-10-602-494-313	Sequence 313, App
c1377	44.8	3.3	5020	18	US-10-473-126-99	Sequence 99, Appl
c1378	44.8	3.3	5020	18	US-10-473-126-245	Sequence 245, App
1379	44.8	3.3	5875	15	US-10-311-455-261	Sequence 261, App
1380	44.8	3.3	5917	14	US-10-087-464-9	Sequence 9, Appli
1381	44.8	3.3	6222	15	US-10-311-455-211	Sequence 211, App
1382	44.8	3.3	6228	17	US-10-221-613-393	Sequence 393, App
c1383	44.8	3.3	6397	15	US-10-311-455-792	Sequence 792, App
1384	44.8	3.3	6627	15	US-10-311-455-1547	Sequence 1547, Ap
c1385	44.8	3.3	6662	15	US-10-311-455-371	Sequence 371, App
1386	44.8	3.3	6676	18	US-10-433-793-44	Sequence 44, Appl
c1387	44.8	3.3	6904	15	US-10-311-455-185	Sequence 185, App
c1388	44.8	3.3	7201	15	US-10-311-455-309	Sequence 309, App
c1389	44.8	3.3	7319	15	US-10-311-455-2018	Sequence 2018, Ap
c1390	44.8	3.3	7823	14	US-10-239-676-198	Sequence 198, App
c1391	44.8	3.3	7823	15	US-10-311-455-2034	Sequence 2034, Ap
c1392	44.8	3.3	7823	15	US-10-240-453-292	Sequence 292, App
c1393	44.8	3.3	8952	17	US-10-221-714A-167	Sequence 167, App
c1394	44.8	3.3	8962	15	US-10-311-455-660	Sequence 660, App
c1395	44.8	3.3	11092	15	US-10-311-455-1486	Sequence 1486, Ap
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c1397	44.8	3.3	128034	17	US-10-282-174-187	Sequence 187, App
c1398	44.8	3.3	128034	19	US-10-600-009-186	Sequence 186, App
c1399	44.8	3.3	128034	19	US-10-600-009-187	Sequence 187, App
1400	44.8	3.3	202100	17	US-10-282-174-484	Sequence 484, App
1401	44.8	3.3	202100	19	US-10-600-009-484	Sequence 484, App
c1402	44.6	3.3	363	10	US-09-814-353-4589	Sequence 4589, Ap
c1403	44.6	3.3	363	10	US-09-814-353-10888	Sequence 10888, A
c1404	44.6	3.3	393	9	US-09-960-352-4582	Sequence 4582, Ap
1405	44.6	3.3	440	18	US-10-425-115-173202	Sequence 173202,
c1406	44.6	3.3	465	10	US-09-814-353-17748	Sequence 17748, A
c1407	44.6	3.3	648	13	US-10-027-632-132827	Sequence 132827,
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c1410	44.6	3.3	6031	17	US-10-221-714A-343	Sequence 343, App
c1411	44.6	3.3	6853	15	US-10-311-455-283	Sequence 283, App
c1412	44.6	3.3	6853	16	US-10-240-452-31	Sequence 31, Appl
c1413	44.6	3.3	7351	15	US-10-311-455-1	Sequence 1, Appli
c1414	44.6	3.3	8056	18	US-10-473-126-385	Sequence 385, App
c1415	44.6	3.3	8607	17	US-10-240-589C-111	Sequence 111, App
c1416	44.6	3.3	11964	18	US-10-433-793-56	Sequence 56, Appl
c1417	44.6	3.3	14987	15	US-10-311-455-604	Sequence 604, App
c1418	44.6	3.3	15732	14	US-10-239-676-95	Sequence 95, Appl
c1419	44.6	3.3	15732	15	US-10-240-453-107	Sequence 107, App
c1420	44.6	3.3	15951	15	US-10-311-455-1654	Sequence 1654, Ap
c1421	44.6	3.3	15951	15	US-10-240-485-134	Sequence 134, App
c1422	44.6	3.3	17959	15	US-10-311-455-548	Sequence 548, App
c1423	44.6	3.3	17959	16	US-10-240-452-42	Sequence 42, Appl
c1424	44.6	3.3	19082	15	US-10-311-455-599	Sequence 599, App
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c1432	44.4	3.3	647	10	US-09-814-353-11262	Sequence 11262, A
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1435	44.4	3.3	2217	17	US-10-191-803-555	Sequence 555, App
1436	44.4	3.3	2217	17	US-10-152-319A-2185	Sequence 2185, Ap
1437	44.4	3.3	5487	15	US-10-311-455-1571	Sequence 1571, Ap
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1440	44.4	3.3	6227	15	US-10-311-455-1560	Sequence 1560, Ap
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c1442	44.4	3.3	6375	15	US-10-311-455-1998	Sequence 1998, Ap
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1444	44.4	3.3	7374	17	US-10-257-166-118	Sequence 118, App
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c1449	44.4	3.3	15674	15	US-10-311-455-335	Sequence 335, App
c1450	44.4	3.3	15674	15	US-10-240-485-29	Sequence 29, Appl
c1451	44.4	3.3	16750	15	US-10-311-455-494	Sequence 494, App
c1452	44.4	3.3	16750	17	US-10-221-714A-36	Sequence 36, Appl
1453	44.4	3.3	17131	15	US-10-311-455-1026	Sequence 1026, Ap
1454	44.4	3.3	17594	15	US-10-311-455-2000	Sequence 2000, Ap
c1455	44.4	3.3	17848	14	US-10-239-676-28	Sequence 28, Appl
c1456	44.4	3.3	17848	15	US-10-240-453-38	Sequence 38, Appl
c1457	44.4	3.3	17848	17	US-10-257-166-58	Sequence 58, Appl
c1458	44.4	3.3	18683	15	US-10-311-455-286	Sequence 286, App
c1459	44.4	3.3	18683	16	US-10-240-452-34	Sequence 34, Appl
c1460	44.4	3.3	81167	18	US-10-719-993-6925	Sequence 6925, Ap
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1462	44.4	3.3	177380	19	US-10-484-577-683	Sequence 683, App
1463	44.2	3.3	323	17	US-10-242-535A-44408	Sequence 44408, A
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c1470	44.2	3.3	1425	17	US-10-282-122A-16862	Sequence 16862, A
1471	44.2	3.3	2341	18	US-10-723-860-6973	Sequence 6973, Ap
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c1474	44.2	3.3	3046	18	US-10-433-793-81	Sequence 81, Appl
c1475	44.2	3.3	5421	15	US-10-311-455-106	Sequence 106, App
c1476	44.2	3.3	6145	15	US-10-311-455-945	Sequence 945, App
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1478	44.2	3.3	6343	18	US-10-473-126-334	Sequence 334, App
c1479	44.2	3.3	6652	18	US-10-433-793-17	Sequence 17, Appl
1480	44.2	3.3	6821	15	US-10-311-455-1575	Sequence 1575, Ap
c1481	44.2	3.3	8889	15	US-10-311-455-183	Sequence 183, App
1482	44.2	3.3	9289	17	US-10-221-714A-224	Sequence 224, App
c1483	44.2	3.3	17967	15	US-10-311-455-987	Sequence 987, App
1484	44.2	3.3	18283	17	US-10-221-613-326	Sequence 326, App
1485	44.2	3.3	277616	18	US-10-367-094-83	Sequence 83, Appl

1486	44.2	3.3	786431	16	US-10-412-277-3	Sequence 3, Appli
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1490	44	3.3	793	17	US-10-424-599-84417	Sequence 84417, A
1491	44	3.3	1111	8	US-08-781-986A-756	Sequence 756, App
1492	44	3.3	1111	17	US-10-329-624-756	Sequence 756, App
1493	44	3.3	1909	10	US-09-759-130B-121	Sequence 121, App
1494	44	3.3	1909	18	US-10-741-790-121	Sequence 121, App
1495	44	3.3	2105	18	US-10-357-930-23225	Sequence 23225, A
1496	44	3.3	2105	18	US-10-357-930-29097	Sequence 29097, A
c1497	44	3.3	5536	15	US-10-311-455-151	Sequence 151, App
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c1499	44	3.3	5979	15	US-10-240-453-26	Sequence 26, Appl
c1500	44	3.3	6070	15	US-10-311-455-1652	Sequence 1652, Ap

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Job time : 811.34 secs

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OM nucleic - nucleic search, using sw model

Run on: February 24, 2005, 19:17:16 ; Search time 4295.67 Seconds
(without alignments)
11927.005 Million cell updates/sec

Title: US-09-989-724-386
Perfect score: 1346
Sequence: 1 gaaagaatgttgtggctgct.....aaaaaaaaaaaaaaaaaaaa 1346

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	751.2	55.8	978	4	BI762437	BI762437 603048828
	3	746.8	55.5	779	4	BG217185	BG217185 RST36886
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	5	736.6	54.7	826	4	BG194741	BG194741 RST13907
	6	732	54.4	788	4	BG211841	BG211841 RST31414
	7	729	54.2	801	4	BG218203	BG218203 RST37930
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	9	706.8	52.5	780	4	BG429174	BG429174 602498032
	10	704.4	52.3	754	4	BG181765	BG181765 RST618 At
	11	695.2	51.6	792	4	BG400845	BG400845 602464068
	12	675.4	50.2	791	4	BG400319	BG400319 602464526
	13	665.8	49.5	1081	4	BM811234	BM811234 AGENCOURT
	14	661.6	49.2	855	4	BG427247	BG427247 602494304
	15	657	48.8	669	9	AY399636	AY399636 Homo sapi
	16	649.4	48.2	866	4	BG429618	BG429618 602501304
	17	648.2	48.2	804	4	BG429705	BG429705 602493709
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	20	637	47.3	782	4	BG433974	BG433974 602497274
	21	636.8	47.3	688	4	BG776793	BG776793 602663969
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	23	631.4	46.9	736	4	BG399402	BG399402 602441161
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	36	579.2	43.0	866	4	BG188580	BG188580 RST7605 A
	37	569	42.3	678	4	BG429011	BG429011 602501924
	38	568.8	42.3	584	1	AI792241	AI792241 ov04f11.y
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	46	544	40.4	828	4	BG195252	BG195252 RST14433
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	54	516.4	38.4	845	6	CA491504	CA491504 AGENCOURT
	55	515.8	38.3	755	6	CB955052	CB955052 AGENCOURT
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	58	509.6	37.9	874	7	CF550832	CF550832 AGENCOURT
	59	509	37.8	797	4	BI101134	BI101134 602886818
	60	507.2	37.7	853	6	CA494852	CA494852 AGENCOURT
	61	507	37.7	842	4	BI101926	BI101926 602887622
	62	505	37.5	529	6	CB134037	CB134037 K-EST0185
	63	505	37.5	529	6	CB139939	CB139939 K-EST0193
	64	504.6	37.5	800	6	CA480818	CA480818 AGENCOURT
	65	504.6	37.5	820	6	CA480734	CA480734 AGENCOURT
c	66	502.6	37.3	512	2	BF589928	BF589928 naa32h04.
	67	502.6	37.3	830	6	CA468084	CA468084 AGENCOURT
c	68	501.8	37.3	505	1	AA999850	AA999850 ov04f11.s
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	71	497.8	37.0	897	6	CA467586	CA467586 AGENCOURT
	72	496	36.8	782	4	BG969864	BG969864 602838808
	73	495	36.8	656	4	BI143454	BI143454 602907630
	74	494	36.7	981	2	BF784771	BF784771 602111117
	75	492.8	36.6	544	4	BG399046	BG399046 602440713
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	77	491.8	36.5	915	2	BF789250	BF789250 602105150
	78	491	36.5	515	6	CB139958	CB139958 K-EST0193
	79	489.4	36.4	724	6	CB599934	CB599934 AGENCOURT
	80	487.8	36.2	844	6	CA492750	CA492750 AGENCOURT
	81	485	36.0	626	7	CK625203	CK625203 mi30d02.y
c	82	484.4	36.0	493	1	AI911520	AI911520 ty73b02.x
	83	479.8	35.6	832	4	BG402158	BG402158 602465708
	84	479	35.6	858	6	CA467976	CA467976 AGENCOURT
	85	478.6	35.6	734	4	BG183334	BG183334 RST2228 A
c	86	476.8	35.4	514	1	AI765078	AI765078 wh56h04.x
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	88	474.8	35.3	822	4	BG402232	BG402232 602465795
	89	474.6	35.3	728	4	BG426067	BG426067 602492749
	90	474.6	35.3	874	6	CA491517	CA491517 AGENCOURT
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	92	473.4	35.2	864	4	BG401869	BG401869 602466568
	93	470.2	34.9	822	6	CA491889	CA491889 AGENCOURT
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	95	467.6	34.7	874	6	CA493040	CA493040 AGENCOURT
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	97	467	34.7	496	4	BG430790	BG430790 602498560

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	101	461	34.2	868	6	CA481303	CA481303 AGENCOURT
	102	456.6	33.9	730	6	CD241570	CD241570 AGENCOURT
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	105	454.8	33.8	742	4	BG969794	BG969794 602838708
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c	126	425	31.6	426	2	BE465778	BE465778 hw22h10.x
c	127	425	31.6	448	1	AI671437	AI671437 wc30c08.x
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c	129	423.8	31.5	430	2	AW299600	AW299600 xs52b09.x
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	131	414.2	30.8	554	1	AI788483	AI788483 uk57g07.y
	132	411.4	30.6	534	4	BM022547	BM022547 id61g10.y
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	136	407.4	30.3	928	7	CF582583	CF582583 AGENCOURT
	137	406	30.2	892	6	CA468414	CA468414 AGENCOURT
	138	405	30.1	547	4	BI965141	BI965141 id34a06.y
	139	405	30.1	569	4	BI966990	BI966990 id27a07.y
	140	404	30.0	546	1	AI789448	AI789448 uk99d02.y
	141	402.4	29.9	539	2	AW012244	AW012244 ul88g07.y
	142	394.6	29.3	508	2	BF550608	BF550608 UI-R-C1-k
	143	393.6	29.2	511	7	CK624505	CK624505 mi22a01.y
	144	393.4	29.2	499	1	AJ681737	AJ681737 AJ681737
	145	392.8	29.2	586	4	BI345729	BI345729 374635 MA
	146	392.4	29.2	582	5	BP370260	BP370260 BP370260
	147	392	29.1	574	2	AW045074	AW045074 um17d10.y
	148	391	29.0	891	6	CA469320	CA469320 AGENCOURT
	149	390	29.0	525	1	AI882207	AI882207 ul31g03.y
	150	389.8	29.0	505	1	AI746613	AI746613 ul01d01.y
	151	388.6	28.9	794	6	CB955392	CB955392 AGENCOURT
	152	387.6	28.8	513	1	AA445683	AA445683 vf62h07.r
	153	386.8	28.7	804	4	BG431368	BG431368 602499982
	154	385.4	28.6	519	1	AI747322	AI747322 ul05a06.y
c	155	384.2	28.5	428	1	AI431850	AI431850 ti25h12.x
	156	382	28.4	549	7	CN369195	CN369195 170006000
	157	381	28.3	405	6	CB137251	CB137251 K-EST0189
	158	376.4	28.0	763	5	BX926439	BX926439 BX926439
	159	374.2	27.8	541	1	AA131483	AA131483 zo08e05.r
	160	373.8	27.8	485	2	AW106894	AW106894 um34h05.y
	161	373.4	27.7	881	6	CA468090	CA468090 AGENCOURT
	162	368.8	27.4	504	1	AJ682987	AJ682987 AJ682987
c	163	368.6	27.4	779	7	CK778629	CK778629 965794 MA
	164	368.4	27.4	547	6	CB222923	CB222923 1JEJ17E10
	165	366.4	27.2	536	1	AI663506	AI663506 uk33f11.y
	166	361.8	26.9	533	1	AI663460	AI663460 uk33b03.y
	167	361.6	26.9	778	7	CR451583	CR451583 CR451583
	168	361	26.8	499	1	AI882240	AI882240 ul56b05.y
	169	353.8	26.3	489	2	AW259149	AW259149 um89b04.y
	170	352.8	26.2	452	1	AA289223	AA289223 vc93f01.r
	171	352.8	26.2	463	1	AA275670	AA275670 vc33c12.r
	172	352.2	26.2	925	2	BF784692	BF784692 602111325
	173	347.8	25.8	566	2	AW475605	AW475605 un68h06.y
	174	340.4	25.3	482	1	AA273463	AA273463 vc37b10.r
	175	334	24.8	644	7	CK627074	CK627074 mj31a04.y
	176	326.4	24.2	436	6	CB163923	CB163923 K-EST0224
	177	326.2	24.2	696	1	AJ660081	AJ660081 AJ660081
c	178	323.4	24.0	360	4	BG182824	BG182824 RST1685 A
	179	322.4	24.0	474	1	AI931440	AI931440 ul68d11.y
	180	318.6	23.7	457	5	BY006328	BY006328 BY006328
	181	317	23.6	405	1	AA109637	AA109637 mm01f02.r
	182	316.6	23.5	532	9	CG532959	CG532959 OST117705
	183	315.6	23.4	427	2	BB847292	BB847292 BB847292
	184	315	23.4	437	2	BB844940	BB844940 BB844940
	185	308	22.9	413	2	BB847970	BB847970 BB847970
c	186	308	22.9	697	7	CO683419	CO683419 DG11-169e
	187	307.8	22.9	416	2	BB848103	BB848103 BB848103
	188	303.8	22.6	716	4	BG400370	BG400370 602464583
	189	303.6	22.6	410	1	AA066328	AA066328 mm14d08.r
	190	303	22.5	408	2	BB848163	BB848163 BB848163
	191	298.2	22.2	361	4	BG181204	BG181204 RST129 At
	192	293.8	21.8	416	2	BB846622	BB846622 BB846622
	193	291.8	21.7	386	1	AA109535	AA109535 mm01g04.r
c	194	289.4	21.5	688	7	CO681115	CO681115 DG11-125l
	195	288.6	21.4	479	5	BP769681	BP769681 BP769681
	196	287.6	21.4	392	2	AW260024	AW260024 um82c07.y
	197	287.4	21.4	437	2	BB844950	BB844950 BB844950
	198	287	21.3	412	5	BY006356	BY006356 BY006356
	199	286.8	21.3	427	2	BB848288	BB848288 BB848288
	200	284.2	21.1	429	5	BY006674	BY006674 BY006674
c	201	282.8	21.0	293	1	AI470468	AI470468 tj44c08.x
	202	282.8	21.0	838	6	CA494798	CA494798 AGENCOURT
	203	282	21.0	509	9	CG611484	CG611484 OST296516
	204	281.4	20.9	506	9	CG668483	CG668483 OST464441
	205	278.6	20.7	426	2	BB847279	BB847279 BB847279
c	206	278.2	20.7	677	7	CO679660	CO679660 DG11-104g
	207	276.4	20.5	375	2	BB843933	BB843933 BB843933
	208	275.6	20.5	421	2	BB848169	BB848169 BB848169
	209	275.6	20.5	492	1	AA065156	AA065156 zm50a10.r
	210	274.8	20.4	428	2	AW259271	AW259271 um89h04.y
	211	274	20.4	372	2	BB843467	BB843467 BB843467
c	212	274	20.4	459	2	AW244613	AW244613 BR_END09H
	213	270.8	20.1	640	4	BM439885	BM439885 pgr1n.pk0
c	214	270.4	20.1	903	7	CF582582	CF582582 AGENCOURT
c	215	267	19.8	667	7	CO693790	CO693790 DG11-67n1
	216	266.2	19.8	369	2	BB843868	BB843868 BB843868
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	218	265.4	19.7	407	2	BB845600	BB845600 BB845600
	219	264.2	19.6	698	6	CD217554	CD217554 pgr1n.pk0
	220	263	19.5	458	2	BB846267	BB846267 BB846267
	221	262.8	19.5	290	6	CB137087	CB137087 K-EST0189
c	222	260.6	19.4	610	7	CO696699	CO696699 DG32-100j
	223	259.8	19.3	430	5	BY006046	BY006046 BY006046
c	224	257.4	19.1	281	1	AI473091	AI473091 th56a03.x
	225	255	18.9	375	2	BB843929	BB843929 BB843929
	226	255	18.9	450	1	AJ655099	AJ655099 AJ655099
c	227	254.2	18.9	608	7	CO683836	CO683836 DG11-175g
	228	254	18.9	455	2	BB845438	BB845438 BB845438
	229	253.4	18.8	345	5	BY005657	BY005657 BY005657
	230	252.4	18.8	341	2	BB846895	BB846895 BB846895
	231	249.6	18.5	418	2	BB848084	BB848084 BB848084
c	232	249	18.5	602	9	CE845885	CE845885 tigr-gss-
c	233	248.6	18.5	606	7	CO693615	CO693615 DG11-65i1
c	234	248	18.4	610	7	CO685560	CO685560 DG11-201f
	235	245.2	18.2	340	2	BB843625	BB843625 BB843625
	236	245	18.2	366	2	BB847608	BB847608 BB847608
	237	244.8	18.2	307	4	BG185958	BG185958 RST4913 A
	238	244.6	18.2	378	5	BY086677	BY086677 BY086677
c	239	244.4	18.2	613	7	CO694612	CO694612 DG11-74j1
	240	243.8	18.1	693	2	BF031348	BF031348 601559115
	241	243.4	18.1	248	1	AA345162	AA345162 EST51144
	242	242	18.0	372	2	BB843455	BB843455 BB843455
c	243	239.8	17.8	652	5	BP769682	BP769682 BP769682

	244	239.6	17.8	338	2	BB847006	BB847006 BB847006
	245	238.8	17.7	527	6	CB954911	CB954911 AGENCOURT
	246	237.4	17.6	304	1	AA068066	AA068066 ml77h10.r
	247	237.2	17.6	1064	2	BF212565	BF212565 601813769
	248	234	17.4	366	2	BB843831	BB843831 BB843831
	249	233	17.3	430	5	BY006662	BY006662 BY006662
	250	232.8	17.3	472	1	AJ693058	AJ693058 AJ693058
	251	232.6	17.3	355	1	AA076448	AA076448 zm91d10.r
	252	231.2	17.2	358	5	BY005603	BY005603 BY005603
	253	229.2	17.0	322	4	BG193281	BG193281 RST12409
	254	229	17.0	303	1	AI119252	AI119252 ue24c07.y
c	255	228.2	17.0	537	6	CB535092	CB535092 768475 MA
c	256	227.8	16.9	608	7	CO696480	CO696480 DG11-99f2
	257	227.6	16.9	1113	6	CA493126	CA493126 AGENCOURT
	258	222.8	16.6	329	4	BG189097	BG189097 RST8135 A
	259	222.4	16.5	317	2	BB848179	BB848179 BB848179
	260	221.6	16.5	494	2	BF654521	BF654521 278735 MA
	261	221	16.4	407	5	BY006237	BY006237 BY006237
c	262	220.6	16.4	615	2	AW107491	AW107491 um17d10.x
	263	220.2	16.4	375	2	BB843943	BB843943 BB843943
	264	219.8	16.3	326	2	AW259274	AW259274 um89h10.y
	265	218.4	16.2	345	2	BB843573	BB843573 BB843573
	266	216	16.0	857	7	CN059437	CN059437 Salamande
c	267	214.2	15.9	285	4	BG184375	BG184375 RST3299 A
	268	213	15.8	335	2	BB847020	BB847020 BB847020
	269	211.8	15.7	473	1	AJ672187	AJ672187 AJ672187
	270	211.2	15.7	762	2	BB432035	BB432035 BB432035
	271	208.8	15.5	312	7	CN790738	CN790738 4125362 B
	272	207	15.4	373	2	BB843794	BB843794 BB843794
	273	206.8	15.4	355	4	BG184374	BG184374 RST3298 A
c	274	205	15.2	618	5	BP771569	BP771569 BP771569
	275	203.8	15.1	621	4	BI394480	BI394480 pgp1n.pk0
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	277	195.6	14.5	702	4	BG971735	BG971735 602838272
	278	193.8	14.4	237	1	AA239693	AA239693 mv23h03.r
c	279	192	14.3	549	5	BP772682	BP772682 BP772682
c	280	191	14.2	676	5	BP770276	BP770276 BP770276
c	281	190.6	14.2	199	2	BE501448	BE501448 hw31h12.x
c	282	189.4	14.1	581	5	BP771186	BP771186 BP771186
	283	188.8	14.0	249	1	AI317693	AI317693 uj16e02.y
	284	187.6	13.9	267	2	BB599302	BB599302 BB599302
	285	184.2	13.7	728	7	CF521338	CF521338 AGENCOURT
	286	183.8	13.7	429	4	BM432807	BM432807 1JEJ6A6.a
c	287	183.8	13.7	531	5	BP770846	BP770846 BP770846
	288	183.2	13.6	733	7	CF522498	CF522498 AGENCOURT
c	289	183	13.6	563	1	AI790388	AI790388 uk99e12.x
c	290	183	13.6	593	1	AI132404	AI132404 ue24c06.x
c	291	182.6	13.6	557	7	CO691734	CO691734 DG11-36n2
	292	182.6	13.6	730	7	CF522204	CF522204 AGENCOURT
	293	182.6	13.6	743	7	CF519814	CF519814 AGENCOURT
	294	182.6	13.6	749	7	CF521728	CF521728 AGENCOURT
	295	182.6	13.6	776	7	CF547505	CF547505 AGENCOURT
	296	182.6	13.6	854	6	CB559638	CB559638 AGENCOURT
	297	182.6	13.6	874	6	CB559915	CB559915 AGENCOURT
	298	182.6	13.6	876	5	BU904475	BU904475 AGENCOURT
	299	181.6	13.5	845	5	BU904947	BU904947 AGENCOURT
c	300	181	13.4	570	1	AI648982	AI648982 uk33f11.x
c	301	180	13.4	505	1	AI882052	AI882052 ul56b05.x
	302	179.2	13.3	217	1	AA197784	AA197784 mv03g11.r
c	303	179.2	13.3	493	2	AW018367	AW018367 ul95b01.x
c	304	179	13.3	549	2	AW146036	AW146036 um36c07.x
	305	178.6	13.3	927	5	BU904108	BU904108 AGENCOURT
	306	176.6	13.1	565	4	BI848315	BI848315 470723 MA
c	307	176.6	13.1	654	1	AI314694	AI314694 uj27f01.x
	308	175.4	13.0	310	5	BY005681	BY005681 BY005681
c	309	174.2	12.9	721	9	AG545490	AG545490 Mus muscu
c	310	172.8	12.8	590	1	AI790369	AI790369 uk99d02.x
c	311	172.6	12.8	488	1	AI891567	AI891567 ul31g03.x
c	312	171.4	12.7	551	1	AA131170	AA131170 zo08e05.s
	313	170.6	12.7	260	2	BB598752	BB598752 BB598752
c	314	170.6	12.7	985	2	BF781108	BF781108 602106752
	315	170.4	12.7	919	5	BU904746	BU904746 AGENCOURT
c	316	169.6	12.6	597	1	AI790451	AI790451 ul01d01.x
c	317	168.2	12.5	502	2	AW012648	AW012648 ul88g07.x
c	318	167	12.4	445	7	CO683642	CO683642 DG11-172h
c	319	163.2	12.1	555	1	AI790249	AI790249 uk57g07.x
c	320	162.8	12.1	498	1	AI931957	AI931957 ul68d11.x
c	321	161.6	12.0	513	2	AW260517	AW260517 um82c07.x
	322	160.6	11.9	461	2	BB746418	BB746418 BB746418
	323	160.6	11.9	462	2	BB746246	BB746246 BB746246
	324	160.6	11.9	465	2	BB744788	BB744788 BB744788
	325	160.6	11.9	465	2	BB747285	BB747285 BB747285
c	326	159.4	11.8	590	5	BP772872	BP772872 BP772872
	327	158.8	11.8	307	2	BB843809	BB843809 BB843809
	328	157.8	11.7	209	2	AW916399	AW916399 EST347690
	329	156.8	11.6	374	5	BY042134	BY042134 BY042134
	330	155.8	11.6	285	2	BB843715	BB843715 BB843715
	331	155.2	11.5	453	2	BB747298	BB747298 BB747298
	332	153.8	11.4	476	2	BB745286	BB745286 BB745286
c	333	153.2	11.4	430	7	CO685254	CO685254 DG11-199g
	334	153.2	11.4	451	2	BB748492	BB748492 BB748492
	335	152.4	11.3	448	2	BB747771	BB747771 BB747771
c	336	151.8	11.3	465	2	AW106962	AW106962 um34h05.x
	337	151.4	11.2	454	2	BB748020	BB748020 BB748020
	338	151	11.2	350	1	AA065710	AA065710 mm44c03.r
	339	150.4	11.2	481	2	BB745265	BB745265 BB745265
	340	150	11.1	335	7	CK961894	CK961894 4076310 B
	341	150	11.1	446	2	BB748378	BB748378 BB748378
c	342	149.4	11.1	476	5	BP770536	BP770536 BP770536
	343	149.2	11.1	462	2	BB746032	BB746032 BB746032
	344	148	11.0	441	2	BB748039	BB748039 BB748039
c	345	148	11.0	442	4	BM569572	BM569572 ih97a02.x
	346	147.8	11.0	444	2	BB744897	BB744897 BB744897
c	347	147.4	11.0	486	2	AW519434	AW519434 un04b12.x
	348	146.8	10.9	184	4	BG196762	BG196762 RST15989
c	349	146.6	10.9	450	1	AA084135	AA084135 zn03h05.s
	350	146.4	10.9	456	2	BB747928	BB747928 BB747928
c	351	145.8	10.8	487	1	AI746288	AI746288 ul05a06.x
	352	145.8	10.8	617	6	CA342735	CA342735 672680 NC
	353	145.8	10.8	765	5	BX887952	BX887952 BX887952
	354	145.8	10.8	767	5	BX868900	BX868900 BX868900
	355	144.8	10.8	769	5	BX913677	BX913677 BX913677
	356	144.2	10.7	750	5	BX879965	BX879965 BX879965
	357	144	10.7	437	2	BB738866	BB738866 BB738866
	358	143.8	10.7	182	1	AA104963	AA104963 mm65a05.r
	359	143.6	10.7	391	5	BY050206	BY050206 BY050206
	360	142.8	10.6	437	2	BB747257	BB747257 BB747257
	361	142.2	10.6	433	2	BB738749	BB738749 BB738749
	362	142.2	10.6	492	1	AV002459	AV002459 AV002459
	363	141	10.5	445	2	BB746531	BB746531 BB746531
	364	140.6	10.4	791	5	BX304379	BX304379 BX304379
c	365	140.4	10.4	442	2	AW319911	AW319911 un11g10.x
	366	139.8	10.4	464	2	BB744139	BB744139 BB744139
c	367	138.6	10.3	498	4	BM022245	BM022245 id61g10.x
	368	137.6	10.2	443	2	BB746485	BB746485 BB746485
	369	137.6	10.2	464	2	BB744916	BB744916 BB744916
	370	137.6	10.2	532	1	AA273481	AA273481 vc37c10.r
	371	137.2	10.2	443	2	BB747760	BB747760 BB747760
c	372	136.2	10.1	517	1	AA065157	AA065157 zm50a10.s
	373	136	10.1	426	2	BB742258	BB742258 BB742258
	374	135.2	10.0	425	2	BB738804	BB738804 BB738804
	375	135.2	10.0	425	2	BB743073	BB743073 BB743073
	376	133.6	9.9	425	2	BB743062	BB743062 BB743062
	377	132.8	9.9	412	2	BB739107	BB739107 BB739107
	378	131.4	9.8	397	2	BB739208	BB739208 BB739208
	379	131.4	9.8	441	5	BY369950	BY369950 BY369950
c	380	131.4	9.8	522	4	BI290719	BI290719 UI-R-DK0-
	381	130.2	9.7	365	5	BY368375	BY368375 BY368375
	382	130.2	9.7	399	2	BB739479	BB739479 BB739479
	383	130.2	9.7	401	2	BB738279	BB738279 BB738279
	384	130.2	9.7	403	2	BB738392	BB738392 BB738392
	385	130.2	9.7	416	2	BB738479	BB738479 BB738479
	386	128.8	9.6	747	6	CA491783	CA491783 AGENCOURT
	387	128.2	9.5	389	2	BB738199	BB738199 BB738199
	388	128.2	9.5	429	5	BY452423	BY452423 BY452423
c	389	128.2	9.5	564	2	BE115317	BE115317 UI-R-CA0-

	390	128	9.5	852	7	CK237456	CK237456 AGENCOURT
	391	127.8	9.5	703	5	BU376588	BU376588 603809540
	392	127.4	9.5	410	2	BB739012	BB739012 BB739012
	393	127.4	9.5	810	7	CK239284	CK239284 AGENCOURT
	394	127.4	9.5	909	6	CA975643	CA975643 AGENCOURT
	395	127	9.4	377	2	BB738099	BB738099 BB738099
	396	126.8	9.4	784	7	CF348736	CF348736 AGENCOURT
	397	126.8	9.4	787	7	CN512318	CN512318 AGENCOURT
	398	126.8	9.4	860	7	CK016244	CK016244 AGENCOURT
	399	126.2	9.4	1035	1	AL551235	AL551235 AL551235
c	400	126	9.4	242	4	BI403931	BI403931 MI-P-CP1-
	401	125.8	9.3	804	6	CD758550	CD758550 AGENCOURT
	402	125.8	9.3	818	6	CD759140	CD759140 AGENCOURT
	403	125.8	9.3	836	7	CK236662	CK236662 AGENCOURT
	404	125.6	9.3	386	1	AV001269	AV001269 AV001269
	405	125.4	9.3	389	2	BB737963	BB737963 BB737963
	406	125.4	9.3	392	2	BB737949	BB737949 BB737949
	407	125	9.3	1690	3	CR599955	CR599955 full-leng
	408	125	9.3	3337	3	BC032938	BC032938 Homo sapi
	409	125	9.3	3339	3	BC048144	BC048144 Homo sapi
	410	124.8	9.3	302	9	CG668510	CG668510 OST464486
	411	124.6	9.3	762	5	BX304380	BX304380 BX304380
	412	124.2	9.2	767	7	CK239480	CK239480 AGENCOURT
	413	124.2	9.2	773	7	CK239430	CK239430 AGENCOURT
	414	124.2	9.2	888	6	CA787423	CA787423 AGENCOURT
	415	124.2	9.2	965	6	CA473387	CA473387 AGENCOURT
	416	124	9.2	376	1	AV002739	AV002739 AV002739
	417	124	9.2	397	5	BY368461	BY368461 BY368461
	418	123.8	9.2	381	2	BB739767	BB739767 BB739767
	419	123.4	9.2	448	2	BB748146	BB748146 BB748146
	420	122.8	9.1	370	1	AV000544	AV000544 AV000544
	421	122.6	9.1	816	7	CK236057	CK236057 AGENCOURT
	422	122.6	9.1	836	7	CK238801	CK238801 AGENCOURT
	423	121.4	9.0	430	2	BB742993	BB742993 BB742993
	424	120.6	9.0	360	1	AA066112	AA066112 ml66e05.r
c	425	120	8.9	599	1	AI408820	AI408820 EST237111
c	426	120	8.9	631	1	AI105157	AI105157 EST214446
	427	118	8.8	854	6	CA474850	CA474850 AGENCOURT
c	428	117.6	8.7	404	1	AI058885	AI058885 UI-R-C1-k
	429	117	8.7	862	6	CA471692	CA471692 AGENCOURT
c	430	116.8	8.7	459	1	AI233636	AI233636 EST230324
	431	116.6	8.7	891	6	CA472074	CA472074 AGENCOURT
c	432	115.8	8.6	600	1	AA891752	AA891752 EST195555
	433	115.4	8.6	829	6	CA496216	CA496216 AGENCOURT
c	434	115	8.5	395	2	AW320077	AW320077 un14e03.x
	435	114.6	8.5	423	2	BB743814	BB743814 BB743814
c	436	114.6	8.5	459	1	AI105375	AI105375 EST214664
	437	114.2	8.5	733	5	BX862922	BX862922 BX862922
	438	114.2	8.5	1013	7	CO581670	CO581670 ILLUMIGEN
c	439	111.4	8.3	435	1	AA076449	AA076449 zm91d10.s
	440	110	8.2	659	6	CA364229	CA364229 639103 NC
	441	109.8	8.2	1603	3	AK008530	AK008530 Mus muscu
	442	107.2	8.0	620	5	BU472823	BU472823 603761782
	443	106.6	7.9	370	2	BB741610	BB741610 BB741610
c	444	106.6	7.9	492	2	AW260204	AW260204 um74f04.x
	445	106.4	7.9	590	4	BI884757	BI884757 fo68g09.y
	446	105.6	7.8	426	2	BB742307	BB742307 BB742307
	447	105.4	7.8	265	2	BB561901	BB561901 BB561901
c	448	105	7.8	388	1	AI648938	AI648938 uk33b03.x
	449	104.8	7.8	685	6	CA965680	CA965680 CcLX05a15
	450	103.4	7.7	421	1	AA273564	AA273564 vc38f10.r
	451	101.4	7.5	447	5	BY153686	BY153686 BY153686
	452	101.2	7.5	773	6	CB559001	CB559001 AGENCOURT
c	453	100.4	7.5	499	1	AI931939	AI931939 ul68b06.x
	454	100.2	7.4	246	2	BB561792	BB561792 BB561792
	455	99.8	7.4	381	5	BY153900	BY153900 BY153900
	456	98.6	7.3	316	2	BB434065	BB434065 BB434065
	457	96.8	7.2	584	5	BP371391	BP371391 BP371391
	458	96.6	7.2	301	2	BB436492	BB436492 BB436492
	459	96.6	7.2	787	5	BX911789	BX911789 BX911789
	460	96	7.1	765	5	BX878953	BX878953 BX878953
	461	96	7.1	777	5	BX867294	BX867294 BX867294
	462	95.6	7.1	694	7	CK957623	CK957623 4097741 B
	463	94.8	7.0	480	6	CA965795	CA965795 CcLX05a19
	464	93.2	6.9	423	6	CD284299	CD284299 G39172.71
	465	92.6	6.9	293	2	BB745854	BB745854 BB745854
	466	92.4	6.9	773	6	CB308042	CB308042 AGENCOURT
	467	90.6	6.7	1154	4	BM460886	BM460886 AGENCOURT
	468	90.4	6.7	308	2	BB435895	BB435895 BB435895
	469	90.4	6.7	359	1	AV004150	AV004150 AV004150
	470	90.2	6.7	330	5	BY368561	BY368561 BY368561
	471	90.2	6.7	369	5	BY398655	BY398655 BY398655
	472	89.8	6.7	689	5	BX878867	BX878867 BX878867
	473	89	6.6	304	2	BB499397	BB499397 BB499397
	474	89	6.6	772	5	BX877877	BX877877 BX877877
	475	89	6.6	794	5	BX880013	BX880013 BX880013
	476	88.2	6.6	552	5	BX086254	BX086254 BX086254
	477	87.6	6.5	674	7	CK948392	CK948392 4073275 B
	478	87.6	6.5	695	7	CK950473	CK950473 4075812 B
	479	86.8	6.4	837	6	CA473716	CA473716 AGENCOURT
	480	86.4	6.4	732	5	BX867401	BX867401 BX867401
	481	86.4	6.4	863	7	CF663100	CF663100 CcLX07a30
	482	86.2	6.4	314	2	BB502721	BB502721 BB502721
	483	85.2	6.3	310	2	BB436562	BB436562 BB436562
	484	84	6.2	294	2	BB498684	BB498684 BB498684
	485	83	6.2	1101	9	CNS00EVL	AL069706 Drosophil
	486	82.8	6.2	778	4	BI831019	BI831019 603080858
	487	82.4	6.1	688	6	BY708410	BY708410 BY708410
	488	82.2	6.1	483	2	BF938662	BF938662 fm79g08.y
	489	81.8	6.1	315	2	BB500625	BB500625 BB500625
	490	81.2	6.0	418	2	BB687602	BB687602 BB687602
	491	81.2	6.0	832	6	CB197355	CB197355 AGENCOURT
	492	80.6	6.0	204	2	BB741525	BB741525 BB741525
	493	80.4	6.0	322	2	BB146668	BB146668 BB146668
	494	80	5.9	189	2	BB747903	BB747903 BB747903
	495	80	5.9	282	2	BB434595	BB434595 BB434595
c	496	79.4	5.9	574	1	AI116021	AI116021 ue25h10.x
	497	78.4	5.8	201	1	AA207583	AA207583 mv81a11.r
	498	78	5.8	293	2	BB435508	BB435508 BB435508
c	499	77.4	5.8	1101	9	CNS0039G	AL063921 Drosophil
	500	77.2	5.7	512	2	BB748027	BB748027 BB748027
	501	77	5.7	283	2	BB054531	BB054531 BB054531
c	502	77	5.7	1156	6	CD508270	CD508270 CDA89-H06
	503	76.8	5.7	266	1	AV003912	AV003912 AV003912
	504	76.8	5.7	269	2	BB497254	BB497254 BB497254
	505	76.8	5.7	1092	9	CNS020K7	AL175696 Tetraodon
	506	76.6	5.7	679	5	BX319688	BX319688 BX319688
	507	76.4	5.7	637	7	CN984278	CN984278 53231_126
c	508	75.4	5.6	392	2	BF334479	BF334479 MR1-CT035
c	509	75.2	5.6	1101	9	CNS00EVL	AL069706 Drosophil
	510	74.4	5.5	192	1	AV004210	AV004210 AV004210
	511	74.4	5.5	311	2	BB500810	BB500810 BB500810
	512	74.4	5.5	337	2	BB497528	BB497528 BB497528
	513	74.4	5.5	944	6	CB180137	CB180137 AGENCOURT
	514	72.8	5.4	680	5	BX319687	BX319687 BX319687
	515	72.6	5.4	241	1	AV003248	AV003248 AV003248
	516	72	5.3	241	2	BB010750	BB010750 BB010750
	517	72	5.3	1101	9	CNS00EO7	AL069440 Drosophil
	518	71.6	5.3	290	2	BB009853	BB009853 BB009853
	519	71.6	5.3	296	2	BB005788	BB005788 BB005788
	520	71.6	5.3	306	2	BB497018	BB497018 BB497018
c	521	71.6	5.3	669	6	CA043283	CA043283 ssalphc00
c	522	71.4	5.3	699	6	CD810900	CD810900 RTInt_1-C
	523	71.2	5.3	269	2	BB435424	BB435424 BB435424
	524	71	5.3	243	2	BB741599	BB741599 BB741599
	525	70.8	5.3	277	2	BB006347	BB006347 BB006347
	526	70.8	5.3	308	2	BB361016	BB361016 BB361016
	527	70.6	5.2	305	2	BB433431	BB433431 BB433431
	528	70.4	5.2	789	7	CN975696	CN975696 25583_125
	529	70.4	5.2	867	7	CN975873	CN975873 25775_125
	530	70	5.2	273	2	BB010292	BB010292 BB010292
	531	69.2	5.1	545	2	BE684228	BE684228 184549 MA
c	532	69.2	5.1	649	1	AA893216	AA893216 EST197019
	533	68.4	5.1	303	1	AV235006	AV235006 AV235006
	534	68.4	5.1	718	5	BU262937	BU262937 603508618
c	535	68.2	5.1	1024	9	CNS030D0	AL222093 Tetraodon

536	67.8	5.0	1190	9	CNS02ON7	AL206908	Tetraodon
537	67.6	5.0	710	5	BX912444	BX912444	BX912444
538	67.4	5.0	207	5	BY368458	BY368458	BY368458
539	67	5.0	567	5	BX086253	BX086253	BX086253
540	67	5.0	759	9	CNS06QXV	AL411257	T7 end of
541	66.8	5.0	233	2	BB051098	BB051098	BB051098
542	66.8	5.0	274	2	BB529929	BB529929	BB529929
543	66.6	4.9	289	4	BG200773	BG200773	RST20223
c 544	66.6	4.9	1101	9	CNS003BD	AL064091	Drosophil
c 545	66.4	4.9	928	9	CNS00DKY	AL071865	Drosophil
546	65.8	4.9	738	5	BX884918	BX884918	BX884918
c 547	65.8	4.9	1101	9	CNS00EO7	AL069440	Drosophil
c 548	65.6	4.9	426	1	AI035384	AI035384	uc90d12.x
c 549	65.6	4.9	651	9	CR121547	CR121547	Reverse s
550	65.2	4.8	277	2	BB434322	BB434322	BB434322
c 551	65	4.8	230	1	AA893296	AA893296	EST197099
552	65	4.8	452	4	BG428060	BG428060	602501471
553	64.4	4.8	1124	9	CNS073BM	AL427304	clone BA0
554	64.2	4.8	928	9	CNS00DKY	AL071865	Drosophil
c 555	64.2	4.8	1043	9	CNS0145P	AL103735	Drosophil
c 556	63.8	4.7	1391	9	CG754863	CG754863	P050-2-G0
557	63.2	4.7	945	9	CNS04D0K	AL285149	Tetraodon
c 558	63.2	4.7	1169	9	CNS06KHQ	AL402900	T3 end of
559	62.6	4.7	991	9	CL139092	CL139092	ISB1-111O
c 560	62	4.6	838	9	AG489918	AG489918	Mus muscu
c 561	62	4.6	938	9	CNS006TJ	AL065906	Drosophil
c 562	62	4.6	1191	9	CL104745	CL104745	ISB1-43I1
c 563	62	4.6	2081	9	AG280593	AG280593	Mus muscu
c 564	61.8	4.6	1101	9	CNS012TP	AL102007	Drosophil
c 565	61.6	4.6	1431	9	AG365607	AG365607	Mus muscu
c 566	61.6	4.6	1896	9	CG753083	CG753083	P048-1-C0
c 567	61.4	4.6	1101	9	CNS00KAE	AL077628	Drosophil
c 568	61	4.5	1007	9	CNS00JOV	AL076752	Drosophil
c 569	61	4.5	1101	9	CNS00EPO	AL069493	Drosophil
c 570	60.8	4.5	639	9	CNS038CX	AL232458	Tetraodon
c 571	60.6	4.5	618	6	CB502807	CB502807	ssalmge50
572	60.6	4.5	1101	9	CNS00EPO	AL069493	Drosophil
573	60.6	4.5	1101	9	CNS00Z2U	AL097152	Drosophil
c 574	60.6	4.5	1118	9	CL147481	CL147481	ISB1-234H
575	60.4	4.5	1592	9	CG750135	CG750135	P044-3-D0
576	60.2	4.5	753	9	AG610797	AG610797	Mus muscu
577	60.2	4.5	1202	9	CL477268	CL477268	SAIL_26_E
c 578	60.2	4.5	1489	9	AG350139	AG350139	Mus muscu
c 579	60	4.5	937	7	CK415737	CK415737	AUF_IpPit
580	60	4.5	1084	9	CNS071NH	AL425139	clone BA0
581	60	4.5	1101	9	CNS008X3	AL052544	Drosophil
582	59.8	4.4	600	6	CB504196	CB504196	ssalplnb5
c 583	59.8	4.4	776	9	CE561073	CE561073	tigr-gss-
c 584	59.8	4.4	892	9	CW020046	CW020046	ZMMBLc001
c 585	59.8	4.4	1027	9	CNS02T50	AL212733	Tetraodon
c 586	59.8	4.4	1101	9	CNS014XJ	AL104737	Drosophil
c 587	59.8	4.4	1268	9	AG347098	AG347098	Mus muscu
c 588	59.6	4.4	615	6	CA041633	CA041633	ssalmge00
589	59.6	4.4	1101	9	CNS003BD	AL064091	Drosophil
c 590	59.4	4.4	1146	9	CNS021G2	AL176843	Tetraodon
591	59.2	4.4	322	7	CK676494	CK676494	ZF101-P00
c 592	59.2	4.4	590	7	CN584985	CN584985	USDA-FP_1
593	59.2	4.4	1101	9	CNS0180R	AL108741	Drosophil
c 594	59.2	4.4	1542	9	AG386981	AG386981	Mus muscu
595	59	4.4	309	2	BB436540	BB436540	BB436540
596	58.8	4.4	1101	9	CNS00BO1	AL057419	Drosophil
c 597	58.8	4.4	1101	9	CNS016LI	AL106896	Drosophil
c 598	58.8	4.4	1260	9	AG430117	AG430117	Mus muscu
c 599	58.8	4.4	1326	9	AG387192	AG387192	Mus muscu
c 600	58.8	4.4	1624	9	CL466243	CL466243	SAIL_1253
601	58.6	4.4	895	9	CNS06FSV	AL396821	T7 end of
c 602	58.4	4.3	1780	9	AG320553	AG320553	Mus muscu
c 603	58.2	4.3	609	9	CNS025K2	AL182171	Tetraodon
c 604	58	4.3	844	8	AZ528979	AZ528979	ENTCP05TF
c 605	58	4.3	1092	9	CNS020K7	AL175696	Tetraodon
606	57.8	4.3	1229	3	CR731677	CR731677	Tetraodon
c 607	57.6	4.3	1201	9	CNS0167M	AL106396	Drosophil
c 608	57.4	4.3	660	8	BH183498	BH183498	023_L_07-
c 609	57.4	4.3	660	9	CNS07ONJ	AL620449	T3 end of
c 610	57.4	4.3	811	1	AL514901	AL514901	AL514901
c 611	57.4	4.3	1003	9	CL472292	CL472292	SAIL_175_
612	57.4	4.3	1225	8	CC238324	CC238324	CH261-192
c 613	57.4	4.3	1225	9	CNS0161D	AL106171	Drosophil
c 614	57.4	4.3	1227	9	AG430010	AG430010	Mus muscu
c 615	57.4	4.3	1242	9	CL068807	CL068807	CH216-115
c 616	57.2	4.2	932	9	CL479576	CL479576	SAIL_308_
617	57.2	4.2	1626	7	CF238805	CF238805	AGENCOURT
c 618	57	4.2	873	9	CNS024M5	AL180950	Tetraodon
619	56.8	4.2	663	8	BH990661	BH990661	oen99c01.
c 620	56.8	4.2	697	9	CNS047O7	AL278224	Tetraodon
621	56.8	4.2	742	8	BH673165	BH673165	BOMHA94TR
c 622	56.8	4.2	1101	9	CNS00FYG	AL071206	Drosophil
623	56.8	4.2	1101	9	CNS0151X	AL104895	Drosophil
624	56.8	4.2	1225	9	CNS0161D	AL106171	Drosophil
c 625	56.8	4.2	1229	3	CR731677	CR731677	Tetraodon
626	56.8	4.2	2300	3	CR734152	CR734152	Tetraodon
627	56.6	4.2	569	8	BH480068	BH480068	BOHRO17TF
c 628	56.6	4.2	843	9	CNS00CS1	AL059666	Drosophil
c 629	56.6	4.2	1021	9	CNS014DY	AL104032	Drosophil
c 630	56.6	4.2	1101	9	CNS001FB	AL060732	Drosophil
631	56.4	4.2	970	6	CB208406	CB208406	AGENCOURT
632	56.4	4.2	1101	9	CNS003B4	AL064082	Drosophil
c 633	56.4	4.2	1190	9	CNS02ON7	AL206908	Tetraodon
c 634	56.4	4.2	1805	9	CL080711	CL080711	CH216-159
635	56.2	4.2	527	1	AI476983	AI476983	fb58b12.y
c 636	56.2	4.2	1025	9	CNS014J2	AL104216	Drosophil
637	56.2	4.2	1094	9	CNS012FZ	AL101513	Drosophil
638	56.2	4.2	1101	9	CNS0039G	AL063921	Drosophil
639	56.2	4.2	1101	9	CNS003BB	AL064089	Drosophil
640	56.2	4.2	1101	9	CNS0106X	AL098595	Drosophil
c 641	56	4.2	969	9	CL492468	CL492468	SAIL_567_
642	56	4.2	1101	9	CNS00EQL	AL069526	Drosophil
643	56	4.2	1187	8	B11102	B11102	F19C22-T7 I
c 644	56	4.2	1348	9	CG749499	CG749499	P043-4-A0
c 645	55.8	4.1	836	9	CNS01100	AL099642	Drosophil
646	55.8	4.1	845	8	AQ745537	AQ745537	HS_2272_A
647	55.8	4.1	994	9	CNS04NOJ	AL298972	Tetraodon
648	55.8	4.1	1184	9	CNS04P4P	AL300850	Tetraodon
649	55.8	4.1	1896	3	CR722884	CR722884	Tetraodon
650	55.8	4.1	1896	9	CG753083	CG753083	P048-1-C0
c 651	55.6	4.1	943	9	CL145947	CL145947	ISB1-146I
652	55.6	4.1	968	9	CNS00KOS	AL078247	Drosophil
c 653	55.6	4.1	979	9	CNS0161W	AL106190	Drosophil
c 654	55.6	4.1	1101	9	CNS00BEU	AL056987	Drosophil
655	55.6	4.1	1111	7	CF764200	CF764200	CES004349
656	55.6	4.1	1176	9	CNS03R83	AL256908	Tetraodon
c 657	55.6	4.1	1210	3	CR721108	CR721108	Tetraodon
c 658	55.4	4.1	674	7	CV117970	CV117970	AGENCOURT
659	55.4	4.1	987	9	CNS014PQ	AL104456	Drosophil
c 660	55.4	4.1	1010	6	CD171719	CD171719	AGENCOURT
661	55.4	4.1	1118	5	BX462896	BX462896	BX462896
c 662	55.4	4.1	1164	8	CC218891	CC218891	CH261-14M
663	55.2	4.1	905	9	CNS00KHX	AL077798	Drosophil
c 664	55.2	4.1	927	8	AZ046250	AZ046250	nbeb0091D
c 665	55.2	4.1	987	9	CNS014PQ	AL104456	Drosophil
666	55.2	4.1	1011	6	CA787481	CA787481	AGENCOURT
c 667	55.2	4.1	1101	9	CNS004ZW	AL055440	Drosophil
668	55.2	4.1	1141	9	CNS07206	AL425596	clone BA0
669	55.2	4.1	1146	9	CNS021G2	AL176843	Tetraodon
c 670	55.2	4.1	1202	9	AG338379	AG338379	Mus muscu
c 671	55.2	4.1	1530	9	AG382019	AG382019	Mus muscu
c 672	55.2	4.1	2077	3	CR667281	CR667281	Tetraodon
c 673	55	4.1	553	7	CF769995	CF769995	DSBF1_5_C
c 674	55	4.1	1101	9	CNS003BB	AL064089	Drosophil
c 675	55	4.1	1118	5	BX462896	BX462896	BX462896
c 676	55	4.1	1291	9	AG430338	AG430338	Mus muscu
677	55	4.1	1398	9	CL022024	CL022024	CH216-13B
c 678	55	4.1	1402	9	AG382069	AG382069	Mus muscu
c 679	55	4.1	1471	9	AG390851	AG390851	Mus muscu
c 680	54.8	4.1	704	9	CL151012	CL151012	104_333_1
681	54.8	4.1	843	9	CNS00CS1	AL059666	Drosophil

	682	54.8	4.1	1042	9	CL461494	CL461494 SAIL_1148
	683	54.8	4.1	1101	9	CNS00FYG	AL071206 Drosophil
c	684	54.8	4.1	1259	9	AG360787	AG360787 Mus muscu
c	685	54.8	4.1	1354	9	CG744717	CG744717 P037-2-F0
c	686	54.8	4.1	1355	9	AG346348	AG346348 Mus muscu
c	687	54.8	4.1	1456	9	AG382339	AG382339 Mus muscu
c	688	54.6	4.1	725	8	BH180166	BH180166 016_I_02-
c	689	54.6	4.1	798	9	CG795035	CG795035 ZMMBBb032
c	690	54.6	4.1	901	9	AG494506	AG494506 Mus muscu
c	691	54.6	4.1	945	9	CNS04D0K	AL285149 Tetraodon
c	692	54.6	4.1	948	9	CNS0159T	AL105179 Drosophil
c	693	54.6	4.1	1029	9	CNS01ZGM	AL174271 Tetraodon
	694	54.6	4.1	1101	9	CNS0021J	AL061936 Drosophil
c	695	54.6	4.1	1332	9	AG429508	AG429508 Mus muscu
	696	54.4	4.0	559	5	BU496707	BU496707 PfESToab5
	697	54.4	4.0	708	7	CK676883	CK676883 ZF101-P00
	698	54.4	4.0	736	8	BZ474913	BZ474913 BOOAO91TR
	699	54.4	4.0	866	8	AZ675767	AZ675767 ENTID09TF
c	700	54.4	4.0	947	9	CL112501	CL112501 ISB1-57D2
	701	54.4	4.0	1086	9	CNS00YXK	AL096962 Drosophil
	702	54.2	4.0	876	9	CNS009G1	AL053529 Drosophil
c	703	54.2	4.0	1101	9	CNS000B8	AL063632 Drosophil
c	704	54.2	4.0	1324	9	AG376784	AG376784 Mus muscu
c	705	54.2	4.0	1607	9	AG390717	AG390717 Mus muscu
	706	54	4.0	391	2	BB748359	BB748359 BB748359
c	707	54	4.0	421	4	BJ748996	BJ748996 BJ748996
c	708	54	4.0	584	1	AJ442092	AJ442092 AJ442092
c	709	54	4.0	731	8	BH937351	BH937351 odd75a01.
	710	54	4.0	886	8	BH177277	BH177277 008_L_22-
	711	54	4.0	886	9	CNS07JUX	AL614235 T3 end of
c	712	54	4.0	1101	9	CNS00B3U	AL056389 Drosophil
c	713	54	4.0	1168	9	CL078758	CL078758 CH216-153
	714	54	4.0	1210	9	CG749728	CG749728 P044-1-C0
c	715	54	4.0	1210	9	CG749728	CG749728 P044-1-C0
c	716	54	4.0	1283	9	CL641341	CL641341 CH213-9O1
c	717	54	4.0	1352	9	AG381852	AG381852 Mus muscu
	718	53.8	4.0	500	1	AU086866	AU086866 AU086866
	719	53.8	4.0	836	9	CNS01100	AL099642 Drosophil
	720	53.8	4.0	1032	9	CNS02OIP	AL206746 Tetraodon
c	721	53.8	4.0	2157	9	CL081966	CL081966 CH216-165
	722	53.8	4.0	2621	9	AG311235	AG311235 Mus muscu
	723	53.6	4.0	822	7	CK416977	CK416977 AUF_IpInt
	724	53.6	4.0	910	9	CNS0112R	AL099741 Drosophil
	725	53.6	4.0	924	9	CNS02Q6S	AL208909 Tetraodon
	726	53.6	4.0	933	7	CK413862	CK413862 AUF_IpGil
c	727	53.6	4.0	1101	9	CNS0039R	AL063932 Drosophil
c	728	53.6	4.0	1101	9	CNS00EQL	AL069526 Drosophil
	729	53.6	4.0	1101	9	CNS00KAE	AL077628 Drosophil
c	730	53.6	4.0	1113	7	CF994845	CF994845 AGENCOURT
c	731	53.6	4.0	1132	8	BZ695089	BZ695089 SP__Ba005
	732	53.6	4.0	1201	9	CNS016E1	AL106627 Drosophil
	733	53.6	4.0	1227	9	AG430010	AG430010 Mus muscu
	734	53.4	4.0	699	8	BH958596	BH958596 odi30a04.
c	735	53.4	4.0	828	8	AQ739398	AQ739398 HS_5482_B
	736	53.4	4.0	878	9	AG595634	AG595634 Mus muscu
c	737	53.4	4.0	1210	9	AG390601	AG390601 Mus muscu
	738	53.4	4.0	1300	4	BM468018	BM468018 AGENCOURT
c	739	53.4	4.0	1315	3	CR657214	CR657214 Tetraodon
c	740	53.4	4.0	1364	9	CG757986	CG757986 P053-2-D0
	741	53.4	4.0	1444	9	AG390892	AG390892 Mus muscu
c	742	53.4	4.0	1539	9	AG340947	AG340947 Mus muscu
c	743	53.2	4.0	342	5	BQ576839	BQ576839 PfESToab1
c	744	53.2	4.0	542	8	AQ307428	AQ307428 HS_2236_A
	745	53.2	4.0	715	6	CD494891	CD494891 CDA13-D01
	746	53.2	4.0	816	9	CL855754	CL855754 OR_CBa008
c	747	53.2	4.0	876	9	CNS009G1	AL053529 Drosophil
c	748	53.2	4.0	959	9	CNS017OR	AL108309 Drosophil
	749	53.2	4.0	988	9	CL087333	CL087333 ISB1-9A17
	750	53.2	4.0	1013	9	CNS06RPQ	AL412260 T7 end of
	751	53.2	4.0	1043	9	CNS0145P	AL103735 Drosophil
c	752	53.2	4.0	1095	9	CNS016E8	AL106634 Drosophil
	753	53	3.9	230	6	CA969172	CA969172 CcLX06a21
c	754	53	3.9	904	9	CL096484	CL096484 ISB1-28B4
c	755	53	3.9	964	9	CNS07E8R	AL441457 T7 end of
c	756	53	3.9	994	9	CNS04NOJ	AL298972 Tetraodon
	757	53	3.9	1085	9	CNS0124K	AL101102 Drosophil
c	758	53	3.9	1254	9	AG349719	AG349719 Mus muscu
c	759	53	3.9	1614	9	AG365768	AG365768 Mus muscu
c	760	52.8	3.9	493	9	CG804135	CG804135 1118048A0
c	761	52.8	3.9	710	8	BZ052236	BZ052236 jnr69g02.
c	762	52.8	3.9	713	8	AQ576566	AQ576566 nbxb0089K
	763	52.8	3.9	804	9	AG519931	AG519931 Mus muscu
c	764	52.8	3.9	992	9	CL068931	CL068931 CH216-115
c	765	52.8	3.9	1177	9	AG365683	AG365683 Mus muscu
c	766	52.8	3.9	1309	2	BE420736	BE420736 HWM002.A0
c	767	52.8	3.9	1388	5	BQ279227	BQ279227 AGENCOURT
	768	52.6	3.9	468	5	BU767578	BU767578 SJEATF03
c	769	52.6	3.9	637	9	CNS036CC	AL229845 Tetraodon
	770	52.6	3.9	945	8	BH158204	BH158204 ENTST43TF
	771	52.6	3.9	964	9	CNS006N9	AL065781 Drosophil
c	772	52.6	3.9	1002	8	BZ695524	BZ695524 SP__Ba006
c	773	52.6	3.9	1101	9	CNS003DQ	AL064580 Drosophil
	774	52.6	3.9	1101	9	CNS016LI	AL106896 Drosophil
c	775	52.6	3.9	1131	9	CNS034FO	AL227373 Tetraodon
c	776	52.6	3.9	1139	8	AQ897537	AQ897537 HS_3153_A
c	777	52.6	3.9	1160	9	AG396428	AG396428 Mus muscu
c	778	52.6	3.9	1186	9	CL649642	CL649642 CH213-243
c	779	52.6	3.9	1246	9	AG341400	AG341400 Mus muscu
c	780	52.6	3.9	1279	9	AG347333	AG347333 Mus muscu
	781	52.6	3.9	1594	9	CL067787	CL067787 CH216-112
	782	52.6	3.9	1745	9	AG338221	AG338221 Mus muscu
c	783	52.4	3.9	278	1	AA480295	AA480295 ne32d11.s
	784	52.4	3.9	670	9	AG103636	AG103636 Pan trogl
c	785	52.4	3.9	867	9	CNS075BG	AL429890 clone BA0
	786	52.4	3.9	895	8	AZ692422	AZ692422 ENTML11TR
	787	52.4	3.9	937	7	CK415737	CK415737 AUF_IpPit
c	788	52.4	3.9	1001	9	CNS0140O	AL103554 Drosophil
c	789	52.4	3.9	1030	9	CL489693	CL489693 SAIL_528_
c	790	52.4	3.9	1202	8	CC262481	CC262481 CH261-167
	791	52.4	3.9	1216	9	AG519648	AG519648 Mus muscu
c	792	52.4	3.9	1271	9	AG360730	AG360730 Mus muscu
c	793	52.4	3.9	1289	9	AG347097	AG347097 Mus muscu
	794	52.4	3.9	1313	7	CK997149	CK997149 ip15c02.b
c	795	52.4	3.9	1554	9	AG390786	AG390786 Mus muscu
	796	52.4	3.9	1780	9	AG320553	AG320553 Mus muscu
	797	52.4	3.9	2131	9	AG435609	AG435609 Mus muscu
	798	52.2	3.9	308	5	BU497685	BU497685 PfESToab8
	799	52.2	3.9	323	4	BG894029	BG894029 kt17b10.y
c	800	52.2	3.9	418	8	AQ816183	AQ816183 HS_4638_A
c	801	52.2	3.9	500	1	AU086935	AU086935 AU086935
c	802	52.2	3.9	524	9	CNS01U9O	AL167541 Tetraodon
c	803	52.2	3.9	559	5	BP510931	BP510931 BP510931
	804	52.2	3.9	648	5	BU124645	BU124645 603147949
	805	52.2	3.9	661	9	CNS02QVJ	AL209800 Tetraodon
	806	52.2	3.9	672	4	BM164124	BM164124 EST566647
	807	52.2	3.9	700	8	BH951634	BH951634 odi16b10.
c	808	52.2	3.9	737	9	BX149919	BX149919 Danio rer
c	809	52.2	3.9	842	9	CNS00ACO	AL055007 Drosophil
	810	52.2	3.9	878	7	CO389521	CO389521 AGENCOURT
c	811	52.2	3.9	945	6	CD580439	CD580439 EST_PSF01
c	812	52.2	3.9	950	9	CL090599	CL090599 ISB1-18B1
	813	52.2	3.9	996	9	CNS00FUH	AL071063 Drosophil
c	814	52.2	3.9	1240	9	AG365596	AG365596 Mus muscu
c	815	52.2	3.9	1378	9	AG350209	AG350209 Mus muscu
c	816	52	3.9	622	7	CV181140	CV181140 tai73g07.
c	817	52	3.9	764	7	CF289381	CF289381 AGENCOURT
c	818	52	3.9	817	9	CL491655	CL491655 SAIL_559_
	819	52	3.9	949	7	CK424488	CK424488 AUF_IpSto
	820	52	3.9	1017	9	CL101048	CL101048 ISB1-36O4
c	821	52	3.9	1067	6	CD386564	CD386564 AGENCOURT
	822	52	3.9	1101	9	CNS00FMC	AL070972 Drosophil
	823	52	3.9	1200	9	CNS016CO	AL106578 Drosophil
c	824	52	3.9	1331	9	AG311246	AG311246 Mus muscu
c	825	52	3.9	1626	7	CF238805	CF238805 AGENCOURT
	826	52	3.9	1758	9	CL509408	CL509408 SAIL_811_
c	827	51.8	3.8	464	4	BI813853	BI813853 PfESToaa1

c 828	51.8	3.8	500	1	AU088106	AU088106	AU088106
c 829	51.8	3.8	531	8	AQ250500	AQ250500	T8A9-T7 T
830	51.8	3.8	673	9	CNS06UWL	AL416395	T7 end of
831	51.8	3.8	678	4	BJ371051	BJ371051	BJ371051
c 832	51.8	3.8	768	9	CE367723	CE367723	tigr-gss-
833	51.8	3.8	781	9	CNS009DO	AL053444	Drosophil
834	51.8	3.8	784	8	BH696092	BH696092	BOHYK47TR
c 835	51.8	3.8	841	9	CNS03MUC	AL251229	Tetraodon
c 836	51.8	3.8	854	8	BH647103	BH647103	BOMGR23TF
c 837	51.8	3.8	900	9	CNS03M11	AL250174	Tetraodon
c 838	51.8	3.8	919	9	AG610809	AG610809	Mus muscu
c 839	51.8	3.8	958	9	CNS0074D	AL066801	Drosophil
c 840	51.8	3.8	971	7	CK416518	CK416518	AUF_IpInt
c 841	51.8	3.8	1100	8	BZ696700	BZ696700	SP__Ba008
842	51.8	3.8	1258	9	CL508886	CL508886	SAIL_804_
c 843	51.8	3.8	1594	9	CL110653	CL110653	ISB1-53P2
844	51.6	3.8	303	4	BG652798	BG652798	sad84c02.
845	51.6	3.8	761	9	CNS02MEY	AL204019	Tetraodon
846	51.6	3.8	852	9	CG928074	CG928074	MBEBS72TR
847	51.6	3.8	965	9	CL505797	CL505797	SAIL_755_
c 848	51.6	3.8	969	9	CL469446	CL469446	SAIL_1303
849	51.6	3.8	1000	9	CL063091	CL063091	CH216-99H
c 850	51.6	3.8	1101	9	CNS00AY1	AL056483	Drosophil
851	51.6	3.8	1160	8	BZ579469	BZ579469	msh2_637.
852	51.6	3.8	1201	9	CNS0168L	AL106431	Drosophil
c 853	51.6	3.8	1243	9	AG390983	AG390983	Mus muscu
c 854	51.6	3.8	1249	9	AG347294	AG347294	Mus muscu
855	51.6	3.8	1306	9	CG754607	CG754607	P050-1-D0
c 856	51.6	3.8	1415	9	CL646438	CL646438	CH213-115
857	51.6	3.8	1563	8	CC206942	CC206942	CH261-191
c 858	51.6	3.8	1592	9	CG750135	CG750135	P044-3-D0
c 859	51.4	3.8	144	7	CK348666	CK348666	hggfha3C1
860	51.4	3.8	478	7	CV200064	CV200064	km25e02.y
c 861	51.4	3.8	642	6	CB303805	CB303805	wsa0030_I
862	51.4	3.8	661	8	BZ001419	BZ001419	oeh95f09.
c 863	51.4	3.8	786	9	CNS009A5	AL053317	Drosophil
c 864	51.4	3.8	798	7	CK777040	CK777040	964032 MA
c 865	51.4	3.8	826	9	AG579614	AG579614	Mus muscu
866	51.4	3.8	915	4	BG520365	BG520365	ps20c09.y
c 867	51.4	3.8	1013	2	BE039874	BE039874	OC09D08 O
c 868	51.4	3.8	1037	5	BQ648574	BQ648574	AGENCOURT
869	51.4	3.8	1052	5	BU560001	BU560001	AGENCOURT
870	51.4	3.8	1101	9	CNS016GE	AL106712	Drosophil
871	51.4	3.8	1168	9	AG526033	AG526033	Mus muscu
c 872	51.4	3.8	1178	8	BZ696021	BZ696021	SP__Ba007
c 873	51.2	3.8	382	7	CR465430	CR465430	CR465430
c 874	51.2	3.8	812	8	BH178455	BH178455	011_J_02-
c 875	51.2	3.8	812	9	CNS07KRM	AL615412	T3 end of
876	51.2	3.8	944	9	CL131790	CL131790	ISB1-101C
877	51.2	3.8	976	9	CL516956	CL516956	SAIL_98_C
c 878	51.2	3.8	981	9	CNS02BD8	AL189701	Tetraodon
c 879	51.2	3.8	1015	9	CL135318	CL135318	ISB1-106F
c 880	51.2	3.8	1101	9	CNS0039Q	AL063931	Drosophil
881	51.2	3.8	1101	9	CNS00B3U	AL056389	Drosophil
c 882	51.2	3.8	1101	9	CNS00DSU	AL075280	Drosophil
c 883	51.2	3.8	1101	9	CNS00FVE	AL071298	Drosophil
c 884	51.2	3.8	1101	9	CNS0107S	AL098626	Drosophil
c 885	51.2	3.8	1198	9	CL080414	CL080414	CH216-158
886	51.2	3.8	1201	9	CNS016A0	AL106482	Drosophil
c 887	51.2	3.8	1254	3	CR720510	CR720510	Tetraodon
888	51	3.8	171	4	BJ334134	BJ334134	BJ334134
889	51	3.8	332	4	BI747908	BI747908	rm47c08.y
c 890	51	3.8	558	2	BF060145	BF060145	Hc_d11_11
891	51	3.8	718	8	AQ416310	AQ416310	RPCI-11-1
c 892	51	3.8	722	7	CV481731	CV481731	AGENCOURT
c 893	51	3.8	783	9	AG574491	AG574491	Mus muscu
c 894	51	3.8	846	7	CO245816	CO245816	AGENCOURT
895	51	3.8	859	8	BH155122	BH155122	ENTTR67TF
c 896	51	3.8	876	8	AZ548068	AZ548068	ENTDI79TR
c 897	51	3.8	917	9	CL472978	CL472978	SAIL_190_
c 898	51	3.8	961	9	CNS008HI	AL051882	Drosophil
899	51	3.8	976	9	CNS04E5M	AL286627	Tetraodon
c 900	51	3.8	976	9	CNS04E5M	AL286627	Tetraodon
901	51	3.8	1027	9	CNS02T50	AL212733	Tetraodon
902	51	3.8	1101	9	CNS05GFT	AL336242	Tetraodon
903	51	3.8	1200	9	CL031866	CL031866	CH216-33I
c 904	51	3.8	1313	7	CK997149	CK997149	ip15c02.b
c 905	51	3.8	1346	9	AG382256	AG382256	Mus muscu
906	51	3.8	1617	5	BM910724	BM910724	AGENCOURT
907	50.8	3.8	392	5	BQ595878	BQ595878	PfESToab2
908	50.8	3.8	451	2	BE722366	BE722366	190570 MA
909	50.8	3.8	578	7	CN477453	CN477453	rx37g10.y
910	50.8	3.8	617	9	CL763005	CL763005	OR_BBa013
911	50.8	3.8	773	4	BG854434	BG854434	1024040A0
c 912	50.8	3.8	773	8	BH186746	BH186746	032_E_23-
c 913	50.8	3.8	773	9	CNS07R5M	AL623692	T7 end of
914	50.8	3.8	790	8	BH542306	BH542306	BOGGP61TR
c 915	50.8	3.8	821	9	CNS0090X	AL052985	Drosophil
c 916	50.8	3.8	890	8	AQ026918	AQ026918	CIT-HSP-2
c 917	50.8	3.8	944	9	CL131790	CL131790	ISB1-101C
918	50.8	3.8	1101	9	CNS000D1	AL065414	Drosophil
c 919	50.8	3.8	1208	9	CG752428	CG752428	P047-1-F1
c 920	50.8	3.8	1211	9	AG349657	AG349657	Mus muscu
c 921	50.8	3.8	1268	8	BZ577630	BZ577630	msh2_550.
c 922	50.8	3.8	1333	9	AG390651	AG390651	Mus muscu
923	50.6	3.8	500	1	AU086770	AU086770	AU086770
924	50.6	3.8	588	9	CE763852	CE763852	tigr-gss-
c 925	50.6	3.8	756	8	AZ192623	AZ192623	SP_1021_B
c 926	50.6	3.8	784	9	CNS043VT	AL273314	Tetraodon
927	50.6	3.8	858	9	CNS008AQ	AL051436	Drosophil
928	50.6	3.8	959	9	CNS017OR	AL108309	Drosophil
929	50.6	3.8	996	9	CNS00DIX	AL070681	Drosophil
930	50.6	3.8	1001	9	CNS0155H	AL105023	Drosophil
c 931	50.6	3.8	1061	9	CL145135	CL145135	ISB1-145G
c 932	50.6	3.8	1101	9	CNS006DU	AL065139	Drosophil
c 933	50.6	3.8	1198	9	AG371377	AG371377	Mus muscu
c 934	50.6	3.8	1206	8	BZ695529	BZ695529	SP__Ba006
c 935	50.6	3.8	1350	9	CG744271	CG744271	P036-4-C0
c 936	50.6	3.8	1571	9	AG435593	AG435593	Mus muscu
c 937	50.4	3.7	680	6	BY717385	BY717385	BY717385
938	50.4	3.7	727	9	CG093979	CG093979	PUFZF48TB
939	50.4	3.7	734	9	CNS010MP	AL099163	Drosophil
c 940	50.4	3.7	829	9	CNS011NU	AL100500	Drosophil
c 941	50.4	3.7	857	9	CG093980	CG093980	PUFZF48TD
c 942	50.4	3.7	867	9	CNS00CX5	AL060052	Drosophil
c 943	50.4	3.7	910	9	AG526131	AG526131	Mus muscu
c 944	50.4	3.7	1046	9	CL452308	CL452308	ZMMBBb047
c 945	50.4	3.7	1056	9	CL492538	CL492538	SAIL_567_
c 946	50.4	3.7	1101	9	CNS016RR	AL107121	Drosophil
c 947	50.4	3.7	1101	9	CNS017V2	AL108536	Drosophil
c 948	50.4	3.7	1187	8	B11102	B11102	F19C22-T7 I
c 949	50.4	3.7	1193	9	CG745316	CG745316	P038-1-G0
950	50.4	3.7	1201	9	CNS0163T	AL106259	Drosophil
c 951	50.4	3.7	1228	9	CL104752	CL104752	ISB1-43I1
952	50.4	3.7	1581	9	AG390984	AG390984	Mus muscu
953	50.4	3.7	1603	9	AG321536	AG321536	Mus muscu
954	50.4	3.7	1715	9	AG288305	AG288305	Mus muscu
955	50.2	3.7	256	5	BQ596447	BQ596447	PfESToab3
956	50.2	3.7	337	7	CO886672	CO886672	BovGen_14
c 957	50.2	3.7	459	9	CL811413	CL811413	OR_CBa002
c 958	50.2	3.7	488	2	AW332942	AW332942	S15C1 AGS
c 959	50.2	3.7	583	8	AQ774291	AQ774291	HS_3086_A
960	50.2	3.7	591	9	CC945272	CC945272	BOICY05TF
961	50.2	3.7	706	8	BH970112	BH970112	odg01g02.
c 962	50.2	3.7	707	8	AZ942250	AZ942250	2M0202N14
c 963	50.2	3.7	802	9	CNS010Z2	AL099608	Drosophil
c 964	50.2	3.7	916	2	AW155504	AW155504	mgie0028I
965	50.2	3.7	1001	9	CNS0140O	AL103554	Drosophil
c 966	50.2	3.7	1101	9	CNS016T6	AL107172	Drosophil
c 967	50.2	3.7	1106	9	CL103937	CL103937	ISB1-42D1
968	50.2	3.7	1159	9	CNS015XR	AL106041	Drosophil
969	50.2	3.7	1202	8	CC262481	CC262481	CH261-167
c 970	50.2	3.7	1258	9	CL508886	CL508886	SAIL_804_
971	50.2	3.7	1277	8	CC253231	CC253231	CH261-180
972	50.2	3.7	1962	9	AG390999	AG390999	Mus muscu
c 973	50	3.7	272	7	CV499293	CV499293	63635.1 M

974	50	3.7	339	7	CN477679	CN477679 rx40f01.y
975	50	3.7	500	1	AU086076	AU086076 AU086076
976	50	3.7	515	6	CD683014	CD683014 rj29d08.y
c 977	50	3.7	649	7	CN758899	CN758899 ID0AAA24A
978	50	3.7	666	6	CD267647	CD267647 tab92c02.
c 979	50	3.7	796	7	CK474754	CK474754 AGENCOURT
c 980	50	3.7	804	8	B12681	B12681 F27D1-Sp6.1
981	50	3.7	820	7	CO930994	CO930994 AGENCOURT
c 982	50	3.7	865	7	CK424316	CK424316 AUF_IpSto
c 983	50	3.7	866	8	AQ258984	AQ258984 nbxb0021P
984	50	3.7	910	8	AZ669796	AZ669796 ENTGU42TF
985	50	3.7	911	9	CL478691	CL478691 SAIL_294_
986	50	3.7	932	4	BM416498	BM416498 OP21593 M
c 987	50	3.7	974	9	CNS00ITT	AL075432 Drosophil
988	50	3.7	1010	6	CD171719	CD171719 AGENCOURT
c 989	50	3.7	1043	8	BZ696704	BZ696704 SP__Ba008
c 990	50	3.7	1043	9	CL135901	CL135901 ISB1-107D
c 991	50	3.7	1091	7	CF934550	CF934550 TrEST-B10
992	50	3.7	1101	9	CNS004ZW	AL055440 Drosophil
c 993	50	3.7	1101	9	CNS00FMC	AL070972 Drosophil
994	50	3.7	1101	9	CNS00FVE	AL071298 Drosophil
c 995	50	3.7	1139	8	BH162532	BH162532 ENTQU13TF
996	50	3.7	1239	9	CL017886	CL017886 CH216-2M1
c 997	50	3.7	1348	9	AG397099	AG397099 Mus muscu
c 998	49.8	3.7	332	5	BU498600	BU498600 PfESToab9
999	49.8	3.7	338	5	BQ576968	BQ576968 PfESToab1
c1000	49.8	3.7	446	9	BX240321	BX240321 Danio rer
c1001	49.8	3.7	514	7	CO275038	CO275038 EK116257.
1002	49.8	3.7	658	9	CNS03NK1	AL252154 Tetraodon
c1003	49.8	3.7	710	8	BZ018176	BZ018176 oeh06c09.
c1004	49.8	3.7	716	7	CF344309	CF344309 AGENCOURT
1005	49.8	3.7	727	8	BH972818	BH972818 odd62e11.
c1006	49.8	3.7	806	4	BG784945	BG784945 SEAUMC004
c1007	49.8	3.7	872	7	CK022958	CK022958 AGENCOURT
c1008	49.8	3.7	878	7	CO389521	CO389521 AGENCOURT
c1009	49.8	3.7	905	9	CNS028U9	AL186426 Tetraodon
c1010	49.8	3.7	916	8	B09084	B09084 F6L16-T7 IG
1011	49.8	3.7	932	9	CL479576	CL479576 SAIL_308_
c1012	49.8	3.7	1053	7	CF469008	CF469008 P14C1 Pla
c1013	49.8	3.7	1074	8	BZ696936	BZ696936 SP__Ba009
1014	49.8	3.7	1101	9	CNS002FG	AL062437 Drosophil
1015	49.8	3.7	1101	9	CNS003B0	AL064078 Drosophil
1016	49.8	3.7	1101	9	CNS00EA9	AL068837 Drosophil
c1017	49.8	3.7	1101	9	CNS0100X	AL098379 Drosophil
1018	49.8	3.7	1101	9	CNS02URK	AL214841 Tetraodon
c1019	49.8	3.7	1143	3	CR688693	CR688693 Tetraodon
c1020	49.8	3.7	1274	9	AG376620	AG376620 Mus muscu
c1021	49.8	3.7	1372	9	AG381938	AG381938 Mus muscu
1022	49.8	3.7	2466	9	CL508701	CL508701 SAIL_802_
c1023	49.6	3.7	409	5	BQ451684	BQ451684 PfESToab0
c1024	49.6	3.7	495	5	BX555224	BX555224 BX555224
c1025	49.6	3.7	620	6	CB341490	CB341490 CA32EN000
1026	49.6	3.7	697	9	CNS047O7	AL278224 Tetraodon
c1027	49.6	3.7	708	7	CO520109	CO520109 3530_1_13
c1028	49.6	3.7	762	8	BZ058231	BZ058231 ljr44a05.
1029	49.6	3.7	821	9	CNS07DIK	AL440514 T7 end of
1030	49.6	3.7	826	9	AG579614	AG579614 Mus muscu
1031	49.6	3.7	828	7	CN594379	CN594379 TTE000141
c1032	49.6	3.7	863	9	CL840224	CL840224 OR_CBa006
1033	49.6	3.7	874	8	BH438482	BH438482 BOGEO68TF
c1034	49.6	3.7	892	6	CB979056	CB979056 CAB40006_
1035	49.6	3.7	902	9	CL475897	CL475897 SAIL_246_
1036	49.6	3.7	949	9	AG134743	AG134743 Pan trogl
c1037	49.6	3.7	970	6	CB208406	CB208406 AGENCOURT
c1038	49.6	3.7	982	8	AQ325799	AQ325799 nbxb0021B
c1039	49.6	3.7	1001	9	CNS0155H	AL105023 Drosophil
1040	49.6	3.7	1006	9	CNS008I3	AL051903 Drosophil
c1041	49.6	3.7	1031	9	AG432790	AG432790 Mus muscu
c1042	49.6	3.7	1147	6	CD387645	CD387645 AGENCOURT
c1043	49.6	3.7	1174	9	CL110860	CL110860 ISB1-54F2
1044	49.6	3.7	1241	9	AG448181	AG448181 Mus muscu
c1045	49.6	3.7	1392	9	CG757503	CG757503 P052-4-C0
c1046	49.4	3.7	420	9	BX239820	BX239820 Danio rer
1047	49.4	3.7	500	1	AU087057	AU087057 AU087057
1048	49.4	3.7	501	4	BM445902	BM445902 1IL1C3.ab
c1049	49.4	3.7	507	8	AQ181894	AQ181894 HS_3214_B
1050	49.4	3.7	537	8	AQ506817	AQ506817 RPCI-11-2
c1051	49.4	3.7	558	9	CNS01WNC	AL170625 Tetraodon
c1052	49.4	3.7	625	7	CN757372	CN757372 ID0AAA1CF
c1053	49.4	3.7	633	3	AY068940	AY068940 Schmidtea
c1054	49.4	3.7	653	6	CD771757	CD771757 AGENCOURT
c1055	49.4	3.7	712	8	BH953124	BH953124 odi39d09.
1056	49.4	3.7	713	5	BX849266	BX849266 BX849266
c1057	49.4	3.7	797	7	CF933735	CF933735 TrEST-B05
1058	49.4	3.7	807	9	CL489403	CL489403 SAIL_523_
1059	49.4	3.7	828	6	CD979572	CD979572 QAG4e12.x
1060	49.4	3.7	831	8	AZ544934	AZ544934 ENTEO26TR
1061	49.4	3.7	836	9	CNS00KG2	AL077933 Drosophil
1062	49.4	3.7	873	8	BH159040	BH159040 ENTTJ07TF
c1063	49.4	3.7	887	9	AG526041	AG526041 Mus muscu
1064	49.4	3.7	957	8	BH165177	BH165177 ENTRG12TR
c1065	49.4	3.7	968	8	BZ696044	BZ696044 SP__Ba007
c1066	49.4	3.7	992	9	CNS0562R	AL322812 Tetraodon
c1067	49.4	3.7	1009	9	CNS00587	AL057153 Drosophil
c1068	49.4	3.7	1038	9	CNS06L7M	AL403832 T3 end of
1069	49.4	3.7	1058	9	CNS014BM	AL103948 Drosophil
c1070	49.4	3.7	1101	9	CNS00Z2U	AL097152 Drosophil
1071	49.4	3.7	1152	4	BG309087	BG309087 HVSMEc000
c1072	49.4	3.7	1201	9	CNS0164J	AL106285 Drosophil
c1073	49.4	3.7	1267	9	AG346514	AG346514 Mus muscu
c1074	49.4	3.7	1325	9	AG341551	AG341551 Mus muscu
c1075	49.4	3.7	1430	9	CG758458	CG758458 P053-4-H0
c1076	49.4	3.7	1758	9	CL509408	CL509408 SAIL_811_
1077	49.2	3.7	385	7	CF928866	CF928866 laf64h12.
c1078	49.2	3.7	431	9	CG721541	CG721541 1119067G1
c1079	49.2	3.7	481	9	CW017733	CW017733 ZMMBLc001
1080	49.2	3.7	738	8	AQ741125	AQ741125 HS_2272_A
c1081	49.2	3.7	758	9	BX185961	BX185961 Danio rer
1082	49.2	3.7	795	9	AG044101	AG044101 Pan trogl
c1083	49.2	3.7	816	9	CL855754	CL855754 OR_CBa008
c1084	49.2	3.7	853	9	CNS014EA	AL104044 Drosophil
1085	49.2	3.7	899	8	BH134306	BH134306 ENTNE78TF
1086	49.2	3.7	952	6	CD049079	CD049079 AGENCOURT
c1087	49.2	3.7	1052	5	BU560001	BU560001 AGENCOURT
1088	49.2	3.7	1101	9	CNS00Z38	AL097166 Drosophil
1089	49.2	3.7	1101	9	CNS0504G	AL315097 Tetraodon
1090	49.2	3.7	1104	9	CL041829	CL041829 CH216-53H
c1091	49.2	3.7	1160	8	BZ579469	BZ579469 msh2_637.
1092	49.2	3.7	1193	9	CG745316	CG745316 P038-1-G0
c1093	49.2	3.7	1200	3	CR661177	CR661177 Tetraodon
c1094	49.2	3.7	1204	9	CNS016E2	AL106628 Drosophil
1095	49.2	3.7	1205	9	CL143963	CL143963 ISB1-123O
1096	49.2	3.7	1260	9	CL491610	CL491610 SAIL_559_
c1097	49.2	3.7	1297	9	AG346663	AG346663 Mus muscu
c1098	49.2	3.7	1356	9	AG360895	AG360895 Mus muscu
c1099	49.2	3.7	1364	9	CG757970	CG757970 P053-2-C0
c1100	49.2	3.7	1446	9	CL490465	CL490465 SAIL_539_
c1101	49.2	3.7	1696	9	AG346840	AG346840 Mus muscu
c1102	49	3.6	308	1	AL663787	AL663787 AL663787
c1103	49	3.6	526	4	BG602598	BG602598 EST501688
1104	49	3.6	537	7	CO079921	CO079921 GR__Ea43A
1105	49	3.6	566	9	BX139720	BX139720 Danio rer
c1106	49	3.6	702	8	AZ526564	AZ526564 256PbH06
1107	49	3.6	730	5	BU453964	BU453964 603767942
c1108	49	3.6	782	7	CV484987	CV484987 AGENCOURT
1109	49	3.6	846	7	CF781629	CF781629 AGENCOURT
1110	49	3.6	852	2	BF617318	BF617318 HVSMEc001
1111	49	3.6	859	9	CNS00KLL	AL077728 Drosophil
c1112	49	3.6	860	9	CNS018BP	AL109135 Drosophil
c1113	49	3.6	939	6	BY720774	BY720774 BY720774
c1114	49	3.6	949	7	CK424488	CK424488 AUF_IpSto
1115	49	3.6	966	8	AZ543015	AZ543015 ENTDA24TR
1116	49	3.6	984	8	AZ544394	AZ544394 ENTCZ84TR
1117	49	3.6	989	9	CL098368	CL098368 ISB1-31D3
c1118	49	3.6	1039	9	CNS02ADN	AL188420 Tetraodon
c1119	49	3.6	1045	9	CNS03YE4	AL266197 Tetraodon

c1120	49	3.6	1101	9	CNS00BO1	AL057419	Drosophil	1193	48.4	3.6	179	4	BJ334175	BJ334175	BJ334175
1121	49	3.6	1101	9	CNS00DT7	AL075293	Drosophil	1194	48.4	3.6	179	4	BJ334928	BJ334928	BJ334928
1122	49	3.6	1101	9	CNS00KB5	AL077453	Drosophil	1195	48.4	3.6	179	4	BJ338148	BJ338148	BJ338148
c1123	49	3.6	1172	3	CR734084	CR734084	Tetraodon	1196	48.4	3.6	180	4	BJ330530	BJ330530	BJ330530
1124	49	3.6	1184	3	CR665955	CR665955	Tetraodon	1197	48.4	3.6	180	4	BJ337662	BJ337662	BJ337662
c1125	49	3.6	1199	9	AG288433	AG288433	Mus muscu	1198	48.4	3.6	181	4	BJ366687	BJ366687	BJ366687
c1126	49	3.6	1237	9	AG390880	AG390880	Mus muscu	1199	48.4	3.6	182	4	BJ335858	BJ335858	BJ335858
1127	49	3.6	1292	4	BM463105	BM463105	AGENCOURT	1200	48.4	3.6	203	4	BJ371047	BJ371047	BJ371047
c1128	49	3.6	1704	4	BG170937	BG170937	602323914	1201	48.4	3.6	210	4	BJ332837	BJ332837	BJ332837
1129	48.8	3.6	431	9	CL879140	CL879140	abf36b06.	1202	48.4	3.6	210	4	BJ337381	BJ337381	BJ337381
c1130	48.8	3.6	450	4	BM275484	BM275484	PfESToaa5	1203	48.4	3.6	211	4	BJ333851	BJ333851	BJ333851
1131	48.8	3.6	550	8	BZ369762	BZ369762	id10d11.g	1204	48.4	3.6	212	4	BJ334886	BJ334886	BJ334886
c1132	48.8	3.6	567	6	CB616361	CB616361	AMGNNUC:U	1205	48.4	3.6	242	7	CF319709	CF319709	HD--10-F0
1133	48.8	3.6	607	7	CV490737	CV490737	AGENCOURT	c1206	48.4	3.6	262	7	CV184748	CV184748	taj09d04.
c1134	48.8	3.6	615	7	CN755256	CN755256	ID0AAA15B	c1207	48.4	3.6	316	5	BP765680	BP765680	BP765680
c1135	48.8	3.6	650	6	CD594427	CD594427	RK091A2F0	1208	48.4	3.6	345	5	BU497054	BU497054	PfESToab5
1136	48.8	3.6	693	1	AV682300	AV682300	AV682300	c1209	48.4	3.6	433	9	BX137793	BX137793	Danio rer
c1137	48.8	3.6	713	7	CV042107	CV042107	tai66d03.	c1210	48.4	3.6	489	4	BM274551	BM274551	PfESToaa4
1138	48.8	3.6	722	9	CW009855	CW009855	ZMMBLa001	c1211	48.4	3.6	500	1	AU087306	AU087306	AU087306
c1139	48.8	3.6	734	8	BZ457345	BZ457345	BONCQ35TF	c1212	48.4	3.6	529	5	BQ265038	BQ265038	NISC_ff03
c1140	48.8	3.6	765	8	BZ058576	BZ058576	lky34a07.	1213	48.4	3.6	599	9	CNS008XP	AL052566	Drosophil
1141	48.8	3.6	771	8	BH482529	BH482529	BOHAG58TF	1214	48.4	3.6	620	8	BH594715	BH594715	BOHSA81TF
c1142	48.8	3.6	772	8	BZ040564	BZ040564	lka43a04.	1215	48.4	3.6	652	9	CNS03HOU	AL244551	Tetraodon
c1143	48.8	3.6	781	9	BX145762	BX145762	Danio rer	1216	48.4	3.6	680	9	BX155076	BX155076	Danio rer
1144	48.8	3.6	800	9	AG590972	AG590972	Mus muscu	c1217	48.4	3.6	708	7	CN763389	CN763389	ID0AAA6DF
1145	48.8	3.6	805	1	AJ537921	AJ537921	AJ537921	c1218	48.4	3.6	762	4	BM160418	BM160418	EST562941
1146	48.8	3.6	824	6	CA195303	CA195303	SCEZSB109	c1219	48.4	3.6	770	7	CK471256	CK471256	AGENCOURT
c1147	48.8	3.6	837	9	AG524361	AG524361	Mus muscu	c1220	48.4	3.6	778	7	CO388288	CO388288	AGENCOURT
1148	48.8	3.6	909	9	CNS06U6T	AL415467	T3 end of	c1221	48.4	3.6	869	9	CL478380	CL478380	SAIL_289_
1149	48.8	3.6	928	8	AZ549545	AZ549545	ENTDS54TF	c1222	48.4	3.6	906	9	AG555384	AG555384	Mus muscu
1150	48.8	3.6	940	9	CNS02GSH	AL196730	Tetraodon	1223	48.4	3.6	908	9	CNS04KS8	AL295217	Tetraodon
c1151	48.8	3.6	941	7	CF935040	CF935040	TrEST-B39	1224	48.4	3.6	939	6	BY720774	BY720774	BY720774
1152	48.8	3.6	1012	9	CL044464	CL044464	CH216-61F	c1225	48.4	3.6	963	9	CNS0075X	AL066857	Drosophil
1153	48.8	3.6	1101	9	CNS006DU	AL065139	Drosophil	c1226	48.4	3.6	965	9	CL505797	CL505797	SAIL_755_
1154	48.8	3.6	1101	9	CNS017KE	AL108152	Drosophil	c1227	48.4	3.6	1037	9	AG520556	AG520556	Mus muscu
c1155	48.8	3.6	1123	6	CD325190	CD325190	AGENCOURT	1228	48.4	3.6	1052	9	AG520832	AG520832	Mus muscu
c1156	48.8	3.6	1160	9	AG289903	AG289903	Mus muscu	1229	48.4	3.6	1055	5	BQ876453	BQ876453	AGENCOURT
c1157	48.8	3.6	1335	9	CL646802	CL646802	CH213-123	1230	48.4	3.6	1085	9	AG075009	AG075009	Pan trogl
c1158	48.8	3.6	1981	9	AG321457	AG321457	Mus muscu	c1231	48.4	3.6	1101	9	CNS00LVP	AL078809	Drosophil
1159	48.8	3.6	2077	3	CR667281	CR667281	Tetraodon	1232	48.4	3.6	1123	9	CL078696	CL078696	CH216-152
1160	48.8	3.6	2142	3	CR730230	CR730230	Tetraodon	c1233	48.4	3.6	1152	9	CL499024	CL499024	SAIL_662_
c1161	48.6	3.6	197	7	CR439668	CR439668	CR439668	c1234	48.4	3.6	1201	8	BZ695091	BZ695091	SP__Ba005
1162	48.6	3.6	211	4	BJ337607	BJ337607	BJ337607	c1235	48.4	3.6	1204	9	AG365769	AG365769	Mus muscu
1163	48.6	3.6	365	9	DR22F13S	AL744394	Danio rer	c1236	48.4	3.6	1251	9	AG377050	AG377050	Mus muscu
c1164	48.6	3.6	400	9	T09838	T09838	0415m3 gmbP	c1237	48.4	3.6	1563	8	CC206942	CC206942	CH261-191
c1165	48.6	3.6	422	8	BH126293	BH126293	BARC-Sat_	1238	48.2	3.6	365	9	CG824120	CG824120	SOYFH26TV
1166	48.6	3.6	500	5	BX736522	BX736522	BX736522	c1239	48.2	3.6	457	2	AW013848	AW013848	UI-H-BI0-
1167	48.6	3.6	539	7	CO722076	CO722076	TgESTzyq2	1240	48.2	3.6	500	1	AU088313	AU088313	AU088313
c1168	48.6	3.6	564	9	AG258155	AG258155	Lotus cor	c1241	48.2	3.6	531	7	CK743616	CK743616	nad03-4cs
1169	48.6	3.6	577	7	CN477441	CN477441	rx37f08.y	1242	48.2	3.6	625	7	CN757372	CN757372	ID0AAA1CF
1170	48.6	3.6	639	9	CNS017QD	AL108367	Drosophil	c1243	48.2	3.6	649	8	BH687718	BH687718	BOMLO56TF
c1171	48.6	3.6	657	7	CR411374	CR411374	CR411374	1244	48.2	3.6	656	8	BH343603	BH343603	CH230-41L
c1172	48.6	3.6	756	7	CF514133	CF514133	CAbud0007	1245	48.2	3.6	682	8	BZ002699	BZ002699	oeg89g06.
c1173	48.6	3.6	798	5	BX729254	BX729254	BX729254	1246	48.2	3.6	717	9	AG291454	AG291454	Mus muscu
1174	48.6	3.6	806	8	BZ394525	BZ394525	EINBI13TF	1247	48.2	3.6	721	8	BH921333	BH921333	odi47b12.
c1175	48.6	3.6	817	8	BZ388550	BZ388550	EINCQ55TF	1248	48.2	3.6	734	7	CK410841	CK410841	AUF_IpHdk
1176	48.6	3.6	910	9	CNS01G8P	AL142826	Anopheles	1249	48.2	3.6	744	8	AQ050079	AQ050079	nbxb0003b
1177	48.6	3.6	960	5	BX458080	BX458080	BX458080	1250	48.2	3.6	773	8	BH186746	BH186746	032_E_23-
1178	48.6	3.6	987	9	CL077094	CL077094	CH216-143	1251	48.2	3.6	773	9	CNS07R5M	AL623692	T7 end of
c1179	48.6	3.6	991	9	CL139092	CL139092	ISB1-111O	c1252	48.2	3.6	783	5	BX773950	BX773950	BX773950
1180	48.6	3.6	1014	6	CD048535	CD048535	AGENCOURT	c1253	48.2	3.6	783	7	CR568215	CR568215	CR568215
c1181	48.6	3.6	1101	9	CNS00G0M	AL071284	Drosophil	c1254	48.2	3.6	791	9	AG581577	AG581577	Mus muscu
1182	48.6	3.6	1101	9	CNS00LVZ	AL078819	Drosophil	c1255	48.2	3.6	810	8	BH480090	BH480090	BOGCF72TF
c1183	48.6	3.6	1198	9	AG347181	AG347181	Mus muscu	c1256	48.2	3.6	812	7	CF515338	CF515338	CAP0001_I
1184	48.6	3.6	1221	3	CR720347	CR720347	Tetraodon	c1257	48.2	3.6	836	9	AG466574	AG466574	Mus muscu
c1185	48.6	3.6	1225	8	CC238324	CC238324	CH261-192	1258	48.2	3.6	839	5	BP507382	BP507382	BP507382
c1186	48.6	3.6	1296	9	AG350007	AG350007	Mus muscu	1259	48.2	3.6	853	8	BH156806	BH156806	ENTRC12TF
c1187	48.6	3.6	1416	9	CL648233	CL648233	CH213-168	1260	48.2	3.6	858	9	BX907266	BX907266	Leishmani
1188	48.6	3.6	1461	9	CL081232	CL081232	CH216-161	c1261	48.2	3.6	895	7	CK165376	CK165376	FGAS04932
1189	48.6	3.6	2087	9	AG333887	AG333887	Mus muscu	1262	48.2	3.6	976	9	CL830166	CL830166	OR_CBa005
1190	48.4	3.6	174	4	BJ365704	BJ365704	BJ365704	1263	48.2	3.6	979	9	CNS0161W	AL106190	Drosophil
1191	48.4	3.6	176	4	BJ330919	BJ330919	BJ330919	1264	48.2	3.6	994	9	CNS015XG	AL106030	Drosophil
1192	48.4	3.6	179	4	BJ331846	BJ331846	BJ331846	c1265	48.2	3.6	1063	9	CNS07A2Y	AL436064	T3 end of

1266	48.2	3.6	1101	9	CNS003DX	AL064587	Drosophil
c1267	48.2	3.6	1101	9	CNS008ZA	AL052623	Drosophil
1268	48.2	3.6	1101	9	CNS01740	AL107562	Drosophil
c1269	48.2	3.6	1200	9	CNS016CO	AL106578	Drosophil
c1270	48.2	3.6	1227	9	CL650455	CL650455	CH213-288
1271	48.2	3.6	1315	3	CR657214	CR657214	Tetraodon
c1272	48.2	3.6	1473	9	AG278179	AG278179	Mus muscu
1273	48.2	3.6	1496	9	CL505519	CL505519	SAIL_751_
c1274	48.2	3.6	1664	9	AG430612	AG430612	Mus muscu
c1275	48.2	3.6	1733	9	AG278266	AG278266	Mus muscu
1276	48	3.6	171	4	BJ338944	BJ338944	BJ338944
1277	48	3.6	185	4	BJ702485	BJ702485	BJ702485
1278	48	3.6	198	5	BU096447	BU096447	tca-932 t
c1279	48	3.6	199	1	AA713657	AA713657	nv69a12.s
1280	48	3.6	248	4	BJ682856	BJ682856	BJ682856
1281	48	3.6	252	6	CB073895	CB073895	taa21f12.
1282	48	3.6	253	4	BJ678675	BJ678675	BJ678675
1283	48	3.6	263	4	BJ700223	BJ700223	BJ700223
1284	48	3.6	361	7	CV223521	CV223521	taj63h11.
1285	48	3.6	366	4	BJ680254	BJ680254	BJ680254
1286	48	3.6	367	6	CB072913	CB072913	taa25f03.
1287	48	3.6	371	6	CA301774	CA301774	taa07h07.
c1288	48	3.6	375	7	CN545397	CN545397	EST 17341
1289	48	3.6	393	6	CB244291	CB244291	UI-M-FY0-
1290	48	3.6	433	6	CA855369	CA855369	PfESToac3
1291	48	3.6	442	7	CF919884	CF919884	EST4184 Z
1292	48	3.6	485	1	AU087880	AU087880	AU087880
c1293	48	3.6	495	6	CB976462	CB976462	CAB40002_
1294	48	3.6	528	5	BP750062	BP750062	BP750062
c1295	48	3.6	537	8	AQ506817	AQ506817	RPCI-11-2
1296	48	3.6	544	7	CF357769	CF357769	rm95d08.y
c1297	48	3.6	575	5	BQ595910	BQ595910	PfESToab2
c1298	48	3.6	607	7	CF201659	CF201659	RR890915N
c1299	48	3.6	611	6	CD451883	CD451883	USDA-FP_1
c1300	48	3.6	640	8	BH453674	BH453674	BOGXG82TR
c1301	48	3.6	646	9	BX218216	BX218216	Danio rer
1302	48	3.6	693	7	CV061738	CV061738	BNEL71d2
c1303	48	3.6	720	8	BH938099	BH938099	odf11g03.
1304	48	3.6	720	9	CL917654	CL917654	OA_ABa002
c1305	48	3.6	779	6	CB975921	CB975921	CAB40001_
c1306	48	3.6	816	6	CB971775	CB971775	CAB10005_
1307	48	3.6	827	9	CR034369	CR034369	Forward s
1308	48	3.6	844	4	BM358154	BM358154	GA__Ea000
1309	48	3.6	860	8	BZ073741	BZ073741	lkf35f03.
1310	48	3.6	869	9	CL478380	CL478380	SAIL_289_
1311	48	3.6	877	8	AZ673567	AZ673567	ENTMO82TF
c1312	48	3.6	879	9	CNS01JRG	AL147405	Anopheles
c1313	48	3.6	883	9	CW016544	CW016544	ZMMBLc000
1314	48	3.6	891	9	AG475476	AG475476	Mus muscu
c1315	48	3.6	907	5	BX777578	BX777578	BX777578
c1316	48	3.6	923	8	CC127656	CC127656	NDL.18F15
1317	48	3.6	963	9	CNS0075X	AL066857	Drosophil
c1318	48	3.6	964	9	CNS017HZ	AL108065	Drosophil
1319	48	3.6	967	9	CNS00Z1N	AL097109	Drosophil
1320	48	3.6	978	9	CNS012T4	AL101986	Drosophil
1321	48	3.6	1006	6	CD388276	CD388276	AGENCOURT
c1322	48	3.6	1050	7	CN215928	CN215928	29772 Sus
c1323	48	3.6	1055	9	CL501343	CL501343	SAIL_696_
c1324	48	3.6	1076	8	BH677985	BH677985	BOMJZ90TR
c1325	48	3.6	1084	9	CNS071NH	AL425139	clone BA0
1326	48	3.6	1101	9	CNS016X8	AL107318	Drosophil
1327	48	3.6	1101	9	CNS017E8	AL107930	Drosophil
c1328	48	3.6	1167	9	CNS07360	AL427102	clone BA0
1329	48	3.6	1200	3	CR720801	CR720801	Tetraodon
c1330	48	3.6	1315	9	AG376867	AG376867	Mus muscu
c1331	48	3.6	1327	9	CL644705	CL644705	CH213-79D
c1332	48	3.6	1364	9	AG382422	AG382422	Mus muscu
c1333	48	3.6	1492	9	AG280506	AG280506	Mus muscu
1334	48	3.6	1539	9	AG340947	AG340947	Mus muscu
1335	48	3.6	1669	9	CL500107	CL500107	SAIL_679_
c1336	48	3.6	2270	9	AG279272	AG279272	Mus muscu
c1337	48	3.6	2300	3	CR734152	CR734152	Tetraodon
1338	47.8	3.6	175	7	CN477790	CN477790	rx41h09.y
1339	47.8	3.6	224	6	CB855268	CB855268	ri36f04.y
1340	47.8	3.6	473	4	BM274148	BM274148	PfESToaa6
1341	47.8	3.6	500	5	BP114545	BP114545	BP114545
1342	47.8	3.6	501	9	CL832689	CL832689	OR_CBa005
1343	47.8	3.6	519	8	AQ320292	AQ320292	RPCI11-10
1344	47.8	3.6	596	9	AG240284	AG240284	Lotus cor
1345	47.8	3.6	640	9	CG027925	CG027925	CHGAF76TF
c1346	47.8	3.6	645	8	BH998460	BH998460	oeh25e03.
c1347	47.8	3.6	663	9	CW518121	CW518121	OP__Ba002
1348	47.8	3.6	668	8	BZ397996	BZ397996	EINCO14TR
1349	47.8	3.6	674	8	BZ055157	BZ055157	jnr30h09.
c1350	47.8	3.6	693	1	AV682300	AV682300	AV682300
c1351	47.8	3.6	693	8	BZ007815	BZ007815	oeh48h06.
1352	47.8	3.6	704	8	BZ399913	BZ399913	EINCW92TR
1353	47.8	3.6	712	9	BX179575	BX179575	Danio rer
c1354	47.8	3.6	717	8	BZ032586	BZ032586	oei22f05.
1355	47.8	3.6	721	8	BH975660	BH975660	odi43g09.
c1356	47.8	3.6	759	9	CNS06QXV	AL411257	T7 end of
1357	47.8	3.6	791	8	BH897939	BH897939	Gm_UMb001
c1358	47.8	3.6	815	9	AG471644	AG471644	Mus muscu
c1359	47.8	3.6	820	8	B11728	B11728	T8D18-Sp6.1
c1360	47.8	3.6	839	9	CL090523	CL090523	ISB1-17D2
c1361	47.8	3.6	845	9	CG770922	CG770922	TcB16.3_A
1362	47.8	3.6	852	8	AQ894184	AQ894184	HS_3072_A
1363	47.8	3.6	865	8	BH180441	BH180441	016_H_20-
1364	47.8	3.6	865	9	CNS07MAN	AL617393	T3 end of
c1365	47.8	3.6	884	4	BM358117	BM358117	GA__Ea000
1366	47.8	3.6	890	9	AG414820	AG414820	Mus muscu
1367	47.8	3.6	916	2	AW155504	AW155504	mgie0028I
c1368	47.8	3.6	969	9	CL077158	CL077158	CH216-143
c1369	47.8	3.6	1013	9	CNS00J7I	AL075824	Drosophil
1370	47.8	3.6	1071	9	CNS05AJ7	AL328588	Tetraodon
1371	47.8	3.6	1085	9	CNS016YR	AL107373	Drosophil
c1372	47.8	3.6	1086	9	CNS00YXK	AL096962	Drosophil
1373	47.8	3.6	1090	1	AJ538020	AJ538020	AJ538020
c1374	47.8	3.6	1101	9	CNS01828	AL108794	Drosophil
c1375	47.8	3.6	1188	9	CL650084	CL650084	CH213-275
1376	47.8	3.6	1200	3	CR668650	CR668650	Tetraodon
1377	47.8	3.6	1200	9	CNS0162Z	AL106229	Drosophil
1378	47.8	3.6	1268	9	CL511608	CL511608	SAIL_850_
c1379	47.8	3.6	1275	9	CL033318	CL033318	CH216-36F
c1380	47.8	3.6	1277	8	CC253231	CC253231	CH261-180
1381	47.8	3.6	1300	2	BE420576	BE420576	HWM000.D0
1382	47.8	3.6	1310	9	AG370846	AG370846	Mus muscu
c1383	47.8	3.6	1441	9	AG396166	AG396166	Mus muscu
1384	47.8	3.6	1489	9	AG350139	AG350139	Mus muscu
c1385	47.8	3.6	1743	9	AG321332	AG321332	Mus muscu
1386	47.8	3.6	4087	3	CR749631	CR749631	Homo sapi
1387	47.6	3.5	386	7	CF383917	CF383917	lac11h08.
1388	47.6	3.5	447	7	CF382693	CF382693	lac90d04.
c1389	47.6	3.5	468	4	BM273814	BM273814	PfESToaa5
c1390	47.6	3.5	478	4	BM273862	BM273862	PfESToaa6
1391	47.6	3.5	497	9	CL874718	CL874718	abe98d11.
1392	47.6	3.5	500	1	AU087218	AU087218	AU087218
c1393	47.6	3.5	509	7	CO335025	CO335025	EK315734.
c1394	47.6	3.5	540	9	BX182832	BX182832	Danio rer
c1395	47.6	3.5	553	7	CO334739	CO334739	EK315206.
1396	47.6	3.5	558	5	BM934567	BM934567	UI-M-BH3-
c1397	47.6	3.5	562	4	BM275344	BM275344	PfESToaa6
c1398	47.6	3.5	577	7	CO334579	CO334579	EK314889.
c1399	47.6	3.5	581	7	CO334736	CO334736	EK315203.
1400	47.6	3.5	585	1	AJ537655	AJ537655	AJ537655
1401	47.6	3.5	613	8	BH424393	BH424393	BOHBX17TR
1402	47.6	3.5	623	1	AJ537636	AJ537636	AJ537636
c1403	47.6	3.5	691	8	BH967565	BH967565	odg74b08.
c1404	47.6	3.5	718	9	CR115352	CR115352	Forward s
1405	47.6	3.5	732	8	BZ021891	BZ021891	oei71h07.
c1406	47.6	3.5	775	8	AQ897834	AQ897834	HS_3153_A
1407	47.6	3.5	786	7	CO809669	CO809669	AGENCOURT
1408	47.6	3.5	800	7	CN385594	CN385594	LE2TR04A1
c1409	47.6	3.5	830	8	BH730490	BH730490	BOHUL32TF
c1410	47.6	3.5	835	9	CR306593	CR306593	Medicago
1411	47.6	3.5	836	7	CK867414	CK867414	AGENCOURT

c1412	47.6	3.5	848	5	BX763712	BX763712 BX763712
1413	47.6	3.5	849	7	CK400551	CK400551 AGENCOURT
1414	47.6	3.5	896	8	AZ672632	AZ672632 ENTJK37TF
1415	47.6	3.5	905	8	BH160918	BH160918 ENTRL19TR
1416	47.6	3.5	920	9	CNS01UQL	AL168150 Tetraodon
c1417	47.6	3.5	935	9	CNS00JKN	AL076398 Drosophil
c1418	47.6	3.5	972	8	AZ687424	AZ687424 ENTHY88TR
c1419	47.6	3.5	975	9	CL138471	CL138471 ISB1-111A
c1420	47.6	3.5	1005	6	CD326165	CD326165 AGENCOURT
c1421	47.6	3.5	1013	9	CNS06RPQ	AL412260 T7 end of
c1422	47.6	3.5	1101	9	CNS012BM	AL101356 Drosophil
1423	47.6	3.5	1101	9	CNS014MV	AL104353 Drosophil
c1424	47.6	3.5	1101	9	CNS015ZS	AL106114 Drosophil
1425	47.6	3.5	1101	9	CNS017ZQ	AL108704 Drosophil
1426	47.6	3.5	1104	9	CL080459	CL080459 CH216-158
c1427	47.6	3.5	1182	9	AG278356	AG278356 Mus muscu
1428	47.6	3.5	1201	9	CNS016EQ	AL106652 Drosophil
1429	47.6	3.5	1230	1	AJ537693	AJ537693 AJ537693
1430	47.6	3.5	1256	1	AJ537698	AJ537698 AJ537698
1431	47.6	3.5	1257	1	AJ537701	AJ537701 AJ537701
1432	47.6	3.5	1259	1	AJ537694	AJ537694 AJ537694
1433	47.6	3.5	1265	1	AJ537742	AJ537742 AJ537742
1434	47.6	3.5	1265	1	AJ537929	AJ537929 AJ537929
1435	47.6	3.5	1266	1	AJ537840	AJ537840 AJ537840
1436	47.6	3.5	1267	1	AJ537836	AJ537836 AJ537836
1437	47.6	3.5	1267	1	AJ538026	AJ538026 AJ538026
c1438	47.6	3.5	1267	9	CL650336	CL650336 CH213-288
1439	47.6	3.5	1274	1	AJ537864	AJ537864 AJ537864
1440	47.6	3.5	1274	1	AJ537869	AJ537869 AJ537869
c1441	47.6	3.5	1287	7	CF222655	CF222655 AGENCOURT
c1442	47.6	3.5	1338	9	AG360686	AG360686 Mus muscu
c1443	47.6	3.5	1364	9	AG430498	AG430498 Mus muscu
1444	47.4	3.5	159	4	BI268791	BI268791 NF009A09G
1445	47.4	3.5	214	7	CK593299	CK593299 tad38f10.
1446	47.4	3.5	322	7	CN194468	CN194468 rg94h06.y
1447	47.4	3.5	348	7	CF804173	CF804173 rg69a06.y
1448	47.4	3.5	366	7	CN194410	CN194410 rg94b02.y
c1449	47.4	3.5	394	6	CD450976	CD450976 USDA-FP_1
c1450	47.4	3.5	395	5	BQ739689	BQ739689 PfESTOab4
1451	47.4	3.5	396	6	CA823354	CA823354 R24H06 tw
c1452	47.4	3.5	409	6	CD451545	CD451545 USDA-FP_1
c1453	47.4	3.5	424	6	CD450510	CD450510 USDA-FP_1
c1454	47.4	3.5	438	6	CD451502	CD451502 USDA-FP_1
c1455	47.4	3.5	441	6	CD451988	CD451988 USDA-FP_1
c1456	47.4	3.5	467	6	CB714206	CB714206 AMGNNUC:N
c1457	47.4	3.5	468	1	AI753483	AI753483 cr11c08.x
1458	47.4	3.5	478	7	CN193971	CN193971 rg99e05.y
c1459	47.4	3.5	500	1	AU086736	AU086736 AU086736
c1460	47.4	3.5	533	6	CD449958	CD449958 USDA-FP_1
c1461	47.4	3.5	539	6	CD451834	CD451834 USDA-FP_1
c1462	47.4	3.5	547	4	BG840870	BG840870 MEST12-G1
c1463	47.4	3.5	547	6	CD452295	CD452295 USDA-FP_1
c1464	47.4	3.5	548	6	CD451306	CD451306 USDA-FP_1
1465	47.4	3.5	568	7	CN801370	CN801370 DI8P03673
c1466	47.4	3.5	570	7	CO372944	CO372944 tah61f03.
c1467	47.4	3.5	587	8	AQ842368	AQ842368 CpG1033A
c1468	47.4	3.5	587	9	BX167074	BX167074 Danio rer
1469	47.4	3.5	592	7	CF369532	CF369532 rg60h10.y
1470	47.4	3.5	606	7	CN757131	CN757131 ID0AAA1BC
1471	47.4	3.5	651	9	CW005151	CW005151 ZMMBLa000
c1472	47.4	3.5	671	8	BH997590	BH997590 oee38f02.
1473	47.4	3.5	712	9	CG824983	CG824983 SOYDA28TV
1474	47.4	3.5	744	9	CL623140	CL623140 OR_BBa001
1475	47.4	3.5	755	6	CB318239	CB318239 AGENCOURT
c1476	47.4	3.5	755	8	BZ015835	BZ015835 oei17g12.
c1477	47.4	3.5	762	9	CL469238	CL469238 SAIL_129b
c1478	47.4	3.5	769	8	BH565388	BH565388 BOHHZ61TR
c1479	47.4	3.5	780	7	CK595444	CK595444 AGENCOURT
c1480	47.4	3.5	787	9	CL868429	CL868429 Gma_01_A1
c1481	47.4	3.5	825	9	AG406068	AG406068 Mus muscu
1482	47.4	3.5	831	9	CG811572	CG811572 FSAAR94TF
c1483	47.4	3.5	839	5	BQ151187	BQ151187 NF048A07L
1484	47.4	3.5	841	8	BH586736	BH586736 BOGFX53TF
c1485	47.4	3.5	931	8	BH163084	BH163084 ENTQX60TF
c1486	47.4	3.5	975	8	BH179465	BH179465 014_P_10-
1487	47.4	3.5	1101	9	CNS00YWL	AL096927 Drosophil
c1488	47.4	3.5	1101	9	CNS00Z2H	AL097139 Drosophil
c1489	47.4	3.5	1101	9	CNS01807	AL108721 Drosophil
c1490	47.4	3.5	1107	8	BZ694442	BZ694442 SP__Ba004
c1491	47.4	3.5	1167	9	CL050792	CL050792 CH216-72O
c1492	47.4	3.5	1224	9	CL050332	CL050332 CH216-72B
c1493	47.4	3.5	1272	8	CC264939	CC264939 CH261-19L
c1494	47.4	3.5	1432	9	AG381846	AG381846 Mus muscu
c1495	47.4	3.5	1493	9	AG311017	AG311017 Mus muscu
c1496	47.4	3.5	1981	9	CL082000	CL082000 CH216-165
c1497	47.4	3.5	2087	9	AG333887	AG333887 Mus muscu
1498	47.2	3.5	228	7	CK607525	CK607525 Control_C
1499	47.2	3.5	311	4	BI744074	BI744074 kx55d03.y
1500	47.2	3.5	334	1	AU039580	AU039580 AU039580

ALIGNMENTS

RESULT 1
BI760941
LOCUS BI760941 870 bp mRNA linear EST 25-SEP-2001
DEFINITION 603043142F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5183554 5', mRNA sequence.
ACCESSION BI760941
VERSION BI760941.1 GI:15752519
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 870)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11458 row: c column: 11
High quality sequence stop: 844.

FEATURES Location/Qualifiers
source 1. .870
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5183554"
/lab_host="DH10B"
/clone_lib="NIH_MGC_116"
/note="Organ: pooled colon, kidney, stomach; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 58.8%; Score 791.2; DB 4; Length 870;
Best Local Similarity 97.7%; Pred. No. 8.1e-164;
Matches 813; Conservative 0; Mismatches 18; Indels 1; Gaps 1;

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Qy         11 TGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGTGCAG 70
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Db         12 TGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGTGCAG 71

Qy         71 AAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATATGCCT 130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         72 AAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATATGCCT 131

Qy        131 GGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAAGTTC 190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 GGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAAGTTC 191

Qy        191 CCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGGGTAT 250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        192 CCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGGGTAT 251

Qy        251 CATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAGGTGC 310
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        252 CATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAGGTGC 311

Qy        311 AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAA 370
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        312 AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAA 371

Qy        371 CTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCA 430
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        372 CTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCA 431

Qy        431 TCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGA 490
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Db        432 TCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGA 491

Qy        491 TTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGATGACG 550
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Db        492 TTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGATGACG 551

Qy        551 CTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCCCTGG 610
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Qy        611 ACATGAAGGG-GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGGCTCACCCCTC 669
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Db        672 TCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTGTGTGACTGCT 731

Qy        730 GAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCTTCTTTTGTAA 789
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        732 GAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCATTCTTCTTTTGTAA 791

Qy        790 TAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAACA 841
              |||||||||||||||| |  ||  |   |  || |||| ||     ||| ||
Db        792 TAAATTTTGAATGTGCCTTGAAAAGGTGAAAAAGCAATCATTATACCCACCA 843
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RESULT 2
BI762437

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LOCUS       BI762437                978 bp    mRNA    linear   EST 25-SEP-2001
DEFINITION  603048828F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5189023 5',
            mRNA sequence.
ACCESSION   BI762437
VERSION     BI762437.1  GI:15754015
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 978)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11472  row: g  column: 08
            High quality sequence stop: 826.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5189023"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_116"
                     /note="Organ: pooled colon, kidney, stomach; Vector:
                     pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
                     source anonymous pool of 3 colons, age 26 yo male, 49 yo
                     female, 71 yo male colon; 46 yo male kidney, and pool of 2
                     stomachs, 62 yo male and 70 yo female.  Library is
                     oligo-dT primed and  directionally cloned (EcoRV site is
                     destroyed upon cloning).  Average insert size 1.4 kb,
                     insert size range 1-3 kb.  Library is normalized and
                     enriched for full-length clones and was constructed by C.
                     Gruber  (Invitrogen).  Research Genetics tracking code
                     023. Note: this is a NIH_MGC Library."
ORIGIN
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  Query Match           55.8%;  Score 751.2;  DB 4;  Length 978;
  Best Local Similarity  92.9%;  Pred. No. 5.5e-155;
  Matches  863;  Conservative    0;  Mismatches   53;  Indels   13;  Gaps    7;

Qy         35 CTGCCATTCATGCTGAACTCTGTCAACCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTA 94
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Db          1 CTGCCATTCATGCTGAACTCTGTCAACCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTA 60

Qy         95 GTATCAGAACAGCTCTGGGAGATAAAGCATATGCCTGGGATACCAATGAAGAATACCTCT 154
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Db         61 GTATCAGAACAGCTCTGGGAGATAAAGCATATGCCTGGGATACCAATGAAGAATACCTCT 120

Qy        155 TCAAAGCGATGGTAGCTTTCTCCATGAGAAAAGTTCCCAACAGAGAAGCAACAGAAATTT 214
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Db        121 TCAAAGCGATGGTAGCTTTCTCCATGAGAAAAGTTCCCAACAGAGAAGCAACAGAAATTT 180

Qy        215 CCCA-TGTCCTACTTTGCAATGTAACCCAGAGGGTATCATTCTGGTTTGTGGTTACAGAC 273
              |||| |||||||| ||||||||||||||||||||||||||||| ||||||||||||||
Db        181 CCCAGTGTCCTACTNTGCAATGTAACCCAGAGGGTATCATTCTGGTGTGTGGTTACAGAC 240

Qy        274 CCTTCAAAAAATCACACCCTTCCTGCTGTTGAGGTGCAATCAGCCATAAGAATGAACAAG 333
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Db        241 CCTTCAAAAAATCACACCCTTCCTGCTGNTGAGGTGCAATCAGCCATAAGAATGAACAAG 300

Qy        334 AACCGGATCAACAATGCCTTCTTTCTAAATGACCAAACTCTGGAATTTTTAAAAATCCCT 393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AACCGGATCAACAATGCCTTCTTTCTAAATGACCAAACTCTGGAATTTTTAAAAATCCCT 360

Qy        394 TCCACACTTGCACCACCCATGGACCCATCTGTGCCCATCTGGATTATTATATTTGGTGTG 453
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Db        361 TCCACACTTGCACCACCCATGGACCCATCTGTGCCCATCTGGATTATTATATNTGGTGTG 420

Qy        454 ATATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTATCAGGGATCTGGCAACGT 513
              |||||| |||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        421 ATATTTGGCATCATCATAGTTGCAATGGCACTACTGATTTTATCAGGGATCTGGCAACGT 480

Qy        514 AGAAGAAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGATAAGTGTGAAAACATG 573
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Db        481 AGAAGAAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGATAAGTGTGAAAACATG 540

Qy        574 ATCACAATTGAAAATGGCATCCCCTCTGATCCCCTGGACATGAAGGG-GGGCATATTAAT 632
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                ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        541 ATCACAATTGAAAATGGCATCCCCTCTGATCCCCTGGACATGAAGGGAGGGCATATTAAT 600

Qy        633 GATGCCTTCATGACAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTT 692
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Qy        693 CCTCAAGAAATTAAACATTTGTTTCTGTGTGACTGCTGAGCATCCTGAAATACCAAGAGC 752
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Db        661 CCTCAAGAAATTAAACA-TTGTTTCTGTGTGACTGCTGAGCATCCTGAAATACCAAGAGC 719

Qy        753 AGATCATATATTTTGTTTCACCATTCTTCTTTTGTAATAAATTTTGAATGTGCTTGAAAG 812
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Db        720 AGATCATATATTTNGTTTCACCATTCTTCTTTGGTAATAAATTTGTGAATGTGCTGAAAG 779

Qy        813 TGAAAAGCAATCAATTATACCCACCAACACCACTGAAATCATAAGCTATTCACGACTCAA 872
              |||||||| |||||||||||| || ||   ||||||||||||||||||||| || ||||
Db        780 TGAAAAGC-ATCAATTATACCAACAAA---CACTGAAATCATAAGCTATTCAGGAATCAA 835

Qy        873 AATATTCTAAAATATTTTTCTGACAGTATAGTGTATAAATGTGGTCATGTGGTATTTGTA 932
              |    ||||| |||||||||||| ||    || || |    ||||      | | | | |
Db        836 A--TATCTAAGATATTTTTCTGAAAGATAGGTATAAA----TGGTGGCAGTGGAATGGAA 889

Qy        933 GTTATTGATTTAAGCATTTTTAGAAATAA 961
              ||  | |||| |||  |||  |||   ||
Db        890 GTATTGGATTAAAGATTTTAGAGATTAAA 918


RESULT 3
BG217185
LOCUS       BG217185                779 bp    mRNA    linear   EST 21-APR-2001
DEFINITION  RST36886 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION   BG217185
VERSION     BG217185.1  GI:13743206
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 779)
  AUTHORS   Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
            Cain,S., Leventhal,C., Thornton,M., Ramachandran,R.,
            Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S.,
            Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K.,
            Offenbacher,J., Danzig,J. and Ducar,M.
  TITLE     Creation of genome-wide protein expression libraries using random
            activation of gene expression
  JOURNAL   Nat. Biotechnol. 19 (5), 440-445 (2001)
  MEDLINE   21227151
   PUBMED   11329013
COMMENT     Contact: Scott J. Cain
            Athersys, Inc.
            3201 Carnegie Ave, Cleveland, OH 44115, USA
            Tel: 216 431 9900
            Fax: 216 361 9596
            Email: scain@athersys.com
            High quality sequence stop: 547.
FEATURES             Location/Qualifiers
     source          1. .779
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                     /clone_lib="Athersys RAGE Library"
                     /note="See 'Creation of Genome-wide Protein Expression
                     Libraries using Random Activation of Gene Expression',
                     Nature Biotechnology, in press. Note that even though the
                     cell type indicated is HT1080, since a random activation
                     method was used, these sequence tags are not necessarily
                     expressed in HT1080 under normal circumstances."
ORIGIN

  Query Match             55.5%;  Score 746.8;  DB 4;  Length 779;
  Best Local Similarity   99.0%;  Pred. No. 5e-154;
  Matches  762;  Conservative    0;  Mismatches    7;  Indels    1;  Gaps    1;

Qy        217 CATGTCCTACTTTGCAATGTAACCCAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCT 276
              | ||||||||||    ||||||||||||||||||||||||||||||||||||||||||||
Db         10 CCTGTCCTACTTTTTCATGTAACCCAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCT 69

Qy        277 TCAAAAAATCACACCCTTCCTGCTGTTGAGGTGCAATCAGCCATAAGAATGAACAAGAAC 336
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Db         70 TCAAAAAATCACACCCTTCCTGCTGTTGAGGTGCAATCAGCCATAAGAATGAACAAGAAC 129

Qy        337 CGGATCAACAATGCCTTCTTTCTAAATGACCAAACTCTGGAATTTTTAAAAATCCCTTCC 396
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 CGGATCAACAATGCCTTCTTTCTAAATGACCAAACTCTGGAATTTTTAAAAATCCCTTCC 189

Qy        397 ACACTTGCACCACCCATGGACCCATCTGTGCCCATCTGGATTATTATATTTGGTGTGATA 456
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Db        190 ACACTTGCACCACCCATGGACCCATCTGTGCCCATCTGGATTATTATATTTGGTGTGATA 249

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Db        250 TTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTATCAGGGATCTGGCAACGTAGA 309

Qy        517 AGAAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGATAAGTGTGAAAACATGATC 576
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Qy        577 ACAATTGAAAATGGCATCCCCTCTGATCCCCTGGACATGAAGGG-GGGCATATTAATGAT 635
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Db        370 ACAATTGAAAATGGCATCCCCTCTGATCCCCTGGACATGAAGGGAGGGCATATTAATGAT 429

Qy        636 GCCTTCATGACAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCT 695
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Db        430 GCCTTCATGACAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCT 489

Qy        696 CAAGAAATTAAACATTTGTTTCTGTGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGA 755
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        490 CAAGAAATTAAACATTTGTTTCTGTGTGACTGCTGAGCTTCCTGAAATACCAAGAGCAGA 549

Qy        756 TCATATATTTTGTTTCACCATTCTTCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGA 815
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 TCATATATTTTGTTTCACCATTCTTCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGA 609

Qy        816 AAAGCAATCAATTATACCCACCAACACCACTGAAATCATAAGCTATTCACGACTCAAAAT 875
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        610 AAAGCAATCAATCATACCCACCAACACCACTGAAATCATAAGCTATTCACGACTCAAAAT 669

Qy        876 ATTCTAAAATATTTTTCTGACAGTATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTT 935
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Db        670 ATTCTAAAATATTTTTCTGACAGTATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTT 729

Qy        936 ATTGATTTAAGCATTTTTAGAAATAAGATCAGGCATATGTATATATTTTC 985
              |||||||||||||||||| ||||||||||||||||||||||||||||||
Db        730 ATTGATTTAAGCATTTTTAAAAATAAGATCAGGCATATGTATATATTTTC 779


RESULT 4
BU689227/c
LOCUS       BU689227                782 bp    mRNA    linear   EST 07-OCT-2002
DEFINITION  UI-CF-EC1-adw-i-18-0-UI.s1 UI-CF-EC1 Homo sapiens cDNA clone
            UI-CF-EC1-adw-i-18-0-UI 3', mRNA sequence.
ACCESSION   BU689227
VERSION     BU689227.1  GI:23546785
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 782)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
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  MEDLINE   97044477
    PUBMED  8889548
COMMENT     Contact: McCray, PB
            McCray Lab
            University of Iowa
            2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
            Tel: 319 356 4866
            Fax: 319 356 7171
            Email: paul-mccray@uiowa.edu
            Tissue Procurement: Dr. M. J. Welsh, University of Iowa
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com) or from Open Biosystems
            (www.openbiosystems.com).
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES              Location/Qualifiers
     source           1. .782
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="UI-CF-EC1-adw-i-18-0-UI"
                      /tissue_type="Lung"
                      /dev_stage="Adult and Fetal"
                      /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                      /clone_lib="UI-CF-EC1"
                      /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                      modified polylinker; Site_1: EcoR I; Site_2: Not I;
                      UI-CF-EC1 is a normalized cDNA library containing the
                      following tissue(s): Normal lung from adult and from fetal
                      day 64, day 87, week 19 and week 42. The library was
                      constructed according to Bonaldo, Lennon and Soares,
                      Genome Research, 6:791-806, 1996. First strand cDNA
                      synthesis was primed with an oligo-dT primer containing a
                      Not I site.  Double stranded cDNA was ligated to an EcoR I
                      adaptor, digested with Not I, and cloned directionally
                      into pT7T3-Pac vector. The oligonucleotide used to prime
                      the synthesis of first-strand cDNA contains a library tag
                      sequence that is located between the Not I site and the
                      (dT)18 tail. The sequence tag for this library is
                      AAGTGCTTAC.
                      TAG_TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371
                      and 380-383
                      TAG_LIB=UI-CF-EC1
                      TAG_SEQ=AAGTGCTTAC"
ORIGIN

  Query Match             55.2%;  Score 743.6;  DB 5;  Length 782;
  Best Local Similarity   98.6%;  Pred. No. 2.5e-153;
  Matches  749;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy        585 AAATGGCATCCCCTCTGATCCCCTGGACATGAAGGGGGGCATATTAATGATGCCTTCATG 644
              |||  |||||||||||||||| |||||||||||| ||||||||||||||||||||||||
Db        760 AAAATGCATCCCCTCTGATCCNCTGGACATGAAGGAGGGCATATTAATGATGCCTTCATG 701

Qy        645 ACAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATT 704
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        700 ACAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATT 641

Qy        705 AAACATTTGTTTCTGTGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATT 764
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        640 AAACATTTGTTTCTGTGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATT 581

Qy        765 TTGTTTCACCATTCTTCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATC 824
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db        580 TTGTTTCACCATTCTTCTTTTGTAATAAATTNTGAATGTGCTTGAAAGTGAAAAGCAATC 521

Qy        825 AATTATACCCACCAACACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAA 884
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        520 AATTATACCCACCAACACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAA 461

Qy        885 TATTTTTCTGACAGTATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTA 944
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        460 TATTTTTCTGACAGTATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTA 401

Qy        945 AGCATTTTTAGAAATAAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGG 1004
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        400 AGCATTTTTAGAAATAAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGG 341

Qy       1005 AAAAATAAATTTTCCAGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGA 1064
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        340 AAAAATAAATTTTCCAGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGA 281

Qy       1065 TCCTTTTTGACGATCACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGT 1124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        280 TCCTTTTTGACGATCACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGT 221

Qy       1125 AATTATTGTAAATGGATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCC 1184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 AATTATTGTAAATGGATGGATAAAAATGGAATTACTCATATACAGGGTGGAATTTTATCC 161

Qy       1185 TGTTATCACACCAACAGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATT 1244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        160 TGTTATCACACCAACAGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATT 101

Qy       1245 CTATTTGTTGACCATTTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTA 1304
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        100 CTATTTGTTGACCATTTCTACAATTTGTAAAAGTCCAATTTGTGCTAACTTAATAAAGTA 41

Qy       1305 ATAATCATCTCTTTTTAAAAAAAAAAAAAAAAAAAAAAAA 1344
              |||||||||||||||| |    ||||||||||||||||||
Db         40 ATAATCATCTCTTTTTGATTTGAAAAAAAAAAAAAAAAAA 1

RESULT 5
BG194741
LOCUS       BG194741                826 bp    mRNA    linear   EST 21-APR-2001
DEFINITION  RST13907 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION   BG194741
VERSION     BG194741.1  GI:13716428
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 826)
  AUTHORS   Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
            Cain,S., Leventhal,C., Thornton,M., Ramachandran,R.,
            Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S.,
            Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K.,
            Offenbacher,J., Danzig,J. and Ducar,M.
  TITLE     Creation of genome-wide protein expression libraries using random
            activation of gene expression
  JOURNAL   Nat. Biotechnol. 19 (5), 440-445 (2001)
  MEDLINE   21227151
    PUBMED  11329013
COMMENT     Contact: Scott J. Cain
            Athersys, Inc.
            3201 Carnegie Ave, Cleveland, OH 44115, USA
            Tel: 216 431 9900
            Fax: 216 361 9596
            Email: scain@athersys.com
            High quality sequence stop: 541.
FEATURES              Location/Qualifiers
     source           1. .826
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /cell_line="HT1080"
                      /clone_lib="Athersys RAGE Library"
                      /note="See 'Creation of Genome-wide Protein Expression
                      Libraries using Random Activation of Gene Expression',
                      Nature Biotechnology, in press. Note that even though the
                      cell type indicated is HT1080, since a random activation
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method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

ORIGIN

Query Match 54.7%; Score 736.6; DB 4; Length 826;
Best Local Similarity 96.7%; Pred. No. 8.9e-152;
Matches 792; Conservative 0; Mismatches 23; Indels 4; Gaps 4;

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Qy        324 AATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAACTCTGGAATTTTT 383
              |||     |  ||||| |||||||||||||||||||||||||||||||||||||||||||
Db          8 AATAGNACAANACCGGNTCAACAATGCCTTCTTTCTAAATGACCAAACTCTGG-ATTTTT 66

Qy        384 AAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCATCTGGATTATTAT 443
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 AAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCATCTGGATTATTAT 126

Qy        444 ATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTATCAGGGAT 503
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 ATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTATCAGGGAT 186

Qy        504 CTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGATAAGTG 563
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 CTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGATAAGTG 246

Qy        564 TGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCCCTGGACATGAAGGG-GG 622
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        247 TGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCCCTGGACATGAAGGGAGG 306

Qy        623 GCATATTAATGATGCCTTCATGACAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGT 682
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 GCATATTAATGATGCCTTCATGACAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGT 366

Qy        683 TGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTGTGTGACTGCTGAGCATCCTGAAA 742
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Db        367 TGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTGTGTGACTGCTGAGCATCCTGAAA 426

Qy        743 TACCAAGAGCAGATCATATATTTTGTTTCACCATTCTTCTTTTGTAATAAATTTTGAATG 802
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TACCAAGAGCAGATCATATATTTTGTTTCACCATTCTTCTTTTGTAATAAATTTTGAATG 486

Qy        803 TGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAACACCACTGAAATCATAAGCTATT 862
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TGCTTGAAAGTGAAAAGCAATCAATTATACCCACCAACACCACTGAAATCATAAGCTATT 546

Qy        863 CACGACTCAAAATATTCTAAAATATTTTTCTGACAGTATAGTGTATAAATGTGGTCATGT 922
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 CACGACTCANAATATTCTAAAATATTTTTCTGACAGTATAGTGTATAAATGTGGTCATGT 606

Qy        923 GGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAATAAGATCAGGCATATGTATATA-T 981
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        607 GGTATTTGTAGTTATTGATTTAAGCATTTTTAGAAATAAGATCAGGCATATGTATATATT 666

Qy        982 TTTCACACTTCAAAGACCTAAGGAAAAATAAATTTTCCAGTGGAGAATACATATAATAT- 1040
              |||||||||||||||||||||||| |||||| ||||||||||||||||||||||||||| |
Db        667 TTTCACACTTCAAAGACCTAAGGAAGAATAAAATTTCCAGTGGAGAATACATATAATATG 726

Qy       1041 GGTGTAGAAATCATTGAAAATGGATCCTTTTTGACGATCACTTATATCACTCTGTATATG 1100
              |||| |||||||||||| || |||||||||||| ||||||||||||||||||||||||||
Db        727 GGTGGAGAAATCATTGAGAAAGGATCCTTTTTGGCGATCACTTATATCACTCTGTATATG 786

Qy       1101 ACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAATGG 1139
              |   | ||||| ||||| |||||||||||||||| ||||
Db        787 AACTAAGAAACACAAGTGGGAAGTAATTATTGTAGATGG 825
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RESULT 6
BG211841
LOCUS BG211841 788 bp mRNA linear EST 21-APR-2001
DEFINITION RST31414 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BG211841
VERSION BG211841.1 GI:13733528
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 788)
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.
TITLE Creation of genome-wide protein expression libraries using random activation of gene expression
JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE 21227151
PUBMED 11329013
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
High quality sequence stop: 554.
FEATURES Location/Qualifiers
source 1. .788
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="HT1080"
/clone_lib="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

ORIGIN

Query Match 54.4%; Score 732; DB 4; Length 788;
Best Local Similarity 98.2%; Pred. No. 9.2e-151;
Matches 771; Conservative 0; Mismatches 11; Indels 3; Gaps 3;

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Qy        210 AATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGGGTATCATTCTGGTTTGTGGTTAC 269
              ||||| |||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db          6 AATTTACCATGTCCTACTTTGTCATGTAACCCAGAGGGTATCATTCTGGTTTGTGGTTAC 65

Qy        270 AGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAGGTGCAATCAGCCATAAGAATGAA 329
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 AGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAGGTGCAATCAGCCATAAGAATGAA 125

Qy        330 CAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAACTCTGGAATTTTTAAAAAT 389
              |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        126 CAAGAACCGGATCAACAATGCCTTCTTTCTAAATGA-CAAACTCTGGAATTTTTAAAAAT 184

Qy        390 CCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCATCTGGATTATTATATTTGG 449
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        185 CCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCATCTGGATTATTATATTTGG 244

Qy        450 TGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTATCAGGGATCTGGCA 509
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        245 TGTGATATTTTGCATCATCATAGTTGTAATTGCACTACTGATTTTATCAGGGATCTGGCA 304

Qy        510 ACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGATAAGTGTGAAAA 569
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        305 ACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGATAAGTGTGAAAA 364

Qy        570 CATGATCACAATTGAAAATGGCATCCCCTCTGATCCCCTGGACATGAAGGG-GGGCATAT 628
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        365 CATGATCACAATTGAAAATGGCATCCCCTCTGATCCCCTGGACATGAAGGGAGGGCATAT 424

Qy        629 TAATGATGCCTTCATGACAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGTTGTTCT 688
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Db        425 TAATGATGCCTTCATGACAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGTTGTTCT 484

Qy        689 GCTTCCTCAAGAAATTAAACATTTGTTTCTGTGTGACTGCTGAGCATCCTGAAATACCAA 748
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                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        485 GCTTCCTCAAGAAATTAAACATTTGTTTCTGTGTGACTGCTGAGCATCCTGAAATACCAA 544

Qy        749 GAGCAGATCATATATTTTGTTTCACCATTCTTCTTTTGTAATAAATTTTGAATGTGCTTG 808
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        545 GAGCAGATCATATATTTTGTTTCACCATTCTTCTTTTGTAATAAATTTTGAATGTGCTTG 604

Qy        809 AAAGTGAAAAGCAATCAATTATACCCACCAACACCACTGAAATCATAAGCTATTCACGAC 868
                |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        605 AAAGTGAAAAGCANTCAATTATACCCACCAACACCACTGAAATCATAAGCTATTCACGAC 664

Qy        869 TCAAAATATTCTAAAATATTTTTCTGACAGTATAGTGTATAAATGTGGTCATGTGGTATT 928
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        665 TCAAAATATTCTAAAATATTTTTCTGACAGTATAGTGTATAAATGTGGTCATGTGGGATT 724

Qy        929 TGTAGTTATTGATTTAAGCATTTTTAGAAATAAGATCAGGCATATGTATATATTTTCACA 988
                |||||||||||||||||||||||||| |||| ||||| || |||| ||||||||||||||
Db        725 TGTAGTTATTGATTTAAGCATTTTTAG-AATATGATCAAGCCTATGCATATATTTTCACA 783

Qy        989 CTTCA 993
                ||| |
Db        784 CTTAA 788
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RESULT 7
BG218203

LOCUS	BG218203 801 bp mRNA linear EST 21-APR-2001
DEFINITION	RST37930 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION	BG218203
VERSION	BG218203.1 GI:13744224
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 801)
AUTHORS	Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.
TITLE	Creation of genome-wide protein expression libraries using random activation of gene expression
JOURNAL	Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE	21227151
PUBMED	11329013
COMMENT	Contact: Scott J. Cain Athersys, Inc. 3201 Carnegie Ave, Cleveland, OH 44115, USA Tel: 216 431 9900 Fax: 216 361 9596 Email: scain@athersys.com High quality sequence stop: 534.

FEATURES Location/Qualifiers

source 1. .801
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="HT1080"
/clone_lib="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

ORIGIN

Query Match 54.2%; Score 729; DB 4; Length 801;
Best Local Similarity 96.4%; Pred. No. 4.2e-150;
Matches 767; Conservative 0; Mismatches 26; Indels 3; Gaps 2;

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Qy        213 TTCCCATGTCCTACTTTGCAATGTAACCCAGAGGGTATCATTCTGGTTTGTGGTTACAGA 272
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Db          5 TTTCCATGTCCTACTTTGCAATGTAACCCAGAGGGTATCATTCTGGTTTGTGGTTACAGA 64

Qy        273 CCCTTCAAAAAATCACACCCTTCCTGCTGTTGAGGTGCAATCAGCCATAAGAATGAACAA 332
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Db         65 CCCTTCAAAAAATCACACCCTTCCTGCTGTTGAGGTGCAATCAGCCATAAGAATGAACAA 124

Qy        333 GAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAACTCTGGAATTTTTAAAAATCCC 392
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Db        125 GAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAACTCTGGAATTTTTAAAAATCCC 184

Qy        393 TTCCACACTTGCACCACCCATGGACCCATCTGTGCCCATCTGGATTATTATATTTGGTGT 452
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Db        185 TTCCACACTTGCACCACCCATGGACCCATCTGTGCCCATCTGGATTATTATATTTGGTGT 244

Qy        453 GATATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTATCAGGGATCTGGCAACG 512
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Db        245 GATATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTATCAGGGATCTGGCAACG 304

Qy        513 TAGAAGAAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGATAAGTGTGAAAACAT 572
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Db        305 TAGAAGAAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGATAAGTGTGAAAACAT 364

Qy        573 GATCACAATTGAAAATGGCATCCCCTCTGATCCCCTGGACATGAAGGG-GGGCATATTAA 631
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Db        365 GATCACAATTGAAAATGGCATCCCCTCTGATCCCCTGGACATGAAGGGAGGGCATATTAA 424

Qy        632 TGATGCCTTCATGACAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGTTGTTCTGCT 691
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Qy        692 TCCTCAAGAAATTAAACATTTGTTTCTGTGTGACTGCTGAGCATCCTGAAATACCAAGAG 751
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Db        485 TCCTCAAGAAATTAAACATTTGTTTCTGTGTGACTGCTGAGCATCCTGAAATACCAAGAG 544

Qy        752 CAGATCATATATTTTGTTTCACCATTCTTCTTTTGTAATAAATTTTGAATGTGCTTGAAA 811
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Db        545 CAGACCATATATTTTGTTTCACCATTCTTCTTTTGTAATAAATTTTGAATGTGCTTAAAA 604

Qy        812 GTGAAAAGCAATCAATTATACCCACCAACACCACTGAAATCATAAGCTATTCACGACTCA 871
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Db        605 GTGAAAAGCAATCAATTATACCCACCAACACCACTGAAATCATAGGCTATTCACGACTCA 664

Qy        872 AAATATTCTAAAATATTTTT--CTGACAGTATAGTGTATAAATGTGGTCATGTGGTATTT 929
                |||||||||||||||||||     |||||||  ||||||||||  | ||||||||||||
Db        665 NAATATTCTAAAATATTTTTTCTGAACAGTATTATGTATAAATGACGGCATGTGGTATTT 724

Qy        930 GTAGTTATTGATTTAAGCATTTTTAGAAATAAGATCAGGCATATGTATATATTTTCACAC 989
                | || |||||| |||||||||||||| |||||||||||||||| |||||||||| ||||
Db        725 GGAGGTATTGAATTAAGCATTTTTAAAAATAAGATCAGGCATTTGTATATATTTCCACAT 784

Qy        990 TTCAAAGACCTAAGGA 1005
                |  ||| ||| | | |
Db        785 TCAAAAAACCAAGGAA 800
```

RESULT 8
CA312017/c

LOCUS	CA312017 750 bp mRNA linear EST 04-NOV-2002
DEFINITION	UI-CF-FN0-afj-e-08-0-UI.s1 UI-CF-FN0 Homo sapiens cDNA clone UI-CF-FN0-afj-e-08-0-UI 3', mRNA sequence.
ACCESSION	CA312017
VERSION	CA312017.1 GI:24530115
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 750)
AUTHORS	Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE	Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL	Genome Res. 6 (9), 791-806 (1996)

```
  MEDLINE   97044477
   PUBMED   8889548
COMMENT     Contact: McCray, PB
            McCray Lab
            University of Iowa
            2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
            Tel: 319 356 4866
            Fax: 319 356 7171
            Email: paul-mccray@uiowa.edu
            Tissue Procurement: Dr. M. J. Welsh, University of Iowa
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com) or from Open Biosystems
            (www.openbiosystems.com).
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .750
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-CF-FN0-afj-e-08-0-UI"
                     /tissue_type="Human Lung Epithelial cells"
                     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                     /clone_lib="UI-CF-FN0"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     UI-CF-FN0 is a subtracted cDNA library derived from two
                     normalized Human lung epithelial cell libraries (EN1 and
                     DU1) The library was subtracted according to according to
                     Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                     1996. For additional information, contact:
                     bento-soares@uiowa.edu
                     TAG_TISSUE=Human Lung Epithelial Cell Lines untreated LPS
                     6hr to LPS 24h
                     TAG_LIB=UI-CF-FN0
                     TAG_SEQ=CTGCTCAGGT"
ORIGIN

  Query Match             53.2%;  Score 715.4;  DB 6;  Length 750;
  Best Local Similarity   98.8%;  Pred. No. 4.2e-147;
  Matches  741;  Conservative    0;  Mismatches    7;  Indels    2;  Gaps    2;

Qy        598 TCTGATCCCCTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGACAGAGGATGAG 656
              ||||||| ||||||||||||||| |||||||||||||||||||||||||||||||||||
Db        750 TCTGATCCNCTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGACAGAGGATGAG 691

Qy        657 AGGCTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTT 716
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        690 AGGCTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTT 631

Qy        717 CTGTGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCAT 776
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        630 CTGTGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCAT 571

Qy        777 TCTTCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCAC 836
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        570 TCTTCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGAAAAGCAATCAATTATACCCAC 511

Qy        837 CAACACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGAC 896
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        510 CAACACCACTGAAATCATAAGCTATTCACGACTCAAAATATTCTAAAATATTTTTCTGAC 451

Qy        897 AGTATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGA 956
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        450 AGTATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAAGCATTTTTAGA 391

Qy        957 AATAAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTT 1016
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        390 AATAAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAATTT 331

Qy       1017 TCCAGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACG 1076
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        330 TCCAGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTTTGACG 271

Qy       1077 ATCACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAA 1136
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        270 ATCACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTAAA 211

Qy       1137 TGGATGGATAAAAATGGAATTACTCATATACAG-GGTGGAATTTTATCCTGTTATCACAC 1195
              |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db        210 TGGATGGATAAAAATGGAATTACTCATATACAGNGGTGGAATTTTATCCTGTTATCACAC 151

Qy       1196 CAACAGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGA 1255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        150 CAACAGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTTGTTGA 91

Qy       1256 CCATTTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTC 1315
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          90 CCATTTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTC 31

Qy       1316 TTTTTAAAAAAAAAAAAAAAAAAAAAAAAA 1345
              ||||| |     ||||||||||||||||||
Db          30 TTTTTGATTGTGAAAAAAAAAAAAAAAAA 1


RESULT 9
BG429174
LOCUS       BG429174                780 bp    mRNA    linear   EST 14-MAR-2001
DEFINITION  602498032F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4612062 5',
            mRNA sequence.
ACCESSION   BG429174
VERSION     BG429174.1  GI:13335680
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 780)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
             cDNA Library Preparation: CLONTECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1359  row: o  column: 07
            High quality sequence stop: 718.
FEATURES             Location/Qualifiers
     source          1. .780
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4612062"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_75"
                     /note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and
                     3' adaptors were used in cloning as follows: 5' adaptor
                     sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).  Average insert size 1.65
                     kb (range 0.5-4.0 kb). 15/15 colonies contained  inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech  Laboratories (Palo Alto,
                     CA). Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             52.5%;  Score 706.8;  DB 4;  Length 780;
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 Best Local Similarity   97.4%;  Pred. No. 3.3e-145;
 Matches  750;  Conservative    0;  Mismatches   17;  Indels    3;  Gaps    3;

Qy         36 TGCCATTCATGCTGAACTCTGTCAACCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAG 95
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TGCCATTCATGCTGAACTCTGTCAACCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAG 60

Qy         96 TATCAGAACAGCTCTGGGAGATAAAGCATATGCCTGGGATACCAATGAAGAATACCTCTT 155
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TATCAGAACAGCTCTGGGAGATAAAGCATATGCCTGGGATACCAATGAAGAATACCTCTT 120

Qy        156 CAAAGCGATGGTAGCTTTCTCCATGAGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTC 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CAAAGCGATGGTAGCTTTCTCCATGAGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTC 180

Qy        216 CCATGTCCTACTTTGCAATGTAACCCAGAGGGTATCATTCTGGTTTGTGGTTACAGACCC 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCATGTCCTACTTTGCAATGTAACCCAGAGGGTATCATTCTGGTTTGTGGTTACAGACCC 240

Qy        276 TTCAAAAAATCACACCCTTCCTGCTGTTGAGGTGCAATCAGCCATAAGAATGAACAAGAA 335
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TTCAAAAAATCACACCCTTCCTGCTGTTGAGGTGCAATCAGCCATAAGAATGAACAAGAA 300

Qy        336 CCGGATCAACAATGCCTTCTTTCTAAATGACCAAACTCTGGAATTTTTAAAAATCCCTTC 395
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Db        301 CCGGATCAACAATGCCTTCTTTCTAAATGACCAAACTCTGGAATTTTTAAAAATCCCTTC 360

Qy        396 CACACTTGCACCACCCATGGACCCATCTGTGCCCATCTGGATTATTATATTTGGTGTGAT 455
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CACACTTGCACCACCCATGGACCCATCTGTGCCCATCTGGATTATTATATTTGGTGTGAT 420

Qy        456 ATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTATCAGGGATCTGGCAACGTAG 515
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTATCAGGGATCTGGCAACGTAG 480

Qy        516 AAGAAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGATAAGTGTGAAAACATGAT 575
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AAGAAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGATAAGTGTGAAAACATGAT 540

Qy        576 CACAATTGAAAATGGCATCCCCTCTGATCCCCTGGACATGAAGGG-GGGCATATTAATGA 634
              |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db        541 CACAATTGAAAATGGCATCCCCTCTGATCCCCTGGACATGAAGGGAGGGCATATTAATGA 600

Qy        635 TGCCTTCATGACAGAGGATGAGAGGCTC-ACCCCTCTCTGAAGGGCTGTTGTTCTGCTTC 693
              ||||||||||||||| |||||||||||| |||||||||||||||||||| | |||||
Db        601 TGCCTTCATGACAGACGATGAGAGGCTCAACCCCTCTCTGAAGGGCTGTGTTCTTGCTTT 660

Qy        694 CTCAAGAAATTAAACATTTGTTTCTGT-GTGACTGCTGAGCATCCTGAAATACCAAGAGC 752
              |||| |||||||||||||||||||||| ||||||  ||||||| ||||||||||||||||
Db        661 CTCAGGAAATTAAACATTTGTTTCTGTGGTGACTTGTGAGCATTCTGAAATACCAAGAGC 720

Qy        753 AGATCATATATTTTGTTTCACCATTCTTCTTTTGTAATAAATTTTGAATG 802
              ||||||||||||| |||    | ||||||||||||||||||||| | |||
Db        721 AGATCATATATTTGGTTCACCAATTCTTCTTTTGTAATAAATTTCGGATG 770
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RESULT 10
BG181765
LOCUS       BG181765                754 bp    mRNA    linear   EST 21-APR-2001
DEFINITION  RST618 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION   BG181765
VERSION     BG181765.1  GI:13703452
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 754)
  AUTHORS   Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
            Cain,S., Leventhal,C., Thornton,M., Ramachandran,R.,
            Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S.,
            Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K.,
            Offenbacher,J., Danzig,J. and Ducar,M.
  TITLE     Creation of genome-wide protein expression libraries using random
            activation of gene expression
  JOURNAL   Nat. Biotechnol. 19 (5), 440-445 (2001)
  MEDLINE   21227151
   PUBMED   11329013
COMMENT     Contact: Scott J. Cain
            Athersys, Inc.
            3201 Carnegie Ave, Cleveland, OH 44115, USA
            Tel: 216 431 9900
            Fax: 216 361 9596
            Email: scain@athersys.com
            High quality sequence stop: 548.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /cell_line="HT1080"
                     /clone_lib="Athersys RAGE Library"
                     /note="See 'Creation of Genome-wide Protein Expression
                     Libraries using Random Activation of Gene Expression',
                     Nature Biotechnology, in press. Note that even though the
                     cell type indicated is HT1080, since a random activation
                     method was used, these sequence tags are not necessarily
                     expressed in HT1080 under normal circumstances."
ORIGIN

  Query Match             52.3%;  Score 704.4;  DB 4;  Length 754;
  Best Local Similarity   97.7%;  Pred. No. 1.1e-144;
  Matches  725;  Conservative    0;  Mismatches   16;  Indels    1;  Gaps    1;

Qy        217 CATGTCCTACTTTGCAATGTAACCCAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCT 276
              | ||||||||||||  |||||||||| ||||||||||||||||||||||||||||||||
Db         11 CCTGTCCTACTTTTTCATGTAACCCACAGGGTATCATTCTGGTTTGTGGTTACAGACCCT 70

Qy        277 TCAAAAAATCACACCCTTCCTGCTGTTGAGGTGCAATCAGCCATAAGAATGAACAAGAAC 336
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         71 TCAAAAGATCACACCCTTCCTGCTGTTGAGGTGCAATCAGCCATAAGAATGAACAAGAAC 130

Qy        337 CGGATCAACAATGCCTTCTTTCTAAATGACCAAACTCTGGAATTTTTAAAAATCCCTTCC 396
              |||||||||||||||||||||||| || ||||||||||||||||||||||||||||||
Db        131 CGGATCAACAATGCCTTCTTTCTAAAAGATCAAACTCTGGAATTTTTAAAAATCCCTTCC 190

Qy        397 ACACTTGCACCACCCATGGACCCATCTGTGCCCATCTGGATTATTATATTTGGTGTGATA 456
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        191 ACACTTGCACCACCCATGGACCCATCTGTGCCCATCTGGATTATTATATTTGGTGTGATA 250

Qy        457 TTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTATCAGGGATCTGGCAACGTAGA 516
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 TTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTATCAGGGATCTGGCAACGTAGA 310

Qy        517 AGAAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGATAAGTGTGAAAACATGATC 576
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        311 AGAAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGATAAGTGAGAAAACATGATC 370

Qy        577 ACAATTGAAAATGGCATCCCCTCTGATCCCCTGGACATGAAGGG-GGGCATATTAATGAT 635
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        371 TCAATTGAAAATGGCATCCCCTCTGATCCCCTGGACATGAAGGGAGGGCATATTAATGAT 430

Qy        636 GCCTTCATGACAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCT 695
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        431 GCCTTCATGACAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCT 490

Qy        696 CAAGAAATTAAACATTTGTTTCTGTGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGA 755
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        491 CAAAAAATTAAACATTTGTTTCTGTGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGA 550

Qy        756 TCATATATTTTGTTTCACCATTCTTCTTTTGTAATAAATTTTGAATGTGCTTGAAAGTGA 815
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db        551 TCATATATTTTGTTTCACCATTCTTCTTTTGTAATAAATTTTGAATGTGCTTGACAGTGA 610

Qy        816 AAAGCAATCAATTATACCCACCAACACCACTGAAATCATAAGCTATTCACGACTCAAAAT 875
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        611 AAAGCAATCAATTATACCCACCAACACCACTGAAATCATAAGCTATTCACGACTCAAAAT 670

Qy        876 ATTCTAAAATATTTTTCTGACAGTATAGTGTATAAATGTGGTCATGTGGTATTTGTAGTT 935
              ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        671 ATTCTAAAATATTTTTCTGACAGTATAGTGTATAAATGTGGCCATGTGGTATTTGTAGTT 730

Qy        936 ATTGATTTAAGCATTTTTAGAA 957
              ||||||||||||||||||   ||
Db        731 ATTGATTTAAGCATTTTAGAAA 752


RESULT 11
BG400845
LOCUS       BG400845                792 bp    mRNA    linear   EST 12-MAR-2001
DEFINITION  602464068F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4592296 5',
            mRNA sequence.
ACCESSION   BG400845
VERSION     BG400845.1  GI:13294293
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 792)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
             cDNA Library Preparation: CLONTECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1330  row: g  column: 17
            High quality sequence stop: 784.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4592296"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_75"
                     /note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and
                     3' adaptors were used in cloning as follows: 5' adaptor
                     sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).  Average insert size 1.65
                     kb (range 0.5-4.0 kb). 15/15 colonies contained  inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech  Laboratories (Palo Alto,
                     CA). Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             51.6%;  Score 695.2;  DB 4;  Length 792;
  Best Local Similarity   98.0%;  Pred. No. 1.2e-142;
  Matches  747;  Conservative    0;  Mismatches    8;  Indels    7;  Gaps    4;

Qy          1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         26 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 85

Qy         61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         86 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 145

Qy        121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        146 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 205

Qy        181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        206 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 265

Qy        241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        266 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 325

Qy        301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        326 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 385

Qy        361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        386 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 445

Qy        421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        446 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 505

Qy        481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        506 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 565

Qy        541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        566 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 625

Qy        601 GATCCCCTGGACATGAAGGG---GGGCATATTAATGATGCCTTCA-TGACAGAGGATGAG 656
              ||||||||||||||||||||   || ||||||||||||||||||| ||||||||||||||
Db        626 GATCCCCTGGACATGAAGGGAGCGGCCATATTAATGATGCCTTCATTGACAGAGGATGAG 685

Qy        657 AGGCTCACCCCTCTCTGAAGGGCTGTTGTTCTGC-TTCCTCAAGAAATT--AAACATTTG 713
              ||||||||||||||||||||||||||||||||||||||||||||||||  || ||||||
Db        686 AGGCTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTTCCTCAAGAAATTTGAACCATTTG 745

Qy        714 TTTCTGTGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGA 755
              |||||||||||||||||||| ||| ||   | ||||||||
Db        746 TTTCTGTGTGACTGCTGAGCATTCTGGAAATTCCAGAGCAGA 787


RESULT 12
BG400319
LOCUS       BG400319                791 bp    mRNA    linear   EST 12-MAR-2001
DEFINITION  602464526F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4592575 5',
            mRNA sequence.
ACCESSION   BG400319
VERSION     BG400319.1  GI:13293767
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 791)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
             cDNA Library Preparation: CLONTECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1331  row: c  column: 08
            High quality sequence stop: 711.
FEATURES             Location/Qualifiers
     source          1. .791
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
```

/db_xref="taxon:9606"
/clone="IMAGE:4592575"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_75"
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 50.2%; Score 675.4; DB 4; Length 791;
Best Local Similarity 97.7%; Pred. No. 2.8e-138;
Matches 749; Conservative 0; Mismatches 11; Indels 7; Gaps 6;

```
Qy          1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         25 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 84

Qy         61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 144

Qy        121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 204

Qy        181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 264

Qy        241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 324

Qy        301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 384

Qy        361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 444

Qy        421 TCTGTGCCCATCTGGATTATTATATTT-GGTGTGATATTTTGCATCATCATAGTTGCAAT 479
              ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        445 TCTGTGCCCATCTGGATTATTATATTTCGGTGTGATATTTTGCATCATCATAGTTGCAAT 504

Qy        480 TGCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGA 539
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        505 TGCACTACTGA-TTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGA 563

Qy        540 AGTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTC 599
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 AGTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTC 623

Qy        600 TGATCCCCTGGACATGAAGGG-GGGCATATTAA-TGATGCCTTCATGACAGAGGATGAGA 657
              |||||||||||||||||||| |||||||||||| ||||||||||||||||||||||||||
Db        624 TGATCCCCTGGACATGAAGGGAGGGCATATTAAGTGATGCCTTCATGACAGAGGATGAGA 683

Qy        658 GGCTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCC--TCAAGAAATTAAACATTTGTT 715
              |||||| |||||||||||||||||||||||  ||  | |    |||||||||||||||||||
Db        684 GGCTCAACCCTCTCTGAAGGGCTGTTGTCATGGCTTCGTCAAAGAAATTAAACATTTGTT 743

Qy        716 TCTGTGTGACTGCTGA-GCATCCTGAAATACCAAGAGCAGATCATAT 761
              |||||||| |||||| |||||||||||| ||||||||||||||||
Db        744 ACTGTGTGATTGCTGAGGCATCCTGAAATTCCAAGAGCAGATCATAT 790
```

RESULT 13
BM811234
LOCUS BM811234 1081 bp mRNA linear EST 05-MAR-2002
DEFINITION AGENCOURT_6489717 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5723829 5', mRNA sequence.
ACCESSION BM811234
VERSION BM811234.1 GI:19128057
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1081)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM12712 row: b column: 22
High quality sequence stop: 721.

FEATURES Location/Qualifiers
source 1. .1081
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5723829"
/lab_host="DH10B"
/clone_lib="NIH_MGC_125"
/note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6; Site_1: EcoRV (destroyed); Site_2: NotI; RNA source pool of three ovaries, from females ranging in age from 38 to 49 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 2.1 kb, insert size range 1-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 036."

ORIGIN

Query Match 49.5%; Score 665.8; DB 4; Length 1081;
Best Local Similarity 96.2%; Pred. No. 3.8e-136;
Matches 715; Conservative 0; Mismatches 22; Indels 6; Gaps 3;

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Qy         61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 CGAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 224

Qy        121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 284

Qy        181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 344

Qy        241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 404

Qy        301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 464

Qy        361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 524
```

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Qy        421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 584

Qy        481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 644

Qy        541 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCT 704

Qy        601 GATCCCCTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 659
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        705 GATCCCCTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGG 764

Qy        660 CTCACCCC--TCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTC 717
              ||||||||  ||||||||||||||||||||||  ||||||||||||||||||||||||||
Db        765 CTCACCCCCTCTCTGAAAGGGCTGTTGTTCTGCTTCCCTCCAGAATTAAACATTTGTTTC 824

Qy        718 TGTGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTT---CACC 774
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   ||  ||
Db        825 TGTGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGGTTTCACCCA 884

Qy        775 ATTCTTCTTTTGTAATAAATTTT 797
              |  | ||||| |||||| |||
Db        885 TTCTTCCTTTTGGAATAAAATTT 907
```

RESULT 14
BG427247

```
LOCUS       BG427247                855 bp    mRNA    linear   EST 14-MAR-2001
DEFINITION  602494304F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4608048 5',
            mRNA sequence.
ACCESSION   BG427247
VERSION     BG427247.1  GI:13333753
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 855)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
             cDNA Library Preparation: CLONTECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1349  row: h  column: 01
            High quality sequence stop: 735.
FEATURES             Location/Qualifiers
     source          1. .855
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4608048"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_75"
                     /note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and
                     3' adaptors were used in cloning as follows: 5' adaptor
                     sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).  Average insert size 1.65
                     kb (range 0.5-4.0 kb). 15/15 colonies contained  inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech  Laboratories (Palo Alto,
                     CA). Note: this is a NIH_MGC Library."
ORIGIN
```

Query Match 49.2%; Score 661.6; DB 4; Length 855;
Best Local Similarity 95.2%; Pred. No. 3.1e-135;
Matches 769; Conservative 0; Mismatches 29; Indels 10; Gaps 8;

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Qy          1 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         27 GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAA 86

Qy         61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 146

Qy        121 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 GCATATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 206

Qy        181 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 AGAAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC 266

Qy        241 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 CAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCT 326

Qy        301 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 GTTGAGGTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTA 386

Qy        361 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 AATGACCAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCA 446

Qy        421 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 TCTGTGCCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 506

Qy        481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAAC-AAAGAACCATCTGA 539
              ||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db        507 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAAGAACCATCTGA 566

Qy        540 AGTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTC 599
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        567 AGTGGATGACGCTGAAGAT-AGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTC 625

Qy        600 TGATCCCCTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGAC-AGAGGATGAGA 657
              |||||||||||||||||||| ||||||||||||||||||||||||| |||||||||||
Db        626 TGATCCCCTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGACAAGAGGATGAGA 685

Qy        658 GGCTCA-CCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTAAACATTTGTTT 716
              |||||| |||||||||||||||||||||||||||||||||||||||    | |  ||
Db        686 GGCTCACCCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCTCAAGAAATTA---ACATTGTT 742

Qy        717 CTGTGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGATCATATATTTTGTTTCACCAT 776
              |||||||||| |||||||| | ||| ||||||||| ||| ||||||||  || |    |
Db        743 CTGTGTGACTG-TGAGCATCTTTAAAAACCAAGAGC-GATTATATATTTGTTTCCCATCT 800

Qy        777 TCTTCTTTTGTAATAAATTTTGAATGTG 804
              |||| |  |    | |  |   || |||
Db        801 TCTTGTAATACTTTGATGTGCTAAAGTG 828
```

RESULT 15
AY399636

```
LOCUS       AY399636                669 bp    DNA     linear   GSS 12-DEC-2003
DEFINITION  Homo sapiens HCM0290 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY399636
VERSION     AY399636.1  GI:39755625
KEYWORDS    GSS.
```

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SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 669)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     gene            <1. .>669
                     /locus_tag="HCM0290"
ORIGIN

  Query Match             48.8%;  Score 657;  DB 9;  Length 669;
  Best Local Similarity   99.9%;  Pred. No. 3.2e-134;
  Matches  668;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          7 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 66
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60

Qy         67 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120

Qy        127 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180

Qy        187 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 240

Qy        247 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 300

Qy        307 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360

Qy        367 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420

Qy        427 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480

Qy        487 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540

Qy        547 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 600

Qy        607 CTGGACATGAAGGG-GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGGCTCACC 665
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGGCTCACC 660

Qy        666 CCTCTCTGA 674
              |||||||||
Db        661 CCTCTCTGA 669


Search completed: February 24, 2005, 22:26:33
Job time : 4435.67 secs
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 25, 2005, 00:51:59 ; Search time 3038 Seconds
(without alignments)
3381.338 Million cell updates/sec

Title: US-09-989-724-387
Perfect score: 1102
Sequence: 1 MLWLLFFLVTAIHAELCQPG.....ENGIPSDPLDMKGGILMMPS 212

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US09989724/runat_22022005_164320_3281/app_query.fasta_1.391
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=1500
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09989724_@CGN_1_1_5600_@runat_22022005_164320_3281 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1102	100.0	1346	6	AR252633	AR252633 Sequence
2	1102	100.0	1346	6	AR528692	AR528692 Sequence
3	1102	100.0	1346	6	AX403499	AX403499 Sequence
4	1102	100.0	1346	6	AX464348	AX464348 Sequence
5	1102	100.0	1346	9	AY359060	AY359060 Homo sapi
6	1089	98.8	666	6	AX083382	AX083382 Sequence
7	1089	98.8	1345	9	AF229179	AF229179 Homo sapi
8	1089	98.8	1347	6	AX083392	AX083392 Sequence
9	1089	98.8	1377	9	BC050606	BC050606 Homo sapi
10	1089	98.8	1440	9	BC015099	BC015099 Homo sapi
11	1089	98.8	1605	9	BC014317	BC014317 Homo sapi
12	1086	98.5	1401	6	BD083420	BD083420 Secreted
13	1082	98.2	1447	6	BD205644	BD205644 97 human
14	1064	96.6	848	6	AR177334	AR177334 Sequence
15	1064	96.6	848	6	BD139270	BD139270 Extended
16	1064	96.6	848	6	BD203799	BD203799 5'EST and
17	1064	96.6	848	6	BD247957	BD247957 5' ESTs f
18	1064	96.6	848	6	CQ771919	CQ771919 Sequence
19	1064	96.6	848	6	AR340701	AR340701 Sequence
20	1064	96.6	848	6	AR412373	AR412373 Sequence
21	1064	96.6	848	6	AX884142	AX884142 Sequence
22	1064	96.6	848	6	AX939008	AX939008 Sequence
23	1064	96.6	848	6	AX968599	AX968599 Sequence
24	1064	96.6	848	6	AX969202	AX969202 Sequence
25	1064	96.6	848	6	BD023757	BD023757 Sequence
26	1064	96.6	848	6	BD073618	BD073618 5'EST of
27	1064	96.6	848	6	BD075896	BD075896 5' EST of
28	1064	96.6	848	6	BD076074	BD076074 5' EST of
29	1064	96.6	848	6	BD076775	BD076775 5' EST of
30	1064	96.6	848	6	BD077436	BD077436 5'EST of
31	1064	96.6	848	6	BD077737	BD077737 5'EST of
32	1064	96.6	848	6	BD085880	BD085880 Elongatio
33	1064	96.6	848	6	BD107926	BD107926 EST and e
34	1064	96.6	848	6	BD131408	BD131408 cDNA enco
35	1062	96.4	1356	6	BD135300	BD135300 110 human
36	938	85.1	1266	10	BC078838	BC078838 Rattus no
37	936	84.9	545	6	CQ714932	CQ714932 Sequence
38	931	84.5	1222	10	BC049912	BC049912 Mus muscu
39	931	84.5	1262	10	AF178085	AF178085 Mus muscu
40	924	83.8	1181	10	AF178086	AF178086 Rattus no
41	694	63.0	439	6	AX939025	AX939025 Sequence
42	694	63.0	439	6	BD077452	BD077452 5'EST of
43	674	61.2	462	6	BD058424	BD058424 Secreted
44	488	44.3	1131	5	BC058203	BC058203 Xenopus l
45	463	42.0	355	6	CQ458858	CQ458858 Sequence
46	405.5	36.8	1877	5	BC065470	BC065470 Danio rer
47	387.5	35.2	1879	5	BC053284	BC053284 Danio rer
48	376	34.1	2415	6	AR135178	AR135178 Sequence
49	376	34.1	2415	6	BD274685	BD274685 Angiotens
50	376	34.1	2415	6	E43987	E43987 ACE-analogo
51	376	34.1	2415	6	AR382342	AR382342 Sequence
52	376	34.1	2415	6	AX418984	AX418984 Sequence
53	376	34.1	2418	6	E39033	E39033 MPROT15 pol
54	376	34.1	2418	9	AY623811	AY623811 Homo sapi
55	376	34.1	2599	6	E43988	E43988 ACE-analogo
56	376	34.1	3325	9	AF291820	AF291820 Homo sapi
57	376	34.1	3334	6	AX047758	AX047758 Sequence
58	376	34.1	3339	9	BC048094	BC048094 Homo sapi
59	376	34.1	3341	9	HSM800880	AL110224 Homo sapi
60	376	34.1	3348	9	BC039902	BC039902 Homo sapi
61	376	34.1	3375	9	BC059378	BC059378 Homo sapi
62	376	34.1	3396	6	AR135177	AR135177 Sequence
63	376	34.1	3396	6	BD274684	BD274684 Angiotens
64	376	34.1	3396	6	AR353104	AR353104 Sequence
65	376	34.1	3396	6	AR382341	AR382341 Sequence
66	376	34.1	3396	6	AX418982	AX418982 Sequence
67	376	34.1	3396	6	AX431513	AX431513 Sequence
68	376	34.1	3405	6	CQ754222	CQ754222 Sequence
69	376	34.1	3405	9	AF241254	AF241254 Homo sapi
70	373	33.8	2599	9	AB046569	AB046569 Homo sapi
71	369	33.5	3732	6	AR528488	AR528488 Sequence
72	369	33.5	3732	6	AX463938	AX463938 Sequence
73	369	33.5	3732	9	AY358714	AY358714 Homo sapi
74	361	32.8	2638	6	AX047762	AX047762 Sequence
75	361	32.8	2638	6	AX047765	AX047765 Sequence
76	361	32.8	2739	6	CQ754224	CQ754224 Sequence
77	361	32.8	2739	10	BC026801	BC026801 Mus muscu

	78	359	32.6	2920	6	AR353103 AR353103 Sequence
	79	358	32.5	1993	10	AB053182 AB053182 Mus muscu
	80	357	32.4	2760	10	AB053181 AB053181 Mus muscu
c	81	340	30.9	159446	9	AC003669 AC003669 Homo sapi
	82	340	30.9	165730	2	AC061988 AC061988 Homo sapi
c	83	335	30.4	213	6	CQ111904 CQ111904 Sequence
c	84	335	30.4	213	6	CQ150704 CQ150704 Sequence
c	85	335	30.4	213	6	CQ184910 CQ184910 Sequence
c	86	335	30.4	213	6	CQ234037 CQ234037 Sequence
c	87	335	30.4	213	6	CQ271795 CQ271795 Sequence
c	88	335	30.4	213	6	CQ309364 CQ309364 Sequence
c	89	335	30.4	213	6	CQ346012 CQ346012 Sequence
c	90	324	29.4	464	6	CQ098839 CQ098839 Sequence
c	91	324	29.4	464	6	CQ137751 CQ137751 Sequence
c	92	324	29.4	464	6	CQ175049 CQ175049 Sequence
c	93	324	29.4	464	6	CQ221115 CQ221115 Sequence
c	94	324	29.4	464	6	CQ259275 CQ259275 Sequence
c	95	324	29.4	464	6	CQ296932 CQ296932 Sequence
c	96	324	29.4	464	6	CQ333335 CQ333335 Sequence
	97	315	28.6	2134	6	CQ714933 CQ714933 Sequence
c	98	302	27.4	225558	2	AC103066 AC103066 Rattus no
	99	302	27.4	226820	2	AC118872 AC118872 Rattus no
	100	289	26.2	1119	5	BX935959 BX935959 Gallus ga
	101	289	26.2	112893	10	AL732294 AL732294 Mouse DNA
	102	289	26.2	234105	10	AC091606 AC091606 Mus Muscu
	103	281	25.5	862	6	BD270445 BD270445 Genes ass
	104	278	25.2	2415	6	AX047760 AX047760 Sequence
	105	262	23.8	2262	6	E39034 E39034 MPROT15 pol
	106	259	23.5	2415	6	AX047764 AX047764 Sequence
	107	238	21.6	3474	6	AX576256 AX576256 Sequence
c	108	233.5	21.2	2350	6	AR263862 AR263862 Sequence
	109	232	21.1	1013	9	AK026461 AK026461 Homo sapi
	110	207.5	18.8	41572	9	AY217547 AY217547 Homo sapi
c	111	207.5	18.8	194492	9	AC097625 AC097625 Homo sapi
	112	187	17.0	192676	10	AL671706 AL671706 Mouse DNA
	113	179	16.2	1659	3	AK113405 AK113405 Ciona int
	114	164	14.9	1155	5	BX934887 BX934887 Gallus ga
	115	125.5	11.4	758	5	BX931879 BX931879 Gallus ga
	116	118.5	10.8	109975	9	AC112497 AC112497 Homo sapi
c	117	111	10.1	144046	2	AC068334 AC068334 Homo sapi
c	118	111	10.1	166016	9	AL591378 AL591378 Human DNA
	119	106.5	9.7	3666	6	AX664156 AX664156 Sequence
	120	105	9.5	253354	2	AC096809 AC096809 Rattus no
	121	104	9.4	164038	2	AC150011 AC150011 Callithri
c	122	103	9.3	39233	9	AC005626 AC005626 Homo sapi
	123	102	9.3	60	6	CQ539130 CQ539130 Sequence
	124	100	9.1	110000	2	PFMAL8P1_09 Continuation (10 o
c	125	100	9.1	146175	8	AC123527 AC123527 Oryza sat
	126	99	9.0	82453	9	AC004558 AC004558 Homo sapi
c	127	99	9.0	110000	2	AC114055_4 Continuation (5 of
c	128	99	9.0	266403	2	AC114693 AC114693 Rattus no
	129	98	8.9	531	6	CQ411925 CQ411925 Sequence
	130	98	8.9	144239	9	AC004015 AC004015 Homo sapi
	131	97.5	8.8	3546	3	GCINTALPH X97283 G.cydonium
	132	96.5	8.8	3039	10	AF041409 AF041409 Mus muscu
	133	95.5	8.7	5515	5	GGA238216 AJ238216 Gallus ga
	134	94	8.5	34337	6	AX398707 AX398707 Sequence
	135	94	8.5	75425	2	AC135034 AC135034 Homo sapi
c	136	94	8.5	166256	9	AC018922 AC018922 Homo sapi
	137	94	8.5	167071	9	AC128649 AC128649 Homo sapi
	138	94	8.5	184193	2	AC109720 AC109720 Rattus no
c	139	94	8.5	222083	2	AC118432 AC118432 Rattus no
c	140	94	8.5	230449	2	AC105504 AC105504 Rattus no
c	141	94	8.5	252988	2	AC105511 AC105511 Rattus no
	142	93.5	8.5	2790	6	CQ611604 CQ611604 Sequence
	143	93	8.4	221179	2	AC099392 AC099392 Rattus no
	144	93	8.4	274148	2	AC132554 AC132554 Rattus no
	145	92.5	8.4	5070	3	AF012531 AF012531 Lymnaea s
	146	92.5	8.4	229752	2	AC127045 AC127045 Rattus no
c	147	92	8.3	93010	10	AL627386 AL627386 Mouse DNA
c	148	92	8.3	137271	2	AC102823 AC102823 Mus muscu
	149	92	8.3	159056	10	AL845368 AL845368 Mouse DNA
c	150	92	8.3	188989	10	AC074224 AC074224 Mus muscu
	151	92	8.3	189994	2	AC109209 AC109209 Mus muscu
	152	91.5	8.3	3564	6	AX379445 AX379445 Sequence
	153	91.5	8.3	4163	10	AY124460 AY124460 Mus muscu
	154	91.5	8.3	4858	6	AX379444 AX379444 Sequence
	155	91.5	8.3	4930	10	BC058716 BC058716 Mus muscu
	156	91	8.3	5149	6	CQ579236 CQ579236 Sequence
c	157	91	8.3	6271	2	AC013078 AC013078 Drosophil
c	158	91	8.3	9783	1	U39699 U39699 Mycoplasma
	159	91	8.3	110000	3	AE003426_1 Continuation (2 of
c	160	91	8.3	110000	6	AR300198_2 Continuation (3 of
	161	91	8.3	179069	2	AC104144 AC104144 Drosophil
c	162	91	8.3	182387	3	AC116543 AC116543 Drosophil
	163	91	8.3	262050	1	AP000985 AP000985 Sulfolobu
c	164	90.5	8.2	163642	9	AC022748 AC022748 Homo sapi
	165	90	8.2	2812	10	MMCAD8 X95600 M.musculus
	166	90	8.2	3126	10	AB010436 AB010436 Rattus ra
	167	90	8.2	3136	6	I34425 I34425 Sequence 41
	168	90	8.2	3136	6	I55092 I55092 Sequence 41
	169	90	8.2	3552	10	BC057581 BC057581 Mus muscu
	170	90	8.2	135940	2	AC119406 AC119406 Trypanoso
	171	90	8.2	219517	2	AC098152 AC098152 Rattus no
	172	90	8.2	234549	2	AC105497 AC105497 Rattus no
	173	89.5	8.1	483	10	AF148797 AF148797 Rattus no
	174	89.5	8.1	2545	6	CQ824165 CQ824165 Sequence
	175	89.5	8.1	2545	9	HUMCA8A L34060 Homo sapien
	176	89.5	8.1	2550	6	I34431 I34431 Sequence 53
	177	89.5	8.1	2550	6	I46829 I46829 Sequence 47
	178	89.5	8.1	2550	6	I55098 I55098 Sequence 53
	179	89.5	8.1	3146	6	AR338786 AR338786 Sequence
	180	89.5	8.1	3150	6	AX332281 AX332281 Sequence
	181	89.5	8.1	3150	6	AX333742 AX333742 Sequence
	182	89.5	8.1	3150	6	AX337415 AX337415 Sequence
	183	89.5	8.1	3150	9	HUMINTEG8A L36531 Homo sapien
	184	89.5	8.1	3868	6	AX377990 AX377990 Sequence
	185	89.5	8.1	6868	3	AF056940 AF056940 Drosophil
c	186	89.5	8.1	136119	9	HS1028D15 AL121886 Human DNA
c	187	89.5	8.1	198070	2	BX649326 BX649326 Danio rer
	188	89.5	8.1	207701	2	BX545856 BX545856 Danio rer
	189	89	8.1	2317	6	CQ719194 CQ719194 Sequence
	190	89	8.1	2742	9	AB035305 AB035305 Homo sapi
	191	89	8.1	2929	6	AX933856 AX933856 Sequence
	192	89	8.1	3502	9	AK124734 AK124734 Homo sapi
	193	89	8.1	4558	3	AF177914 AF177914 Strongylo
	194	89	8.1	110000	1	BX908798_21 Continuation (22 o
c	195	89	8.1	154244	9	AL360231 AL360231 Human DNA
	196	89	8.1	171967	2	AC102710 AC102710 Mus muscu
c	197	89	8.1	212008	2	AC093271 AC093271 Homo sapi
	198	88.5	8.0	2897	14	AB026929 AB026929 TTV-like
	199	88.5	8.0	36056	3	DMC163A10 AL035436 Drosophil
	200	88.5	8.0	158294	2	AC116789 AC116789 Mus muscu
	201	88.5	8.0	169781	10	AF336378 AF336378 Mus muscu
	202	88.5	8.0	188287	9	HS32B1 AL023693 Human DNA
c	203	88.5	8.0	204437	10	AC117678 AC117678 Mus muscu
c	204	88.5	8.0	273740	2	AC132066 AC132066 Rattus no
	205	88	8.0	1177	10	MUSCDA44A M27129 Mouse CD44
	206	88	8.0	1183	10	MUSCDA44B M27130 Mouse CD44
	207	88	8.0	1208	10	MUSPGP1A J05163 Mouse phosp
	208	88	8.0	1337	10	MUSPGP1 M30655 Mouse phago
	209	88	8.0	1418	10	MMPGP1M1M X66081 M.musculus
	210	88	8.0	1520	10	MMPGP1M2M X66082 M.musculus
	211	88	8.0	1766	10	MMPGP1M3M X66083 M.musculus
	212	88	8.0	1997	10	MMPGP1M4M X66084 M.musculus
	213	88	8.0	2613	10	MMU251594 AJ251594 Mus muscu
	214	88	8.0	2799	10	BC005676 BC005676 Mus muscu
	215	88	8.0	3518	10	BC051388 BC051388 Mus muscu
	216	88	8.0	110000	3	AC116984_1 Continuation (2 of
c	217	88	8.0	195863	2	CR847978 CR847978 Danio rer
c	218	88	8.0	200340	9	AC009997 AC009997 Homo sapi
	219	87.5	7.9	2908	6	CQ579237 CQ579237 Sequence
	220	87.5	7.9	117409	2	AC138141 AC138141 Homo sapi
	221	87.5	7.9	128891	9	AF130866 AF130866 Homo sapi
c	222	87.5	7.9	147788	2	AC015840 AC015840 Homo sapi
	223	87.5	7.9	152309	9	AC138185 AC138185 Homo sapi

224	87.5	7.9	160612	9	AP005856	AP005856 Homo sapi
225	87.5	7.9	161238	9	AP003127	AP003127 Homo sapi
226	87.5	7.9	168594	9	AP003970	AP003970 Homo sapi
c 227	87.5	7.9	178929	9	AL359252	AL359252 Human DNA
228	87.5	7.9	181827	2	AC022942	AC022942 Homo sapi
229	87.5	7.9	186812	2	AC023089	AC023089 Homo sapi
c 230	87.5	7.9	192657	1	AP005377	AP005377 Thermosyn
231	87.5	7.9	215789	2	AC103449	AC103449 Rattus no
c 232	87	7.9	847	11	BV048781	BV048781 S212P6020
233	87	7.9	1089	10	CRUCD44	M33827 Hamster hya
234	87	7.9	4129	1	AB098080	AB098080 Paenibaci
235	87	7.9	4631	6	BD261713	BD261713 12 human
236	87	7.9	184457	1	AF079317	AF079317 Sphingomo
237	87	7.9	196408	10	AC142114	AC142114 Mus muscu
c 238	87	7.9	200370	9	AC104035	AC104035 Homo sapi
c 239	87	7.9	202000	1	AP000058	AP000058 Aeropyrum
c 240	87	7.9	250519	2	AC094894	AC094894 Rattus no
241	87	7.9	257860	2	AC127719	AC127719 Rattus no
c 242	86.5	7.8	2147	10	BC010299	BC010299 Mus muscu
243	86.5	7.8	3295	3	AF196553	AF196553 Drosophil
244	86.5	7.8	3521	3	DME289882	AJ289882 Drosophil
c 245	86.5	7.8	11067	1	AE012888	AE012888 Chlorobiu
246	86.5	7.8	15894	14	AB012948	AB012948 Measles v
247	86.5	7.8	15894	14	AB012949	AB012949 Measles v
c 248	86.5	7.8	110000	2	AC151852_1	Continuation (2 of
c 249	86.5	7.8	110000	8	CR382139_16	Continuation (17 o
c 250	86.5	7.8	114576	9	AC074397	AC074397 Homo sapi
c 251	86.5	7.8	154324	2	AC122552	AC122552 Mus muscu
c 252	86.5	7.8	157904	2	AC025150	AC025150 Homo sapi
253	86.5	7.8	166197	10	AC132343	AC132343 Mus muscu
254	86.5	7.8	167691	2	AC103349	AC103349 Mus muscu
255	86.5	7.8	183188	2	AC147927	AC147927 Ovis arie
c 256	86.5	7.8	191635	10	BX119996	BX119996 Mouse DNA
257	86.5	7.8	218800	2	AC094410	AC094410 Rattus no
c 258	86.5	7.8	230116	10	AL732620	AL732620 Mouse DNA
c 259	86.5	7.8	244637	2	AC110473	AC110473 Rattus no
260	86.5	7.8	274710	2	AC131884	AC131884 Rattus no
c 261	86.5	7.8	303249	1	AP001515	AP001515 Bacillus
262	86	7.8	1383	10	RNU52179	U52179 Rattus norv
263	86	7.8	1384	10	RNU46957	U46957 Rattus norv
264	86	7.8	1384	10	AF065147	AF065147 Rattus no
265	86	7.8	1690	1	AF061802	AF061802 Pseudomon
266	86	7.8	1927	10	MAU10881	U10881 Mesocricetu
267	86	7.8	1932	10	BC061531	BC061531 Rattus no
268	86	7.8	2747	6	AX401912	AX401912 Sequence
269	86	7.8	2747	10	RATCD44A	M61875 Rattus norv
270	86	7.8	2962	10	MAU10880	U10880 Mesocricetu
271	86	7.8	3164	10	RATMETAA	M61874 Rattus norv
272	86	7.8	3207	6	I19505	I19505 Sequence 1
273	86	7.8	3580	10	AF135439	AF135439 Mus muscu
274	86	7.8	4038	10	RNU96138	U96138 Rattus norv
c 275	86	7.8	134201	2	AC114976	AC114976 Homo sapi
276	86	7.8	141048	2	AC141679	AC141679 Apis mell
c 277	86	7.8	150902	2	AC018391	AC018391 Homo sapi
c 278	86	7.8	186535	9	AC022272	AC022272 Homo sapi
c 279	86	7.8	210545	5	BX004772	BX004772 Zebrafish
280	86	7.8	253599	2	AC117827	AC117827 Mus muscu
281	86	7.8	259957	2	AC141698	AC141698 Apis mell
c 282	86	7.8	266544	3	AC116956	AC116956 Dictyoste
283	85.5	7.8	3212	9	BC038232	BC038232 Homo sapi
284	85.5	7.8	3447	6	AX366689	AX366689 Sequence
285	85.5	7.8	3557	6	BD160631	BD160631 Primer fo
286	85.5	7.8	3557	6	CQ834028	CQ834028 Sequence
287	85.5	7.8	3557	6	AX302537	AX302537 Sequence
288	85.5	7.8	3557	6	AX366690	AX366690 Sequence
289	85.5	7.8	3557	6	AX366696	AX366696 Sequence
290	85.5	7.8	3557	6	AX883959	AX883959 Sequence
291	85.5	7.8	3557	9	AK024365	AK024365 Homo sapi
292	85.5	7.8	6395	9	AB046769	AB046769 Homo sapi
c 293	85.5	7.8	8186	6	AX344683	AX344683 Sequence
294	85.5	7.8	15894	14	AB016162	AB016162 Measles v
295	85.5	7.8	15894	14	AB032167	AB032167 Measles v
c 296	85.5	7.8	91274	8	ATF18N11	AL132953 Arabidops
c 297	85.5	7.8	110980	8	ATF9K21	AL138657 Arabidops
c 298	85.5	7.8	113951	9	AC007552	AC007552 Homo sapi
299	85.5	7.8	191378	2	AC129960	AC129960 Bos tauru
c 300	85.5	7.8	239945	2	AC094050	AC094050 Rattus no
301	85.5	7.8	248254	2	AC133448	AC133448 Rattus no
302	85	7.7	4756	6	AR380916	AR380916 Sequence
303	85	7.7	4756	6	AX817986	AX817986 Sequence
304	85	7.7	4756	9	HUMPTPS	D37781 Human mRNA
305	85	7.7	24174	3	CBRG35I24	AC084558 Caenorhab
c 306	85	7.7	58498	9	HS410B11	Z86063 Human DNA s
c 307	85	7.7	110000	8	CR380951_5	Continuation (6 of
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309	85	7.7	152802	9	AC018923	AC018923 Homo sapi
c 310	85	7.7	152895	2	AC139973	AC139973 Rattus no
311	85	7.7	164846	2	AC107727	AC107727 Mus muscu
c 312	85	7.7	183051	2	AC120130	AC120130 Mus muscu
c 313	85	7.7	190371	2	AC116830	AC116830 Mus muscu
c 314	85	7.7	192141	2	AC019004	AC019004 Homo sapi
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316	85	7.7	255661	2	AC106084	AC106084 Rattus no
317	85	7.7	273225	2	AC129440	AC129440 Rattus no
318	84.5	7.7	2097	9	IRO322987	AL359064 Homo sapi
319	84.5	7.7	2907	1	BACFLG	M54965 Bacillus su
320	84.5	7.7	3057	9	AF111799	AF111799 Homo sapi
321	84.5	7.7	3564	6	AX379427	AX379427 Sequence
322	84.5	7.7	3601	5	XLU92006	U92006 Xenopus lae
323	84.5	7.7	3983	6	CQ721401	CQ721401 Sequence
324	84.5	7.7	3983	9	AF137378	AF137378 Homo sapi
325	84.5	7.7	5042	6	AX379426	AX379426 Sequence
326	84.5	7.7	38306	6	CQ812178	CQ812178 Sequence
327	84.5	7.7	38306	6	CQ818355	CQ818355 Sequence
328	84.5	7.7	80142	9	AL645465	AL645465 Human DNA
329	84.5	7.7	107947	8	NCB7N14	AL669986 Neurospor
330	84.5	7.7	110000	2	AC117024_3	Continuation (4 of
331	84.5	7.7	157138	2	AC144366	AC144366 Papio anu
c 332	84.5	7.7	165764	2	AC022527	AC022527 Homo sapi
333	84.5	7.7	175191	9	AC010251	AC010251 Homo sapi
c 334	84.5	7.7	198097	10	AC146602	AC146602 Mus muscu
335	84.5	7.7	199906	10	AC098718	AC098718 Mus muscu
336	84.5	7.7	204263	1	BSUB0009	Z99112 Bacillus su
c 337	84.5	7.7	204350	10	AC125056	AC125056 Mus muscu
338	84.5	7.7	207922	10	AL450399	AL450399 Mouse DNA
339	84.5	7.7	211772	2	AC112148	AC112148 Mus muscu
c 340	84.5	7.7	212564	10	AC148983	AC148983 Mus muscu
341	84.5	7.7	216325	10	AC112260	AC112260 Mus muscu
342	84.5	7.7	248297	2	AC094564	AC094564 Rattus no
c 343	84.5	7.7	255790	2	AC117112	AC117112 Rattus no
c 344	84.5	7.7	257934	2	AC111300	AC111300 Rattus no
345	84.5	7.7	258486	2	AC113677	AC113677 Rattus no
c 346	84.5	7.7	290573	2	AC110362	AC110362 Rattus no
c 347	84.5	7.7	311321	1	NMA3Z2491	AL162754 Neisseria
348	84.5	7.7	345730	1	BX957219	BX957219 Methanoco
c 349	84	7.6	2446	3	AB189721	AB189721 Plasmodiu
350	84	7.6	11145	1	AE010606	AE010606 Fusobacte
c 351	84	7.6	60016	2	AC126381	AC126381 Homo sapi
352	84	7.6	104939	9	AL590413	AL590413 Human DNA
353	84	7.6	110000	2	AC151843_2	Continuation (3 of
c 354	84	7.6	110000	2	AL732358_0	AL732358 Homo sapi
c 355	84	7.6	113880	3	PFMAL3P4	AL008970 Plasmodiu
c 356	84	7.6	161797	9	AP005209	AP005209 Homo sapi
357	84	7.6	171158	2	AC023201	AC023201 Homo sapi
358	84	7.6	173657	2	AP001014	AP001014 Homo sapi
c 359	84	7.6	174409	2	AC010788	AC010788 Homo sapi
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c 363	84	7.6	191206	10	AC124573	AC124573 Mus muscu
c 364	84	7.6	217342	2	AC119700	AC119700 Rattus no
365	84	7.6	237317	2	AC097420	AC097420 Rattus no
c 366	84	7.6	271454	2	AC112098	AC112098 Rattus no
367	84	7.6	300150	1	AP004598	AP004598 Oceanobac
c 368	84	7.6	302836	1	AE017253	AE017253 Treponema
369	84	7.6	314415	2	AC106697	AC106697 Rattus no

	370	84	7.6	340750	1	BX294135
	371	83.5	7.6	720	8	CNS01ALC
	372	83.5	7.6	1335	8	BT015858
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	374	83.5	7.6	3529	5	GGINTA8
	375	83.5	7.6	4284	10	AB062913
	376	83.5	7.6	5117	6	AR109903
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	386	83.5	7.6	123454	9	HSBC17A99
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	389	83.5	7.6	157043	2	AC013692
	390	83.5	7.6	170397	2	CR352292
c	391	83.5	7.6	178035	2	AC068680
	392	83.5	7.6	182205	2	BX901930
	393	83.5	7.6	182375	10	AL627089
	394	83.5	7.6	183088	9	AC007600
c	395	83.5	7.6	191906	10	AC132304
c	396	83.5	7.6	194018	2	AC118477
c	397	83.5	7.6	194198	2	AC013298
c	398	83.5	7.6	194632	9	AC096996
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	401	83.5	7.6	203605	2	AC119514
c	402	83.5	7.6	209998	2	AC102681
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	404	83.5	7.6	221958	2	AC021705
c	405	83.5	7.6	235422	2	AC095877
c	406	83.5	7.6	241170	2	AC111268
	407	83.5	7.6	300900	1	AP005939
	408	83.5	7.6	301629	2	AC103342
	409	83	7.5	1581	4	AF055347
c	410	83	7.5	2789	9	AK125149
	411	83	7.5	5588	6	AX401889
	412	83	7.5	5588	10	RNSCA1
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	414	83	7.5	12857	1	U32841
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c	418	83	7.5	110000	2	AC101676_0
c	419	83	7.5	110000	2	AC151852_5
	420	83	7.5	110000	6	BD426631_17
	421	83	7.5	110000	6	AR274513_17
	422	83	7.5	110000	6	AR541453_17
c	423	83	7.5	115173	2	AC012612
	424	83	7.5	133028	2	AC146840
	425	83	7.5	146500	2	AC119500
c	426	83	7.5	146798	2	AC116022
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c	431	83	7.5	171096	14	AY037858
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c	436	83	7.5	223435	2	AC098360
	437	83	7.5	253305	3	PFMAL3P7
c	438	83	7.5	269050	1	AP000987
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c	440	83	7.5	307380	1	AE016939
c	441	83	7.5	324165	2	AC010277
c	442	82.5	7.5	386	6	AX333122

BX294135 Pirellula
AL113080 Botrytis
BT015858 Arabidops
BT015052 Arabidops
X58519 Chicken mRN
AB062913 Mesocrice
AR109903 Sequence
AR308068 Sequence
AX817984 Sequence
U10886 Human densi
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CR352292 Danio rer
AC068680 Homo sapi
BX901930 Danio rer
AL627089 Mouse DNA
AC007600 Homo sapi
AC132304 Mus muscu
AC118477 Mus muscu
AC013298 Homo sapi
AC096996 Homo sapi
AC119512 Rattus no
AC123884 Mus muscu
AC119514 Rattus no
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AF055347 Diceros b
AK125149 Homo sapi
AX401889 Sequence
X91619 R.norvegicu
AE013580 Methanosa
U32841 Haemophilus
AC074274 Homo sapi
AP004475 Lotus cor
AC025463 Homo sapi
AC101676 Mus muscu
Continuation (6 of
Continuation (18 o
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Continuation (18 o
AC012612 Homo sapi
AC146840 Dasypus n
AC119500 Leishmani
AC116022 Homo sapi
AC126040 Mus muscu
AC010250 Homo sapi
AC008447 Homo sapi
AC145046 Sus scrof
AY037858 Cercopith
AC136297 Homo sapi
AC022463 Homo sapi
AC102590 Mus muscu
AC132460 Mus muscu
AC098360 Rattus no
AL034559 Plasmodiu
AP000987 Sulfolobu
AC099597 Mus muscu
AE016939 Bacteroid
AC010277 Homo sapi
AX333122 Sequence

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	448	82.5	7.5	4373	1	SGU61158
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c	454	82.5	7.5	101295	3	CEY48B6A
	455	82.5	7.5	129663	2	AC027081
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c	460	82.5	7.5	166859	2	AC116521
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	464	82.5	7.5	176778	10	AL845336
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c	467	82.5	7.5	182267	2	AC021128
	468	82.5	7.5	191643	2	AC144874
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	470	82.5	7.5	193276	2	BX088575
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	472	82.5	7.5	203124	2	AC101849
	473	82.5	7.5	209071	2	AC134109
c	474	82.5	7.5	213604	2	AC100345
	475	82.5	7.5	214695	2	AC128559
c	476	82.5	7.5	224612	2	AC123726
c	477	82.5	7.5	227111	5	BX085195
	478	82.5	7.5	228353	2	AL445283
c	479	82.5	7.5	245046	2	CR846103
	480	82.5	7.5	300225	1	AE016949
c	481	82.5	7.5	301068	1	AE017231
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c	484	82	7.4	2339	6	CQ583029
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	492	82	7.4	6314	10	RNU40790
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c	498	82	7.4	101324	9	AC010386
	499	82	7.4	103814	2	AC009210
c	500	82	7.4	110000	2	PFMAL13_02
	501	82	7.4	110000	8	CR380947_0
c	502	82	7.4	123153	9	AC069155
	503	82	7.4	152158	2	BX649301
	504	82	7.4	152740	9	AF490843
	505	82	7.4	159145	2	AC027172
c	506	82	7.4	164935	9	AC012513
c	507	82	7.4	166178	3	AC011072
	508	82	7.4	166954	5	BX470178
c	509	82	7.4	168153	2	CR628407
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c	511	82	7.4	179676	2	AC129889
c	512	82	7.4	183483	9	AL161628
c	513	82	7.4	192645	2	AC006763
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c	515	82	7.4	198073	2	AC109146

AY052191 Arabidops
AF318611 Caenorhab
BC067690 Danio rer
AY598943 Tetraodon
AR396528 Sequence
U61158 Staphylococ
BD193747 Enterococ
AL357232 S.pombe c
Z75537 Caenorhabdi
AL158191 Human DNA
AL161743 Human DNA
AL110490 Caenorhab
AC027081 Homo sapi
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AE017231 Mycobacte
AY115572 Rattus no
AR508364 Sequence
CQ583029 Sequence
AF239722 Drosophil
BT003216 Drosophil
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AF109681 Homo sapi
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AX817991 Sequence
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AC024778 Caenorhab
BX649329 Homo sapi
AC087172 Homo sapi
AL807369 Neurospor
AL603882 Human DNA
AC010386 Homo sapi
AC009210 Drosophil
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AC027172 Homo sapi
AC012513 Homo sapi
AC011072 Drosophil
BX470178 Zebrafish
CR628407 Danio rer
AC099593 Mus muscu
AC129889 Papio anu
AL161628 Human DNA
AC006763 Caenorhab
AC113548 Mus muscu
AC109146 Mus muscu

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c 517	82	7.4	214281	2	AC140050	AC140050 Mus muscu
518	82	7.4	258174	2	AC079429	AC079429 Mus muscu
519	82	7.4	303450	1	AP005085	AP005085 Vibrio pa
c 520	82	7.4	316961	3	AE003799	AE003799 Drosophil
521	82	7.4	343558	2	AC117032	AC117032 Rattus no
c 522	81.5	7.4	816	3	CHIHBB5	M17695 C.thummi th
523	81.5	7.4	910	6	CQ847339	CQ847339 Sequence
524	81.5	7.4	910	6	AX440868	AX440868 Sequence
525	81.5	7.4	1191	1	AF346727	AF346727 Staphyloc
c 526	81.5	7.4	1386	10	BC028255	BC028255 Mus muscu
c 527	81.5	7.4	1955	10	AB024427	AB024427 Mus muscu
528	81.5	7.4	2461	8	MSY428052	AJ428052 Malassezi
529	81.5	7.4	2604	3	AF419623	AF419623 Drosophil
530	81.5	7.4	3040	3	AF419622	AF419622 Drosophil
531	81.5	7.4	3147	6	AX481398	AX481398 Sequence
532	81.5	7.4	3234	9	BC064366	BC064366 Homo sapi
533	81.5	7.4	3269	6	AX337787	AX337787 Sequence
534	81.5	7.4	3269	9	HUMORFT	D26067 Homo sapien
535	81.5	7.4	3495	5	CHKVITAA	M60517 Chicken vit
536	81.5	7.4	4334	10	BC060200	BC060200 Mus muscu
537	81.5	7.4	5716	6	CQ719063	CQ719063 Sequence
538	81.5	7.4	5717	6	AR380788	AR380788 Sequence
539	81.5	7.4	5717	6	AX658103	AX658103 Sequence
540	81.5	7.4	5717	9	HUMVTNR	M14648 Human cell
541	81.5	7.4	6952	6	CQ493953	CQ493953 Sequence
542	81.5	7.4	6954	6	CQ412497	CQ412497 Sequence
543	81.5	7.4	8302	1	BSFLAAO	X56049 B. subtilis
c 544	81.5	7.4	17528	2	AC020192	AC020192 Drosophil
545	81.5	7.4	21520	6	AX770894	AX770894 Sequence
546	81.5	7.4	68850	10	AL929258	AL929258 Mouse DNA
547	81.5	7.4	76410	2	AC016093	AC016093 Homo sapi
548	81.5	7.4	81677	3	AC004377	AC004377 Drosophil
549	81.5	7.4	89836	8	AC007188	AC007188 Arabidops
550	81.5	7.4	96642	8	AC002291	AC002291 Arabidops
551	81.5	7.4	136124	9	HS394P21	AL021528 Human DNA
552	81.5	7.4	138217	10	AL669905	AL669905 Mouse DNA
c 553	81.5	7.4	139994	9	AC006462	AC006462 Homo sapi
c 554	81.5	7.4	140327	2	AP003938	AP003938 Oryza sat
555	81.5	7.4	147569	2	BX248417	BX248417 Homo sapi
c 556	81.5	7.4	155112	2	AL357521	AL357521 Homo sapi
c 557	81.5	7.4	158297	2	AL513545	AL513545 Homo sapi
558	81.5	7.4	167442	2	AC112954	AC112954 Mus muscu
559	81.5	7.4	171015	5	BX005395	BX005395 Zebrafish
c 560	81.5	7.4	173373	3	AC008349	AC008349 Drosophil
c 561	81.5	7.4	174811	2	AC013259	AC013259 Homo sapi
562	81.5	7.4	175118	2	AC145247	AC145247 Didelphis
563	81.5	7.4	177384	2	AC091786	AC091786 Mus muscu
c 564	81.5	7.4	177747	10	AC122051	AC122051 Mus muscu
565	81.5	7.4	187277	2	BX901971	BX901971 Danio rer
c 566	81.5	7.4	188802	2	AC113864	AC113864 Rattus no
567	81.5	7.4	192208	2	AC084792	AC084792 Homo sapi
568	81.5	7.4	208609	9	HS389A20	Z93242 Human DNA s
569	81.5	7.4	213541	9	HUAC004381	AC004381 Homo sapi
c 570	81.5	7.4	216726	2	AC097270	AC097270 Pan trogl
571	81.5	7.4	238643	2	AC133255	AC133255 Rattus no
c 572	81.5	7.4	247730	2	AC112120	AC112120 Rattus no
573	81.5	7.4	253522	2	AC130734	AC130734 Rattus no
c 574	81.5	7.4	275209	2	AC097164	AC097164 Rattus no
c 575	81.5	7.4	281904	2	AC132547	AC132547 Rattus no
c 576	81.5	7.4	301146	1	AE017311	AE017311 Desulfovi
c 577	81.5	7.4	307323	3	AE003457	AE003457 Drosophil
578	81.5	7.4	349944	1	BX571871	BX571871 Photorhab
579	81	7.4	1539	6	AR544985	AR544985 Sequence
c 580	81	7.4	3241	3	AF005059	AF005059 Toxoplasm
581	81	7.4	4010	10	MUSINTA7SU	L23423 Mouse (BALB
582	81	7.4	4262	3	AF067658	AF067658 Lytechinu
583	81	7.4	4262	3	LVU22152	U22152 Lytechinus
584	81	7.4	26880	10	AF067129	AF067129 Mus muscu
585	81	7.4	29047	3	CET05A10	Z68108 Caenorhabdi
c 586	81	7.4	38784	2	AC014012	AC014012 Drosophil
587	81	7.4	94728	2	OSIG00030	AL732334 Oryza sat
588	81	7.4	99596	9	AC106873	AC106873 Homo sapi
589	81	7.4	110000	8	CR380959_12	Continuation (13 o
c 590	81	7.4	118331	9	AL391336	AL391336 Human DNA
591	81	7.4	121702	9	AC096723	AC096723 Homo sapi
c 592	81	7.4	126150	9	AC005152	AC005152 Homo sapi
c 593	81	7.4	140797	2	AC118723	AC118723 Mus muscu
c 594	81	7.4	146545	2	AC115221	AC115221 Homo sapi
c 595	81	7.4	148471	9	AC009332	AC009332 Homo sapi
c 596	81	7.4	149844	2	AC144682	AC144682 Rattus no
c 597	81	7.4	153926	2	AC107866	AC107866 Mus muscu
598	81	7.4	158648	2	AC021853	AC021853 Homo sapi
599	81	7.4	170201	2	AC055885	AC055885 Homo sapi
600	81	7.4	170213	5	BX005062	BX005062 Zebrafish
601	81	7.4	170376	9	AC104430	AC104430 Homo sapi
602	81	7.4	170435	9	AC100767	AC100767 Homo sapi
c 603	81	7.4	171451	2	AC064838	AC064838 Homo sapi
604	81	7.4	176054	2	AC022377	AC022377 Homo sapi
c 605	81	7.4	177738	2	AC055886	AC055886 Homo sapi
606	81	7.4	178121	9	AL603840	AL603840 Human DNA
c 607	81	7.4	179350	9	AC026351	AC026351 Homo sapi
608	81	7.4	180957	9	AF267168	AF267168 Homo sapi
c 609	81	7.4	183867	10	AC122237	AC122237 Mus muscu
c 610	81	7.4	187677	2	AC147321	AC147321 Pan trogl
611	81	7.4	187979	10	AC123854	AC123854 Mus muscu
612	81	7.4	188110	2	AC104152	AC104152 Rattus no
613	81	7.4	190644	10	AC122872	AC122872 Mus muscu
614	81	7.4	191379	10	AL845534	AL845534 Mouse DNA
615	81	7.4	194837	10	AL607066	AL607066 Mouse DNA
c 616	81	7.4	196044	9	AC018505	AC018505 Homo sapi
617	81	7.4	198759	2	AC020772	AC020772 Homo sapi
618	81	7.4	202366	2	AL805939	AL805939 Mus muscu
619	81	7.4	209876	9	AC011599	AC011599 Homo sapi
620	81	7.4	210979	10	AC132863	AC132863 Mus muscu
c 621	81	7.4	237286	2	AC113645	AC113645 Rattus no
622	81	7.4	240483	2	AC095955	AC095955 Rattus no
c 623	81	7.4	250119	2	AC111874	AC111874 Rattus no
624	81	7.4	257991	2	AC114028	AC114028 Rattus no
c 625	81	7.4	267546	2	AC125740	AC125740 Rattus no
626	81	7.4	268050	1	AL627266	AL627266 Salmonell
c 627	81	7.4	275460	2	AC114120	AC114120 Rattus no
628	81	7.4	288479	2	AC146814	AC146814 Zea mays
c 629	81	7.4	300029	1	AE016842	AE016842 Salmonell
630	80.5	7.3	568	6	CQ719682	CQ719682 Sequence
c 631	80.5	7.3	597	8	AY557646	AY557646 Saccharom
632	80.5	7.3	1636	6	AX366700	AX366700 Sequence
633	80.5	7.3	2166	10	MUSMUC1A	M84683 Mus musculu
634	80.5	7.3	2242	10	BC005441	BC005441 Mus muscu
635	80.5	7.3	2280	5	DRU41419	U41419 Danio rerio
636	80.5	7.3	2359	3	AB056090	AB056090 Polyandro
637	80.5	7.3	3141	5	DRE311886	AJ311886 Danio rer
638	80.5	7.3	3613	6	CQ851438	CQ851438 Sequence
639	80.5	7.3	3613	9	AK128681	AK128681 Homo sapi
640	80.5	7.3	4184	6	CQ851271	CQ851271 Sequence
641	80.5	7.3	4184	9	AK128856	AK128856 Homo sapi
642	80.5	7.3	4294	8	SCYDR032C	Z74328 S.cerevisia
643	80.5	7.3	5138	5	AF090432	AF090432 Danio rer
644	80.5	7.3	5355	5	AF229450	AF229450 Danio rer
645	80.5	7.3	5469	5	AF229449	AF229449 Danio rer
646	80.5	7.3	10085	8	AB015471	AB015471 Arabidops
c 647	80.5	7.3	13761	1	AE013212	AE013212 Thermoana
c 648	80.5	7.3	15446	1	AE000710	AE000710 Aquifex a
649	80.5	7.3	15894	6	BD137592	BD137592 Mutation
650	80.5	7.3	15894	6	BD137593	BD137593 Mutation
651	80.5	7.3	21112	9	AF361486	AF361486 Homo sapi
652	80.5	7.3	24628	8	SC9673	Z68196 S.cerevisia
c 653	80.5	7.3	29548	3	AF022970	AF022970 Caenorhab
654	80.5	7.3	41523	2	AC101065	AC101065 Mus muscu
c 655	80.5	7.3	60000	9	AP003679	AP003679 Homo sapi
656	80.5	7.3	66765	6	CQ874958	CQ874958 Sequence
657	80.5	7.3	66765	9	AF414442	AF414442 Homo sapi
658	80.5	7.3	110000	1	CR543861_24	Continuation (25 o
c 659	80.5	7.3	110000	2	AC095920_03	Continuation (4 of
660	80.5	7.3	110000	2	AC134360_2	Continuation (3 of
661	80.5	7.3	110000	8	CR380951_1	Continuation (2 of

	662	80.5	7.3	135980	8	AC126224 AC126224 Oryza sat
	663	80.5	7.3	137617	9	AC092107 AC092107 Homo sapi
	664	80.5	7.3	152612	2	AC053515 AC053515 Homo sapi
	665	80.5	7.3	163310	2	AC016147 AC016147 Homo sapi
	666	80.5	7.3	168706	2	AC016151 AC016151 Homo sapi
c	667	80.5	7.3	168794	2	AC026252 AC026252 Homo sapi
	668	80.5	7.3	171058	9	AC073068 AC073068 Homo sapi
	669	80.5	7.3	172949	10	AC122231 AC122231 Mus muscu
c	670	80.5	7.3	174113	2	AC112810 AC112810 Rattus no
	671	80.5	7.3	177048	2	AC128925 AC128925 Rattus no
	672	80.5	7.3	179246	9	AC114877 AC114877 Homo sapi
c	673	80.5	7.3	205985	2	AC148494 AC148494 Otolemur
	674	80.5	7.3	207531	2	AC133061 AC133061 Rattus no
c	675	80.5	7.3	228752	2	AC094632 AC094632 Rattus no
c	676	80.5	7.3	248917	2	AC096017 AC096017 Rattus no
c	677	80.5	7.3	252394	3	AE014833 AE014833 Plasmodiu
	678	80.5	7.3	254278	2	AC095693 AC095693 Rattus no
c	679	80.5	7.3	286162	2	AC117293 AC117293 Rattus no
	680	80.5	7.3	340900	1	SME591791 AL591791 Sinorhizo
	681	80	7.3	669	3	GCSHOX X79054 G.cydonium
	682	80	7.3	1327	3	AF076220 AF076220 Drosophil
	683	80	7.3	1349	6	CQ575619 CQ575619 Sequence
	684	80	7.3	1427	3	AY058251 AY058251 Drosophil
	685	80	7.3	1599	3	AK116812 AK116812 Ciona int
c	686	80	7.3	3711	6	CQ872812 CQ872812 Sequence
	687	80	7.3	4775	5	XELINTA3S L43057 Xenopus lae
	688	80	7.3	10029	1	AE005313 AE005313 Escherich
c	689	80	7.3	11578	1	AE008345 AE008345 Agrobacte
	690	80	7.3	11585	1	AE005277 AE005277 Escherich
	691	80	7.3	12013	1	AE009266 AE009266 Agrobacte
c	692	80	7.3	47483	2	AC141834 AC141834 Apis mell
c	693	80	7.3	76410	2	AC016093 AC016093 Homo sapi
	694	80	7.3	81149	2	AC023338 AC023338 Homo sapi
c	695	80	7.3	81419	5	BX571840 BX571840 Zebrafish
	696	80	7.3	86248	6	BD184766 BD184766 Nucleic a
	697	80	7.3	87563	6	AR204161 AR204161 Sequence
c	698	80	7.3	89479	8	AC006932 AC006932 Genomic s
c	699	80	7.3	100795	5	BX323600 BX323600 Zebrafish
c	700	80	7.3	108716	9	HS101A4 Z93341 Human DNA s
	701	80	7.3	110000	8	CR380948_1 Continuation (2 of
c	702	80	7.3	135686	9	HS473J6 Z83827 Human DNA s
	703	80	7.3	148090	10	AC100737 AC100737 Mus muscu
	704	80	7.3	158475	9	AC097463 AC097463 Homo sapi
	705	80	7.3	165791	10	AC129198 AC129198 Mus muscu
c	706	80	7.3	169414	9	AC068707 AC068707 Homo sapi
c	707	80	7.3	170535	9	CNS05TBO AL163932 Human chr
	708	80	7.3	170559	2	AC026989 AC026989 Homo sapi
	709	80	7.3	170924	2	AC148627 AC148627 Callithri
c	710	80	7.3	171823	14	HHV507799 AJ507799 Human her
c	711	80	7.3	172281	14	EBV V01555 Epstein-Bar
	712	80	7.3	173775	2	AC079933 AC079933 Trypanoso
	713	80	7.3	174965	9	AC036222 AC036222 Homo sapi
c	714	80	7.3	177248	5	AL929093 AL929093 Zebrafish
c	715	80	7.3	182997	9	AL355332 AL355332 Human DNA
c	716	80	7.3	184113	14	HS4B958RAJ M80517 Epstein-Bar
	717	80	7.3	191729	2	AL590872 AL590872 Homo sapi
	718	80	7.3	198703	10	AC129570 AC129570 Mus muscu
c	719	80	7.3	200340	9	AC100797 AC100797 Homo sapi
c	720	80	7.3	201470	2	AC105683 AC105683 Rattus no
	721	80	7.3	204401	2	AC105524 AC105524 Rattus no
c	722	80	7.3	206264	2	CR847572 CR847572 Danio rer
c	723	80	7.3	207411	10	AC114916 AC114916 Mus muscu
	724	80	7.3	208458	10	AC118009 AC118009 Mus muscu
c	725	80	7.3	212664	2	AC123005 AC123005 Rattus no
c	726	80	7.3	212705	10	AC113600 AC113600 Mus muscu
	727	80	7.3	212879	2	AC148552 AC148552 Callithri
	728	80	7.3	229905	2	AC135819 AC135819 Rattus no
c	729	80	7.3	232120	2	AC132712 AC132712 Rattus no
	730	80	7.3	237952	2	AL591116 AL591116 Homo sapi
c	731	80	7.3	247728	2	AC134204 AC134204 Rattus no
c	732	80	7.3	250541	2	AC114390 AC114390 Rattus no
c	733	80	7.3	276326	8	AY574035 AY574035 Zea mays
	734	80	7.3	279331	2	AC097172 AC097172 Rattus no
c	735	80	7.3	290874	2	CR847807 CR847807 Danio rer
	736	80	7.3	291073	1	AE017323 AE017323 Listeria
	737	80	7.3	292423	2	AC113653 AC113653 Rattus no
	738	80	7.3	308766	6	CQ873161 CQ873161 Sequence
	739	80	7.3	327773	1	AP002554 AP002554 Escherich
	740	79.5	7.2	906	6	CQ847194 CQ847194 Sequence
	741	79.5	7.2	906	6	AX440723 AX440723 Sequence
	742	79.5	7.2	1088	3	AF440518 AF440518 Caenorhab
	743	79.5	7.2	1257	9	CGU64092 U64092 Cercopithec
c	744	79.5	7.2	1813	3	AY513386 AY513386 Centrucho
	745	79.5	7.2	1892	3	AF142497 AF142497 Trypanoso
	746	79.5	7.2	3830	10	MMU14135 U14135 Mus musculu
	747	79.5	7.2	4123	10	BC048857 BC048857 Mus muscu
c	748	79.5	7.2	20975	3	CER12H7 Z50755 Caenorhabdi
c	749	79.5	7.2	37889	3	U40797 U40797 Caenorhabdi
c	750	79.5	7.2	40093	2	AY714857 AY714857 Unculture
c	751	79.5	7.2	60709	2	AC107923 AC107923 Homo sapi
	752	79.5	7.2	87435	8	NC103E1 BX294028 Neurospor
	753	79.5	7.2	109018	9	HSJ1129A6 AL096763 Human DNA
c	754	79.5	7.2	110000	1	AE017354_31 Continuation (32 o
	755	79.5	7.2	121506	4	AC087807 AC087807 Felis cat
c	756	79.5	7.2	128091	2	AC139626 AC139626 Takifugu
	757	79.5	7.2	131000	9	AP001017 AP001017 Homo sapi
	758	79.5	7.2	133104	9	AL451070 AL451070 Human DNA
c	759	79.5	7.2	139217	8	AC147925 AC147925 Oryza sat
	760	79.5	7.2	143420	9	AL161422 AL161422 Human DNA
c	761	79.5	7.2	156548	10	AC119214 AC119214 Mus muscu
c	762	79.5	7.2	159413	2	AC018520 AC018520 Homo sapi
c	763	79.5	7.2	160325	9	AC097347 AC097347 Homo sapi
c	764	79.5	7.2	163776	2	AC109289 AC109289 Mus muscu
c	765	79.5	7.2	164103	2	AC037484 AC037484 Homo sapi
c	766	79.5	7.2	164479	9	AC103922 AC103922 Homo sapi
c	767	79.5	7.2	168699	8	CNS08CCV AL954157 Oryza sat
	768	79.5	7.2	169834	9	AC138070 AC138070 Homo sapi
	769	79.5	7.2	170777	2	AC148444 AC148444 Rhinoloph
c	770	79.5	7.2	172388	2	AC027634 AC027634 Homo sapi
	771	79.5	7.2	175707	2	AC022030 AC022030 Homo sapi
	772	79.5	7.2	175759	10	AF220294 AF220294 Mus muscu
c	773	79.5	7.2	178147	8	CNS08CE8 BX001060 Oryza sat
c	774	79.5	7.2	178208	2	AC136432 AC136432 Homo sapi
c	775	79.5	7.2	178928	2	AC121725 AC121725 Rattus no
c	776	79.5	7.2	183479	2	AC114907 AC114907 Mus muscu
	777	79.5	7.2	184819	10	AL845483 AL845483 Mouse DNA
	778	79.5	7.2	188782	9	AC023150 AC023150 Homo sapi
c	779	79.5	7.2	190110	10	AC121564 AC121564 Mus muscu
c	780	79.5	7.2	190701	9	AC022274 AC022274 Homo sapi
	781	79.5	7.2	193444	2	BX510909 BX510909 Danio rer
	782	79.5	7.2	194487	2	AP002896 AP002896 Homo sapi
c	783	79.5	7.2	195895	2	AC117033 AC117033 Rattus no
	784	79.5	7.2	197153	2	AC141966 AC141966 Rattus no
	785	79.5	7.2	202214	10	AC124556 AC124556 Mus muscu
	786	79.5	7.2	204340	9	AC091103 AC091103 Homo sapi
c	787	79.5	7.2	206346	2	AC027438 AC027438 Homo sapi
	788	79.5	7.2	207497	5	BX571675 BX571675 Zebrafish
	789	79.5	7.2	208014	5	BX005008 BX005008 Zebrafish
c	790	79.5	7.2	208661	10	AC072048 AC072048 Mus muscu
c	791	79.5	7.2	210205	1	AY223810 AY223810 Rhodococc
c	792	79.5	7.2	216185	5	BX842696 BX842696 Zebrafish
	793	79.5	7.2	222983	2	AC129695 AC129695 Rattus no
	794	79.5	7.2	224266	2	AC127197 AC127197 Rattus no
	795	79.5	7.2	226651	10	AC130711 AC130711 Mus muscu
	796	79.5	7.2	228645	2	AC094273 AC094273 Rattus no
c	797	79.5	7.2	244929	2	AC094389 AC094389 Rattus no
	798	79.5	7.2	253973	2	AC094544 AC094544 Rattus no
c	799	79.5	7.2	254172	2	CR392035 CR392035 Danio rer
	800	79.5	7.2	257245	2	AC097396 AC097396 Rattus no
c	801	79.5	7.2	258646	2	AC096239 AC096239 Rattus no
c	802	79.5	7.2	268123	10	AC093479 AC093479 Mus muscu
	803	79.5	7.2	271402	2	AC137598 AC137598 Oryza sat
c	804	79.5	7.2	271402	2	AC137598 AC137598 Oryza sat
	805	79.5	7.2	272840	5	BX005328 BX005328 Zebrafish
	806	79.5	7.2	278372	2	AC111812 AC111812 Rattus no
	807	79.5	7.2	283158	2	AC137193 AC137193 Rattus no

808	79.5	7.2	295050	1	AL591982	AL591982 Listeria
c 809	79.5	7.2	300425	1	AP005038	AP005038 Streptomy
810	79.5	7.2	320205	2	AC106178	AC106178 Rattus no
811	79.5	7.2	348632	2	AC096299	AC096299 Rattus no
812	79.5	7.2	349980	6	AX641671	AX641671 Sequence
813	79	7.2	65	6	CQ556364	CQ556364 Sequence
814	79	7.2	543	3	AF301159	AF301159 Eriocheir
c 815	79	7.2	1032	5	AY059001	AY059001 Walterinn
816	79	7.2	1155	10	AF537215	AF537215 Mus muscu
817	79	7.2	1301	10	AF234830	AF234830 Mus muscu
818	79	7.2	1512	6	AX433776	AX433776 Sequence
c 819	79	7.2	1695	6	CQ573504	CQ573504 Sequence
c 820	79	7.2	1749	3	AF242735	AF242735 Drosophil
821	79	7.2	2108	10	BC031488	BC031488 Mus muscu
c 822	79	7.2	2198	3	AF275814	AF275814 Drosophil
823	79	7.2	2296	9	AK074419	AK074419 Homo sapi
824	79	7.2	2546	9	AK074243	AK074243 Homo sapi
825	79	7.2	2664	6	AX285092	AX285092 Sequence
826	79	7.2	2932	6	BD159735	BD159735 Primer fo
827	79	7.2	2932	6	AX882457	AX882457 Sequence
828	79	7.2	2932	9	AK027587	AK027587 Homo sapi
829	79	7.2	3298	10	AF170316	AF170316 Mus muscu
c 830	79	7.2	3750	6	CQ573503	CQ573503 Sequence
831	79	7.2	4952	10	BC050836	BC050836 Mus muscu
832	79	7.2	5018	10	AK129234	AK129234 Mus muscu
833	79	7.2	5205	6	AX451422	AX451422 Sequence
834	79	7.2	6228	3	AY051985	AY051985 Drosophil
835	79	7.2	6490	3	DMDLAR9	U36857 Drosophila
c 836	79	7.2	7265	6	AX602153	AX602153 Sequence
837	79	7.2	7606	3	DROLARM	M27700 D.melanogas
838	79	7.2	7630	6	CQ614817	CQ614817 Sequence
839	79	7.2	9834	9	AY327116	AY327116 Homo sapi
840	79	7.2	10002	9	AB107369	AB107369 Homo sapi
841	79	7.2	10002	9	AY327115	AY327115 Homo sapi
c 842	79	7.2	12978	2	AC014229	AC014229 Drosophil
843	79	7.2	17284	9	HSRINGG	Y07829 Homo sapien
844	79	7.2	21495	1	AE014285	AE014285 Streptoco
845	79	7.2	24766	2	AC014976	AC014976 Drosophil
846	79	7.2	25119	2	AY714839	AY714839 Unculture
c 847	79	7.2	34284	8	SPAC3H5	Z99296 S.pombe chr
848	79	7.2	39434	9	AL162911	AL162911 Human DNA
849	79	7.2	52712	2	AC149925	AC149925 Strongylo
850	79	7.2	73481	9	AC011891	AC011891 Homo sapi
851	79	7.2	80501	9	AC097314	AC097314 Homo sapi
852	79	7.2	87726	2	AC014337	AC014337 Drosophil
853	79	7.2	89050	1	SAG766855	AL766855 Streptoco
854	79	7.2	110000	1	AE017197_05	Continuation (6 of
c 855	79	7.2	110000	1	AE017333_39	Continuation (40 o
c 856	79	7.2	110000	1	CP000002_39	Continuation (40 o
c 857	79	7.2	125528	2	AC027389	AC027389 Homo sapi
c 858	79	7.2	129642	3	AGA438610	AJ438610 Anopheles
859	79	7.2	132354	2	AC017130	AC017130 Drosophil
c 860	79	7.2	138264	10	AC132579	AC132579 Mus muscu
c 861	79	7.2	145327	9	AP004285	AP004285 Homo sapi
c 862	79	7.2	146572	10	AC118259	AC118259 Mus muscu
c 863	79	7.2	147322	2	AC137764	AC137764 Mus muscu
864	79	7.2	147530	9	AC008766	AC008766 Homo sapi
c 865	79	7.2	152130	9	AP000856	AP000856 Homo sapi
c 866	79	7.2	154890	3	AC008136	AC008136 Drosophil
867	79	7.2	155361	2	AC142174	AC142174 Rattus no
868	79	7.2	163990	3	AC009255	AC009255 Drosophil
c 869	79	7.2	164936	2	AC141529	AC141529 Rattus no
c 870	79	7.2	170190	3	AC009911	AC009911 Drosophil
871	79	7.2	170803	9	HSJ344J20	AL080285 Human DNA
872	79	7.2	177487	2	AC117601	AC117601 Mus muscu
873	79	7.2	180699	3	AC008339	AC008339 Drosophil
874	79	7.2	181498	8	OSJN00162	AL662960 Oryza sat
c 875	79	7.2	182603	10	AC141893	AC141893 Mus muscu
c 876	79	7.2	183982	2	AC021884	AC021884 Homo sapi
c 877	79	7.2	184872	10	AL672243	AL672243 Mouse DNA
c 878	79	7.2	185769	10	AC129178	AC129178 Mus muscu
c 879	79	7.2	186066	9	AC090579	AC090579 Homo sapi
c 880	79	7.2	186154	2	AC102651	AC102651 Mus muscu
c 881	79	7.2	186751	9	AC023344	AC023344 Homo sapi
c 882	79	7.2	187314	2	AC026590	AC026590 Homo sapi
c 883	79	7.2	187936	9	AC080003	AC080003 Homo sapi
c 884	79	7.2	191028	8	PPU38804	U38804 Porphyra pu
c 885	79	7.2	199897	2	AC118296	AC118296 Rattus no
c 886	79	7.2	203183	3	AC005721	AC005721 Drosophil
887	79	7.2	203374	2	AC102546	AC102546 Mus muscu
888	79	7.2	206733	2	AC110553	AC110553 Mus muscu
889	79	7.2	206945	2	AC146022	AC146022 Pan trogl
890	79	7.2	215447	10	AC125541	AC125541 Mus muscu
c 891	79	7.2	219664	2	AC146911	AC146911 Mus muscu
c 892	79	7.2	222195	2	AC112890	AC112890 Rattus no
893	79	7.2	224650	1	AL596164	AL596164 Listeria
894	79	7.2	245453	2	AC131004	AC131004 Rattus no
c 895	79	7.2	246585	2	AC108954	AC108954 Rattus no
c 896	79	7.2	253278	2	AC097310	AC097310 Rattus no
c 897	79	7.2	254961	3	AE003706	AE003706 Drosophil
898	79	7.2	290667	3	AE003663	AE003663 Drosophil
c 899	79	7.2	291073	1	AE017323	AE017323 Listeria
900	79	7.2	304758	3	AE003784	AE003784 Drosophil
c 901	79	7.2	349527	1	CR378678	CR378678 Photobact
902	79	7.2	349980	6	CQ655073	CQ655073 Sequence
903	79	7.2	349980	6	AX417041	AX417041 Sequence
904	79	7.2	349980	6	AX453571	AX453571 Sequence
905	79	7.2	349980	6	AX954533	AX954533 Sequence
906	78.5	7.1	1060	6	AX366801	AX366801 Sequence
c 907	78.5	7.1	1173	6	CQ805812	CQ805812 Sequence
c 908	78.5	7.1	1204	8	AY117314	AY117314 Arabidops
909	78.5	7.1	1257	8	AB118147	AB118147 Saussurea
910	78.5	7.1	1320	8	AB118141	AB118141 Saussurea
c 911	78.5	7.1	1365	8	AY064047	AY064047 Arabidops
c 912	78.5	7.1	1419	8	AF419594	AF419594 Arabidops
913	78.5	7.1	1761	6	BD265001	BD265001 Compositi
914	78.5	7.1	1761	6	AR238404	AR238404 Sequence
915	78.5	7.1	1761	6	AR478743	AR478743 Sequence
916	78.5	7.1	1761	6	AX366620	AX366620 Sequence
917	78.5	7.1	2159	5	CR760664	CR760664 Xenopus t
918	78.5	7.1	2608	6	BD265000	BD265000 Compositi
919	78.5	7.1	2608	6	AR238403	AR238403 Sequence
920	78.5	7.1	2608	6	AR478742	AR478742 Sequence
921	78.5	7.1	2608	6	AX366619	AX366619 Sequence
922	78.5	7.1	2996	6	BD264926	BD264926 Compositi
923	78.5	7.1	2996	6	AR238329	AR238329 Sequence
924	78.5	7.1	2996	6	AR257870	AR257870 Sequence
925	78.5	7.1	2996	6	AR478668	AR478668 Sequence
926	78.5	7.1	2996	6	AX156348	AX156348 Sequence
927	78.5	7.1	2996	6	AX366544	AX366544 Sequence
928	78.5	7.1	2996	6	AX366695	AX366695 Sequence
929	78.5	7.1	3101	4	AF317199	AF317199 Bos tauru
930	78.5	7.1	3144	4	AF239958	AF239958 Bos tauru
931	78.5	7.1	3489	10	MUSOSF4	D21253 Mus musculu
932	78.5	7.1	3581	6	AR034821	AR034821 Sequence
933	78.5	7.1	3581	6	E07381	E07381 cDNA encodi
934	78.5	7.1	3646	10	BC046314	BC046314 Mus muscu
935	78.5	7.1	3755	6	CQ604115	CQ604115 Sequence
936	78.5	7.1	3862	6	CQ574215	CQ574215 Sequence
937	78.5	7.1	3863	3	AF184227	AF184227 Drosophil
c 938	78.5	7.1	4102	3	AY070899	AY070899 Drosophil
939	78.5	7.1	4127	6	AX306074	AX306074 Sequence
940	78.5	7.1	4127	10	MMCADL	X77557 M.musculus
941	78.5	7.1	4129	9	BC047454	BC047454 Homo sapi
942	78.5	7.1	4285	5	BC084201	BC084201 Xenopus l
c 943	78.5	7.1	5513	9	AC098796	AC098796 Homo sapi
c 944	78.5	7.1	5755	11	BV179236	BV179236 sqnm10444
945	78.5	7.1	10622	6	AX366802	AX366802 Sequence
c 946	78.5	7.1	11288	6	AR134885	AR134885 Sequence
c 947	78.5	7.1	11288	6	AR182304	AR182304 Sequence
c 948	78.5	7.1	11288	6	AR370519	AR370519 Sequence
c 949	78.5	7.1	11288	6	AR479027	AR479027 Sequence
c 950	78.5	7.1	11288	6	AX269130	AX269130 Sequence
c 951	78.5	7.1	11288	9	HSCRCANTA	Z21818 H.sapiens c
952	78.5	7.1	11743	6	CQ592355	CQ592355 Sequence
c 953	78.5	7.1	12216	6	CQ594536	CQ594536 Sequence

c 954	78.5	7.1	15056	6	BD195539	BD195539 Adenoviru
c 955	78.5	7.1	15056	6	BD224258	BD224258 Adenoviru
c 956	78.5	7.1	15056	6	AR266427	AR266427 Sequence
c 957	78.5	7.1	15056	6	AR474484	AR474484 Sequence
c 958	78.5	7.1	15056	6	AX259954	AX259954 Sequence
c 959	78.5	7.1	15056	6	AX262359	AX262359 Sequence
960	78.5	7.1	47687	2	AC013074	AC013074 Drosophil
961	78.5	7.1	55374	9	AL645474	AL645474 Human DNA
962	78.5	7.1	63940	2	AC017795	AC017795 Drosophil
c 963	78.5	7.1	84961	2	AC014810	AC014810 Drosophil
c 964	78.5	7.1	98303	2	AP004642	AP004642 Oryza sat
c 965	78.5	7.1	110000	8	CR382126_02	Continuation (3 of
c 966	78.5	7.1	110000	8	CR382135_06	Continuation (7 of
967	78.5	7.1	117931	2	AC111066	AC111066 Mus muscu
c 968	78.5	7.1	128785	9	AC105328	AC105328 Homo sapi
969	78.5	7.1	132635	2	AC007577	AC007577 Drosophil
c 970	78.5	7.1	143798	9	AL157409	AL157409 Human DNA
c 971	78.5	7.1	147002	10	AL928882	AL928882 Mouse DNA
972	78.5	7.1	148498	9	AP003473	AP003473 Homo sapi
c 973	78.5	7.1	149284	5	BX323015	BX323015 Zebrafish
c 974	78.5	7.1	149804	2	AC020984	AC020984 Homo sapi
975	78.5	7.1	150221	9	AC004593	AC004593 Homo sapi
c 976	78.5	7.1	150727	2	CR381531	CR381531 Danio rer
c 977	78.5	7.1	151512	2	AC142376	AC142376 Rattus no
c 978	78.5	7.1	152430	9	AC087432	AC087432 Homo sapi
979	78.5	7.1	154768	9	AC015476	AC015476 Homo sapi
c 980	78.5	7.1	157620	9	BS000109	BS000109 Pan trogl
981	78.5	7.1	159758	9	AP005356	AP005356 Homo sapi
982	78.5	7.1	160264	10	AC108412	AC108412 Mus muscu
c 983	78.5	7.1	160410	2	AC020753	AC020753 Homo sapi
c 984	78.5	7.1	162223	8	AC108870	AC108870 Oryza sat
c 985	78.5	7.1	163438	2	AC147759	AC147759 Macropus
c 986	78.5	7.1	163613	2	AC091702	AC091702 Trypanoso
987	78.5	7.1	163996	8	AP003333	AP003333 Oryza sat
c 988	78.5	7.1	165174	8	AP005730	AP005730 Oryza sat
c 989	78.5	7.1	165855	3	AC009342	AC009342 Drosophil
c 990	78.5	7.1	166162	9	AC018814	AC018814 Homo sapi
c 991	78.5	7.1	168421	10	AC113328	AC113328 Mus muscu
c 992	78.5	7.1	168618	2	AC116689	AC116689 Mus muscu
c 993	78.5	7.1	169550	2	AP005617	AP005617 Oryza sat
c 994	78.5	7.1	171072	9	CNS05TE6	AL358335 Human chr
c 995	78.5	7.1	171810	2	AC128062	AC128062 Rattus no
996	78.5	7.1	171973	2	AC013571	AC013571 Homo sapi
997	78.5	7.1	172127	2	AC013572	AC013572 Homo sapi
998	78.5	7.1	173910	2	AC115902	AC115902 Mus muscu
999	78.5	7.1	174729	3	AC008203	AC008203 Drosophil
1000	78.5	7.1	174751	3	AC008288	AC008288 Drosophil
1001	78.5	7.1	176212	2	AC141778	AC141778 Apis mell
c1002	78.5	7.1	177380	6	AX706985	AX706985 Sequence
c1003	78.5	7.1	177380	6	AX707915	AX707915 Sequence
1004	78.5	7.1	177380	9	AC002457	AC002457 Homo sapi
1005	78.5	7.1	180700	2	AC084136	AC084136 Homo sapi
1006	78.5	7.1	181535	9	AL592203	AL592203 Human DNA
c1007	78.5	7.1	181833	2	AC141405	AC141405 Homo sapi
c1008	78.5	7.1	182223	3	AC023674	AC023674 Drosophil
c1009	78.5	7.1	183763	9	AC104036	AC104036 Homo sapi
c1010	78.5	7.1	188432	2	AC018497	AC018497 Homo sapi
1011	78.5	7.1	188555	10	AC122417	AC122417 Mus muscu
1012	78.5	7.1	194034	9	AP005901	AP005901 Homo sapi
1013	78.5	7.1	196967	2	AC108589	AC108589 Rattus no
1014	78.5	7.1	197173	2	AC131036	AC131036 Mus muscu
c1015	78.5	7.1	200933	10	AL805910	AL805910 Mouse DNA
1016	78.5	7.1	201456	10	AC124669	AC124669 Mus muscu
c1017	78.5	7.1	202645	2	AL513330	AL513330 Homo sapi
c1018	78.5	7.1	203593	10	AL663053	AL663053 Mouse DNA
1019	78.5	7.1	204278	10	AC124507	AC124507 Mus muscu
1020	78.5	7.1	206749	2	AC102059	AC102059 Mus muscu
1021	78.5	7.1	208885	2	AC101703	AC101703 Mus muscu
c1022	78.5	7.1	211492	2	AC140877	AC140877 Homo sapi
1023	78.5	7.1	216493	2	AC013530	AC013530 Homo sapi
1024	78.5	7.1	216811	2	AC140808	AC140808 Homo sapi
1025	78.5	7.1	218498	3	AE003746	AE003746 Drosophil
1026	78.5	7.1	220251	2	AC140363	AC140363 Mus muscu
c1027	78.5	7.1	222613	2	AC150742	AC150742 Zea mays
c1028	78.5	7.1	223308	10	AC110920	AC110920 Mus muscu
1029	78.5	7.1	225880	2	AC131693	AC131693 Mus muscu
c1030	78.5	7.1	230232	2	AC104292	AC104292 Rattus no
c1031	78.5	7.1	233589	10	AL683824	AL683824 Mouse DNA
1032	78.5	7.1	237899	10	AC102622	AC102622 Mus muscu
1033	78.5	7.1	240256	2	AC123729	AC123729 Mus muscu
1034	78.5	7.1	259619	2	AC108308	AC108308 Rattus no
c1035	78.5	7.1	282610	1	RPXX01	AJ235270 Rickettsi
c1036	78.5	7.1	284268	3	AE003565	AE003565 Drosophil
1037	78.5	7.1	313050	1	BX321857	BX321857 Nitrosomo
1038	78.5	7.1	344530	2	AC133390	AC133390 Rattus no
c1039	78.5	7.1	348873	3	AE003790	AE003790 Drosophil
1040	78	7.1	872	5	AB090396	AB090396 Paralabid
1041	78	7.1	872	5	AB090397	AB090397 Paralabid
1042	78	7.1	872	5	AB090398	AB090398 Paralabid
1043	78	7.1	872	5	AB090425	AB090425 Gaurochro
1044	78	7.1	872	5	AB090427	AB090427 Astatotil
1045	78	7.1	903	6	CQ847198	CQ847198 Sequence
1046	78	7.1	903	6	AX440727	AX440727 Sequence
1047	78	7.1	1138	5	AY207478	AY207478 Euchilogl
1048	78	7.1	1138	5	AY207479	AY207479 Euchilogl
1049	78	7.1	1838	10	RATRTA	M35297 Rat pot. G
1050	78	7.1	1989	9	BC001293	BC001293 Homo sapi
1051	78	7.1	2436	5	GGCADHB	X58518 Chicken mRN
1052	78	7.1	2615	5	AF001406	AF001406 Carassius
1053	78	7.1	3126	3	AF515783	AF515783 Aplysia c
1054	78	7.1	3307	5	AASPAA	X76108 A.anguilla
1055	78	7.1	3900	1	AJ633552	AJ633552 Sphingomo
1056	78	7.1	3926	5	AB000470	AB000470 Gallus ga
c1057	78	7.1	7173	1	STU94729	U94729 Salmonella
1058	78	7.1	7437	14	RHDVCGS	Z29514 Rabbit hemo
1059	78	7.1	11876	9	AB110940	AB110940 Homo sapi
1060	78	7.1	11877	9	AB110939	AB110939 Homo sapi
c1061	78	7.1	20029	1	AE008755	AE008755 Salmonell
c1062	78	7.1	22700	3	CEF36G3	Z47069 Caenorhabdi
1063	78	7.1	36626	9	HS31E23	AL132993 Homo sapi
c1064	78	7.1	42074	9	AC004202	AC004202 Homo sapi
1065	78	7.1	52928	9	BX322644	BX322644 Human DNA
1066	78	7.1	57264	9	BX005441	BX005441 Human DNA
1067	78	7.1	69294	2	AC091032	AC091032 Homo sapi
1068	78	7.1	73009	9	BX927221	BX927221 Human DNA
c1069	78	7.1	74841	10	AL806529	AL806529 Mouse DNA
1070	78	7.1	78743	2	CR753815	CR753815 Homo sapi
1071	78	7.1	78827	9	CR788282	CR788282 Human DNA
1072	78	7.1	82272	5	BX001004	BX001004 Zebrafish
1073	78	7.1	83684	9	AC105290	AC105290 Homo sapi
c1074	78	7.1	100000	9	AP000518	AP000518 Homo sapi
1075	78	7.1	101333	8	AP004030	AP004030 Oryza sat
1076	78	7.1	104125	3	AC084468	AC084468 Caenorhab
1077	78	7.1	104924	9	CR759838	CR759838 Human DNA
1078	78	7.1	110000	2	AC087331_3	Continuation (4 of
1079	78	7.1	110000	2	AC097795_2	Continuation (3 of
c1080	78	7.1	110000	2	AL672261_1	Continuation (2 of
1081	78	7.1	120206	9	HS439F8	AL021392 Human DNA
1082	78	7.1	121587	1	CR522871	CR522871 Desulfota
1083	78	7.1	123460	8	AB073166	AB073166 Arabidops
c1084	78	7.1	128032	9	AC091730	AC091730 Homo sapi
c1085	78	7.1	139033	2	AC150739	AC150739 Zea mays
1086	78	7.1	144169	9	AL671859	AL671859 Human DNA
1087	78	7.1	149035	8	AC131343	AC131343 Oryza sat
1088	78	7.1	151042	8	AC114011	AC114011 Oryza sat
1089	78	7.1	152487	9	AP000431	AP000431 Homo sapi
1090	78	7.1	153420	10	AL591426	AL591426 Mouse DNA
1091	78	7.1	159178	9	AL669914	AL669914 Human DNA
1092	78	7.1	159620	9	AL354835	AL354835 Human DNA
1093	78	7.1	161099	10	AC132624	AC132624 Mus muscu
c1094	78	7.1	162383	9	AB023054	AB023054 Homo sapi
c1095	78	7.1	162383	9	AB023055	AB023055 Homo sapi
c1096	78	7.1	162760	9	AC007969	AC007969 Homo sapi
1097	78	7.1	165241	10	AC117802	AC117802 Mus muscu
c1098	78	7.1	165516	2	AC105938	AC105938 Homo sapi
c1099	78	7.1	167850	2	AC140114	AC140114 Rattus no

c1100	78	7.1	170225	10	AC122512	AC122512 Mus muscu
1101	78	7.1	174539	2	AC113298	AC113298 Mus muscu
c1102	78	7.1	176464	2	AC102297	AC102297 Mus muscu
c1103	78	7.1	176901	9	AC107623	AC107623 Homo sapi
1104	78	7.1	177681	10	AC122810	AC122810 Mus muscu
1105	78	7.1	178237	9	AF245226	AF245226 Homo sapi
c1106	78	7.1	183386	9	AC005229	AC005229 Homo sapi
c1107	78	7.1	183729	2	AC116352	AC116352 Homo sapi
1108	78	7.1	184346	10	AC122283	AC122283 Mus muscu
1109	78	7.1	184672	2	AP002508	AP002508 Homo sapi
c1110	78	7.1	187831	2	AC149640	AC149640 Zea mays
1111	78	7.1	188782	10	AL713870	AL713870 Mouse DNA
c1112	78	7.1	189768	2	CR753421	CR753421 Homo sapi
1113	78	7.1	190130	10	AC122808	AC122808 Mus muscu
c1114	78	7.1	191901	9	BS000101	BS000101 Pan trogl
1115	78	7.1	192106	9	AC090229	AC090229 Homo sapi
1116	78	7.1	196204	9	AC073957	AC073957 Homo sapi
1117	78	7.1	196398	10	AL604027	AL604027 Mouse DNA
c1118	78	7.1	197069	2	AC090370	AC090370 Homo sapi
1119	78	7.1	200477	9	AC090079	AC090079 Homo sapi
c1120	78	7.1	204430	2	CR792453	CR792453 Danio rer
c1121	78	7.1	204839	2	AC119260	AC119260 Mus muscu
1122	78	7.1	206137	2	AC142455	AC142455 Mus muscu
1123	78	7.1	207058	2	AP001394	AP001394 Homo sapi
1124	78	7.1	214250	2	AC103314	AC103314 Rattus no
1125	78	7.1	214648	2	AC105570	AC105570 Rattus no
c1126	78	7.1	217309	10	AL928632	AL928632 Mouse DNA
c1127	78	7.1	218882	2	AC133692	AC133692 Rattus no
c1128	78	7.1	218974	2	AC139456	AC139456 Homo sapi
1129	78	7.1	221586	2	BX957332	BX957332 Danio rer
c1130	78	7.1	224292	2	AC026873	AC026873 Homo sapi
c1131	78	7.1	226611	10	AC122878	AC122878 Mus muscu
1132	78	7.1	227495	2	AC148480	AC148480 Zea mays
1133	78	7.1	230258	2	AC110106	AC110106 Rattus no
1134	78	7.1	230682	2	BX510307	BX510307 Danio rer
1135	78	7.1	230956	9	AC090614	AC090614 Homo sapi
1136	78	7.1	233050	1	AL627271	AL627271 Salmonell
1137	78	7.1	236428	10	AC147563	AC147563 Mus muscu
1138	78	7.1	236844	2	AC098096	AC098096 Rattus no
c1139	78	7.1	256581	2	CR394526	CR394526 Danio rer
c1140	78	7.1	263603	2	AC114244	AC114244 Rattus no
c1141	78	7.1	266098	2	AC099280	AC099280 Rattus no
c1142	78	7.1	266164	2	AC113507	AC113507 Mus muscu
1143	78	7.1	274975	2	AC099279	AC099279 Rattus no
c1144	78	7.1	279560	2	AC113689	AC113689 Rattus no
c1145	78	7.1	280815	2	AC107562	AC107562 Rattus no
c1146	78	7.1	300523	1	AE016838	AE016838 Salmonell
1147	78	7.1	301877	2	AC096091	AC096091 Rattus no
1148	78	7.1	313143	2	AC120453	AC120453 Rattus no
c1149	78	7.1	316869	2	AC124509	AC124509 Mus muscu
c1150	78	7.1	324876	2	AC114164	AC114164 Rattus no
1151	78	7.1	340000	9	AP001674	AP001674 Homo sapi
c1152	78	7.1	349877	2	AC115218	AC115218 Rattus no
c1153	78	7.1	349980	6	AX344556	AX344556 Sequence
1154	77.5	7.0	945	6	AX489386	AX489386 Sequence
1155	77.5	7.0	1020	1	AF426455	AF426455 Primary e
1156	77.5	7.0	1055	4	CFCD44AG	Z27115 C.familiari
c1157	77.5	7.0	1089	5	AY062004	AY062004 Xenopus l
1158	77.5	7.0	1102	5	AF103007	AF103007 Ictalurus
1159	77.5	7.0	1850	9	BC018652	BC018652 Homo sapi
1160	77.5	7.0	1925	10	BC024072	BC024072 Mus muscu
1161	77.5	7.0	1941	10	BC031717	BC031717 Mus muscu
1162	77.5	7.0	1957	10	BC024123	BC024123 Mus muscu
1163	77.5	7.0	1977	10	AB055004	AB055004 Mus muscu
1164	77.5	7.0	2025	10	AY027919	AY027919 Mus muscu
1165	77.5	7.0	2313	6	AX046352	AX046352 Sequence
1166	77.5	7.0	2651	9	BC050328	BC050328 Homo sapi
c1167	77.5	7.0	2677	5	BC084337	BC084337 Xenopus l
c1168	77.5	7.0	3395	9	HSA420243	AJ420243 Homo sapi
1169	77.5	7.0	3421	1	AF467290	AF467290 Primary e
1170	77.5	7.0	3857	6	AX046398	AX046398 Sequence
c1171	77.5	7.0	4023	9	HUMMHCW2B	M16273 Human MHC c
1172	77.5	7.0	4433	10	AK129390	AK129390 Mus muscu
1173	77.5	7.0	4613	5	CHKCRYP	L32780 Gallus gall
1174	77.5	7.0	6798	8	AY219227	AY219227 Leavenwor
1175	77.5	7.0	6957	6	BD183310	BD183310 Novel gen
1176	77.5	7.0	7548	10	BC079889	BC079889 Mus muscu
c1177	77.5	7.0	7799	9	AF211174	AF211174 Homo sapi
1178	77.5	7.0	8671	9	AB051462	AB051462 Homo sapi
c1179	77.5	7.0	10410	1	AE010782	AE010782 Methanosa
c1180	77.5	7.0	13729	1	AE002415	AE002415 Neisseria
1181	77.5	7.0	15894	6	AR049868	AR049868 Sequence
1182	77.5	7.0	15894	6	BD137590	BD137590 Mutation
1183	77.5	7.0	15894	6	BD137591	BD137591 Mutation
1184	77.5	7.0	15894	6	BD137594	BD137594 Mutation
1185	77.5	7.0	15894	6	BD137595	BD137595 Mutation
1186	77.5	7.0	15894	6	BD137596	BD137596 Mutation
1187	77.5	7.0	15894	6	BD137597	BD137597 Mutation
1188	77.5	7.0	15894	6	E04903	E04903 DNA coding
1189	77.5	7.0	15894	6	I59432	I59432 Sequence 1
1190	77.5	7.0	15894	14	AB046218	AB046218 Measles v
1191	77.5	7.0	15894	14	AF266286	AF266286 Measles v
1192	77.5	7.0	15894	14	AF266287	AF266287 Measles v
1193	77.5	7.0	15894	14	AF266288	AF266288 Measles v
1194	77.5	7.0	15894	14	AF266289	AF266289 Measles v
1195	77.5	7.0	15894	14	AF266290	AF266290 Measles v
1196	77.5	7.0	15894	14	AF266291	AF266291 Measles v
1197	77.5	7.0	15894	14	AY486083	AY486083 Measles v
1198	77.5	7.0	15894	14	AY486084	AY486084 Measles v
1199	77.5	7.0	15894	14	MVEDMBCDN	Z66517 Measles vir
1200	77.5	7.0	15894	14	S58435	S58435 nucleocapsi
1201	77.5	7.0	18967	6	CQ753911	CQ753911 Sequence
1202	77.5	7.0	18967	6	CQ754454	CQ754454 Sequence
1203	77.5	7.0	18967	6	CQ754932	CQ754932 Sequence
1204	77.5	7.0	18967	6	CQ755017	CQ755017 Sequence
1205	77.5	7.0	31731	3	U21318	U21318 Caenorhabdi
1206	77.5	7.0	35040	1	BACYACA	L77246 Bacillus su
1207	77.5	7.0	36462	14	AY530876	AY530876 Simian ad
c1208	77.5	7.0	37570	8	ATU53501	U53501 Arabidopsis
c1209	77.5	7.0	38775	3	U46671	U46671 Caenorhabdi
1210	77.5	7.0	44645	9	AC108058	AC108058 Homo sapi
1211	77.5	7.0	71347	2	AC025308	AC025308 Homo sapi
c1212	77.5	7.0	74645	2	AC009592	AC009592 Homo sapi
1213	77.5	7.0	79976	9	BX537339	BX537339 Human DNA
c1214	77.5	7.0	79990	9	AC010457	AC010457 Homo sapi
1215	77.5	7.0	82144	9	AC099660	AC099660 Homo sapi
1216	77.5	7.0	94487	8	AC012394	AC012394 Arabidops
c1217	77.5	7.0	100806	8	AC015450	AC015450 Arabidops
1218	77.5	7.0	104418	9	AC119740	AC119740 Homo sapi
1219	77.5	7.0	109694	8	F23A5	AC011713 Arabidops
c1220	77.5	7.0	109694	8	F23A5	AC011713 Arabidops
1221	77.5	7.0	110000	1	CR628337_13	Continuation (14 o
1222	77.5	7.0	110000	2	LMFLCHR34_02	Continuation (3 of
c1223	77.5	7.0	110000	8	CR380955_04	Continuation (5 of
c1224	77.5	7.0	116469	8	AC093956	AC093956 Oryza sat
1225	77.5	7.0	121257	2	AC146307	AC146307 Medicago
1226	77.5	7.0	122269	9	HS653H13	AL031466 Human DNA
1227	77.5	7.0	131175	2	CNS08C7L	AL731736 Oryza sat
1228	77.5	7.0	133786	9	AC091839	AC091839 Homo sapi
c1229	77.5	7.0	137139	9	HSBB455A7	AL121580 Human DNA
1230	77.5	7.0	137908	10	AL607024	AL607024 Mouse DNA
1231	77.5	7.0	139155	2	AC149815	AC149815 Zea mays
1232	77.5	7.0	140572	9	AL354743	AL354743 Human DNA
1233	77.5	7.0	147350	2	AC069332	AC069332 Homo sapi
1234	77.5	7.0	148000	9	AP003464	AP003464 Homo sapi
1235	77.5	7.0	148057	5	BX649341	BX649341 Zebrafish
1236	77.5	7.0	148376	2	AC138898	AC138898 Homo sapi
c1237	77.5	7.0	150528	2	AC149242	AC149242 Macaca mu
1238	77.5	7.0	150789	2	AC006885	AC006885 Caenorhab
1239	77.5	7.0	152276	10	AC131763	AC131763 Mus muscu
c1240	77.5	7.0	154112	9	AC074378	AC074378 Homo sapi
c1241	77.5	7.0	154605	2	AC046161	AC046161 Homo sapi
1242	77.5	7.0	156153	10	AC107715	AC107715 Mus muscu
c1243	77.5	7.0	156677	2	AC092550	AC092550 Homo sapi
1244	77.5	7.0	159286	5	BX470149	BX470149 Zebrafish
1245	77.5	7.0	160378	2	AC090076	AC090076 Homo sapi

c1246	77.5	7.0	160603	9	AC096630	AC096630 Pan trogl
c1247	77.5	7.0	165277	5	AL954184	AL954184 Zebrafish
c1248	77.5	7.0	166371	2	BX936382	BX936382 Danio rer
1249	77.5	7.0	166637	9	AC008657	AC008657 Homo sapi
c1250	77.5	7.0	167726	2	CR812892	CR812892 Danio rer
1251	77.5	7.0	167835	2	AC151085	AC151085 Bos tauru
1252	77.5	7.0	168797	2	AC104882	AC104882 Mus muscu
c1253	77.5	7.0	168889	10	AL731779	AL731779 Mouse DNA
c1254	77.5	7.0	171550	9	AC079322	AC079322 Homo sapi
c1255	77.5	7.0	172044	2	AC151530	AC151530 Mus muscu
1256	77.5	7.0	172667	2	CR361541	CR361541 Danio rer
1257	77.5	7.0	172732	10	AC113039	AC113039 Mus muscu
1258	77.5	7.0	175426	2	AC113235	AC113235 Canis fam
1259	77.5	7.0	176436	2	AC148535	AC148535 Macaca mu
1260	77.5	7.0	177171	2	AC128176	AC128176 Rattus no
c1261	77.5	7.0	178071	2	AC145536	AC145536 Lemur cat
1262	77.5	7.0	179271	2	AC136883	AC136883 Sus scrof
c1263	77.5	7.0	179779	2	AC026012	AC026012 Homo sapi
1264	77.5	7.0	180606	2	AC073406	AC073406 Homo sapi
1265	77.5	7.0	181470	9	AC016659	AC016659 Homo sapi
c1266	77.5	7.0	182559	9	AC096590	AC096590 Homo sapi
1267	77.5	7.0	182871	3	AC117176	AC117176 Dictyoste
1268	77.5	7.0	184361	2	AC012481	AC012481 Homo sapi
1269	77.5	7.0	185020	5	BX649431	BX649431 Zebrafish
c1270	77.5	7.0	186720	2	AC122735	AC122735 Mus muscu
1271	77.5	7.0	187938	2	AC117973	AC117973 Rattus no
c1272	77.5	7.0	188532	2	AC145036	AC145036 Homo sapi
c1273	77.5	7.0	189710	10	AL805967	AL805967 Mouse DNA
1274	77.5	7.0	190256	10	AC121302	AC121302 Mus muscu
1275	77.5	7.0	191704	2	AC053529	AC053529 Homo sapi
1276	77.5	7.0	191710	10	AC122489	AC122489 Mus muscu
1277	77.5	7.0	193872	9	AC087369	AC087369 Homo sapi
1278	77.5	7.0	194727	2	AC148553	AC148553 Callithri
c1279	77.5	7.0	195642	2	AC125828	AC125828 Rattus no
c1280	77.5	7.0	201375	1	BSUB0012	Z99115 Bacillus su
c1281	77.5	7.0	201861	9	AC067796	AC067796 Homo sapi
1282	77.5	7.0	202267	9	DJ293M10	AF111167 Homo sapi
1283	77.5	7.0	203638	2	AC135953	AC135953 Macaca mu
1284	77.5	7.0	204741	10	AC145569	AC145569 Mus muscu
c1285	77.5	7.0	205910	2	AC044847	AC044847 Mus muscu
c1286	77.5	7.0	208369	1	AE017195	AE017195 Bacillus
c1287	77.5	7.0	212627	2	CR749167	CR749167 Danio rer
1288	77.5	7.0	214406	2	AC140672	AC140672 Mus muscu
1289	77.5	7.0	216409	2	AC136132	AC136132 Rattus no
1290	77.5	7.0	220407	2	AC121626	AC121626 Rattus no
1291	77.5	7.0	220903	2	CR293532	CR293532 Danio rer
1292	77.5	7.0	227008	2	AP001771	AP001771 Homo sapi
c1293	77.5	7.0	227430	2	AC091590	AC091590 Homo sapi
1294	77.5	7.0	229771	2	AC129242	AC129242 Rattus no
1295	77.5	7.0	230768	2	AC122571	AC122571 Rattus no
c1296	77.5	7.0	233759	2	CR293502	CR293502 Danio rer
c1297	77.5	7.0	235632	5	BX511021	BX511021 Zebrafish
c1298	77.5	7.0	236187	2	AC108287	AC108287 Rattus no
c1299	77.5	7.0	238678	2	AC097692	AC097692 Rattus no
1300	77.5	7.0	243163	2	AC117093	AC117093 Rattus no
c1301	77.5	7.0	250029	3	AE014820	AE014820 Plasmodiu
c1302	77.5	7.0	252410	2	AC095553	AC095553 Rattus no
1303	77.5	7.0	253924	3	AE014822	AE014822 Plasmodiu
1304	77.5	7.0	257028	2	AC129248	AC129248 Rattus no
1305	77.5	7.0	263238	2	AC136483	AC136483 Rattus no
c1306	77.5	7.0	300078	2	AC109067	AC109067 Rattus no
c1307	77.5	7.0	321250	1	SCO939111	AL939111 Streptomy
c1308	77.5	7.0	348430	2	AC130157	AC130157 Rattus no
c1309	77.5	7.0	349980	6	AX044029	AX044029 Sequence
c1310	77.5	7.0	349980	6	AX044030	AX044030 Sequence
1311	77	7.0	2253	8	AK102249	AK102249 Oryza sat
c1312	77	7.0	2337	3	AK114286	AK114286 Ciona int
1313	77	7.0	2383	8	AK103518	AK103518 Oryza sat
1314	77	7.0	2640	3	AY051488	AY051488 Drosophil
1315	77	7.0	2979	6	BD096360	BD096360 WT1 inter
c1316	77	7.0	3189	14	PRR223078	AJ223078 Porcine r
1317	77	7.0	3320	5	AY057072	AY057072 Fundulus
1318	77	7.0	4117	5	PWINTAV	X81108 P.waltl mRN

c1319	77	7.0	5595	10	BC008538	BC008538 Mus muscu
1320	77	7.0	6030	6	CQ591240	CQ591240 Sequence
1321	77	7.0	10029	1	AE015875	AE015875 Shewanell
c1322	77	7.0	10840	1	AE000908	AE000908 Methanoba
c1323	77	7.0	11684	1	AE006647	AE006647 Sulfolobu
c1324	77	7.0	11865	1	AE014797	AE014797 Bifidobac
c1325	77	7.0	13867	1	AE014737	AE014737 Bifidobac
1326	77	7.0	13987	1	AE014745	AE014745 Bifidobac
c1327	77	7.0	14023	1	AE007841	AE007841 Clostridi
1328	77	7.0	14835	1	AE010390	AE010390 Methanopy
1329	77	7.0	15205	1	U67516	U67516 Methanocald
1330	77	7.0	33026	9	AF156673	AF156673 Homo sapi
1331	77	7.0	56105	1	SS56KBFR	Y08257 S.solfatari
c1332	77	7.0	62070	8	NC2E4	AL451022 Neurospor
c1333	77	7.0	65182	2	AC101488	AC101488 Mus muscu
1334	77	7.0	81209	10	AL805942	AL805942 Mouse DNA
c1335	77	7.0	82944	9	AL354999	AL354999 Human DNA
1336	77	7.0	88546	9	AC008435	AC008435 Homo sapi
1337	77	7.0	110000	2	AC105546_1	Continuation (2 of
1338	77	7.0	110000	2	AC105546_2	Continuation (3 of
1339	77	7.0	110000	2	AC114343_0	AC114343 Rattus no
1340	77	7.0	110000	2	AC115635_0	AC115635 Rattus no
c1341	77	7.0	110000	2	BX649565_2	Continuation (3 of
c1342	77	7.0	110000	6	AR271569_08	Continuation (9 of
1343	77	7.0	111560	9	AC073905	AC073905 Homo sapi
1344	77	7.0	116951	9	AC114788	AC114788 Homo sapi
c1345	77	7.0	129198	8	OSJN00275	AL731632 Oryza sat
1346	77	7.0	132077	9	AC005589	AC005589 Homo sapi
1347	77	7.0	132319	10	AL805904	AL805904 Mouse DNA
1348	77	7.0	135873	9	AC008915	AC008915 Homo sapi
c1349	77	7.0	141810	2	CR847532	CR847532 Danio rer
c1350	77	7.0	142331	2	AF307157	AF307157 Homo sapi
1351	77	7.0	143549	2	AC118287	AC118287 Oryza sat
c1352	77	7.0	147172	9	AC022234	AC022234 Homo sapi
c1353	77	7.0	148033	2	AC121513	AC121513 Mus muscu
c1354	77	7.0	149907	4	AC091436	AC091436 Felis cat
c1355	77	7.0	150582	2	AC147805	AC147805 Mus muscu
c1356	77	7.0	160589	10	AL663066	AL663066 Mouse DNA
1357	77	7.0	160681	10	AL844140	AL844140 Mouse DNA
1358	77	7.0	165051	9	AC026950	AC026950 Homo sapi
1359	77	7.0	165723	2	AC150538	AC150538 Bos tauru
1360	77	7.0	168470	2	AC147309	AC147309 Pan trogl
1361	77	7.0	172828	10	AC124187	AC124187 Mus muscu
c1362	77	7.0	175026	2	AL512409	AL512409 Homo sapi
1363	77	7.0	177893	9	AC005089	AC005089 Homo sapi
c1364	77	7.0	179919	2	AC114383	AC114383 Rattus no
1365	77	7.0	181279	2	CR382383	CR382383 Danio rer
c1366	77	7.0	182706	2	AC022374	AC022374 Homo sapi
c1367	77	7.0	185928	2	AC127983	AC127983 Rattus no
1368	77	7.0	187509	2	AC131327	AC131327 Mus muscu
c1369	77	7.0	188219	2	AC022875	AC022875 Homo sapi
c1370	77	7.0	193333	9	AC090958	AC090958 Homo sapi
c1371	77	7.0	193363	10	AL627104	AL627104 Mouse DNA
c1372	77	7.0	193936	9	AL359636	AL359636 Human DNA
c1373	77	7.0	196065	10	AC139060	AC139060 Mus muscu
1374	77	7.0	196263	2	AC131385	AC131385 Homo sapi
1375	77	7.0	196413	2	AC139927	AC139927 Rattus no
c1376	77	7.0	197013	2	AC079552	AC079552 Mus muscu
1377	77	7.0	198264	9	AC018841	AC018841 Homo sapi
c1378	77	7.0	200548	10	AL672026	AL672026 Mouse DNA
c1379	77	7.0	202838	2	CR388230	CR388230 Mus muscu
c1380	77	7.0	204834	9	AC009312	AC009312 Homo sapi
1381	77	7.0	204919	2	AC150766	AC150766 Bos tauru
1382	77	7.0	206093	10	AC087330	AC087330 Mus muscu
c1383	77	7.0	207161	2	AC120651	AC120651 Rattus no
1384	77	7.0	207687	10	AL824706	AL824706 Mouse DNA
c1385	77	7.0	207909	10	AC122318	AC122318 Mus muscu
c1386	77	7.0	208014	10	AL691519	AL691519 Mouse DNA
1387	77	7.0	211668	2	AC115146	AC115146 Rattus no
1388	77	7.0	211930	2	AC123986	AC123986 Mus muscu
c1389	77	7.0	212343	2	AC130007	AC130007 Rattus no
1390	77	7.0	214118	9	BS000047	BS000047 Pan trogl
1391	77	7.0	214178	5	BX640577	BX640577 Zebrafish

c1392	77	7.0	217372	2	AC148224	AC148224 Colobus g
1393	77	7.0	218291	10	AC146610	AC146610 Mus muscu
c1394	77	7.0	218686	2	AC137954	AC137954 Mus muscu
c1395	77	7.0	218696	9	BS000031	BS000031 Pan trogl
1396	77	7.0	223281	2	AC101671	AC101671 Mus muscu
1397	77	7.0	223395	2	AC109386	AC109386 Rattus no
c1398	77	7.0	224390	2	AC124228	AC124228 Mus muscu
c1399	77	7.0	224534	10	AC145076	AC145076 Mus muscu
1400	77	7.0	226883	10	AC112680	AC112680 Mus muscu
1401	77	7.0	228546	2	AC128594	AC128594 Rattus no
1402	77	7.0	231850	2	AC103162	AC103162 Rattus no
1403	77	7.0	233944	2	AC106583	AC106583 Rattus no
1404	77	7.0	235925	2	AC127608	AC127608 Rattus no
1405	77	7.0	238039	2	AC140796	AC140796 Mus muscu
1406	77	7.0	239172	2	AC095885	AC095885 Rattus no
c1407	77	7.0	240628	2	AC129400	AC129400 Rattus no
1408	77	7.0	241607	2	AC113636	AC113636 Rattus no
c1409	77	7.0	243860	2	AC114710	AC114710 Rattus no
1410	77	7.0	244662	2	AC113927	AC113927 Rattus no
1411	77	7.0	247838	2	AC113445	AC113445 Mus muscu
c1412	77	7.0	248308	2	AC073937	AC073937 Mus muscu
1413	77	7.0	248341	2	AC094181	AC094181 Rattus no
c1414	77	7.0	249589	2	AC098962	AC098962 Rattus no
c1415	77	7.0	251933	2	AC133356	AC133356 Rattus no
c1416	77	7.0	256777	2	AC110239	AC110239 Mus muscu
1417	77	7.0	257261	2	AC098513	AC098513 Rattus no
c1418	77	7.0	261522	2	AC099585	AC099585 Mus muscu
1419	77	7.0	265663	2	AC109741	AC109741 Rattus no
1420	77	7.0	274762	1	BX664015	BX664015 Serratia
c1421	77	7.0	283791	2	AC133615	AC133615 Rattus no
c1422	77	7.0	290181	2	AC094516	AC094516 Rattus no
1423	77	7.0	324050	1	BX251410	BX251410 Tropherym
c1424	77	7.0	331039	3	AC116979	AC116979 Dictyoste
c1425	77	7.0	340212	2	AC110386	AC110386 Rattus no
c1426	77	7.0	340425	2	AC137190	AC137190 Rattus no
c1427	77	7.0	346613	1	BX571661	BX571661 Wolinella
c1428	77	7.0	348277	2	AC110391	AC110391 Rattus no
1429	77	7.0	349980	6	AX492785	AX492785 Sequence
c1430	77	7.0	349980	6	AX492785	AX492785 Sequence
c1431	77	7.0	349980	6	AX492787	AX492787 Sequence
1432	77	7.0	349980	6	AX553952	AX553952 Sequence
c1433	77	7.0	349980	6	AX553952	AX553952 Sequence
c1434	77	7.0	349980	6	AX553954	AX553954 Sequence
1435	76.5	6.9	648	9	AY327582	AY327582 Homo sapi
c1436	76.5	6.9	885	5	BX931788	BX931788 Gallus ga
1437	76.5	6.9	912	6	CQ847093	CQ847093 Sequence
1438	76.5	6.9	912	6	AX440622	AX440622 Sequence
c1439	76.5	6.9	960	6	AR395530	AR395530 Sequence
1440	76.5	6.9	981	6	AR544923	AR544923 Sequence
1441	76.5	6.9	1150	5	AY331583	AY331583 Danio rer
1442	76.5	6.9	1300	1	STU20795	U20795 Salmonella
c1443	76.5	6.9	1330	9	AK074197	AK074197 Homo sapi
1444	76.5	6.9	1344	5	XLU90895	U90895 Xenopus lae
1445	76.5	6.9	1399	8	AF151454	AF151454 Cirsium s
1446	76.5	6.9	1650	6	AX411427	AX411427 Sequence
1447	76.5	6.9	1650	6	AX411429	AX411429 Sequence
1448	76.5	6.9	1650	9	AF282874	AF282874 Homo sapi
1449	76.5	6.9	1795	9	GIBMUC1A	L41589 Hylobates l
1450	76.5	6.9	1917	9	BC016982	BC016982 Homo sapi
1451	76.5	6.9	2680	9	BC001336	BC001336 Homo sapi
1452	76.5	6.9	2926	5	BC081156	BC081156 Xenopus l
1453	76.5	6.9	3032	6	CQ720852	CQ720852 Sequence
1454	76.5	6.9	3147	6	AX411425	AX411425 Sequence
1455	76.5	6.9	3237	5	AF002983	AF002983 Xenopus l
1456	76.5	6.9	3291	4	AF170528	AF170528 Oryctolag
1457	76.5	6.9	3552	3	DROINTBETN	L13305 Drosophila
1458	76.5	6.9	3742	4	CFU55028	U55028 Canis famil
1459	76.5	6.9	3900	6	CQ574491	CQ574491 Sequence
1460	76.5	6.9	4617	9	AB011090	AB011090 Homo sapi
1461	76.5	6.9	7572	6	CQ574490	CQ574490 Sequence
1462	76.5	6.9	9819	1	AE014112	AE014112 Buchnera
1463	76.5	6.9	15894	14	MEANPCG	K01711 Measles vir
c1464	76.5	6.9	22348	1	AE008699	AE008699 Salmonell
1465	76.5	6.9	27518	9	HS1032F13	AL031903 Human DNA
c1466	76.5	6.9	32501	9	HSAP2B	Y09912 H.sapiens A
c1467	76.5	6.9	33087	3	U00055	U00055 Caenorhabdi
1468	76.5	6.9	36535	14	AY530878	AY530878 Simian ad
1469	76.5	6.9	38456	3	AF016684	AF016684 Caenorhab
c1470	76.5	6.9	41581	2	AC017258	AC017258 Drosophil
c1471	76.5	6.9	59032	10	BX005046	BX005046 Mouse DNA
1472	76.5	6.9	70104	8	BX908810	BX908810 Neurospor
1473	76.5	6.9	77612	8	NCB8J24	AL669990 Neurospor
c1474	76.5	6.9	85802	10	AL671909	AL671909 Mouse DNA
1475	76.5	6.9	93352	2	AC091707	AC091707 Homo sapi
c1476	76.5	6.9	99103	9	AF202964	AF202964 Homo sapi
c1477	76.5	6.9	102331	8	AC007120	AC007120 Arabidops
1478	76.5	6.9	106746	8	AC139840	AC139840 Solanum d
c1479	76.5	6.9	110000	8	CR382136_02	Continuation (3 of
c1480	76.5	6.9	110000	10	AE014180_0	AE014180 Mus muscu
c1481	76.5	6.9	117072	9	AC010445	AC010445 Homo sapi
1482	76.5	6.9	118049	8	AC104276	AC104276 Oryza sat
c1483	76.5	6.9	118280	9	HSDJ753D5	AL049693 Human DNA
c1484	76.5	6.9	122613	9	AL359642	AL359642 Human DNA
1485	76.5	6.9	123964	2	AC148643	AC148643 Sorex ara
1486	76.5	6.9	136129	2	AC011050	AC011050 Homo sapi
c1487	76.5	6.9	137878	10	AL627252	AL627252 Mouse DNA
c1488	76.5	6.9	142638	9	AL355316	AL355316 Human DNA
c1489	76.5	6.9	143325	2	AL137180	AL137180 Homo sapi
c1490	76.5	6.9	144454	9	BS000637	BS000637 Pan trogl
1491	76.5	6.9	144665	9	CNS07EF7	AL512358 Human chr
1492	76.5	6.9	145115	2	AC092197	AC092197 Homo sapi
c1493	76.5	6.9	146454	14	AF410153	AF410153 Swinepox
c1494	76.5	6.9	148026	2	AC142083	AC142083 Homo sapi
c1495	76.5	6.9	148090	10	AC100737	AC100737 Mus muscu
c1496	76.5	6.9	148751	10	AL929167	AL929167 Mouse DNA
1497	76.5	6.9	151147	2	AC131450	AC131450 Strongylo
c1498	76.5	6.9	151509	9	CNS05TE8	AL358337 Human chr
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1500	76.5	6.9	154080	2	AC024416	AC024416 Homo sapi

ALIGNMENTS

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RESULT 1
AR252633
LOCUS       AR252633                1346 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 386 from patent US 6478825.
ACCESSION   AR252633
VERSION     AR252633.1  GI:27300541
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1346)
  AUTHORS   Winterbottom,J.M., Shimp,L., Boyce,T.M. and Kaes,D.
  TITLE     Implant, method of making same and use of the implant for the
            treatment of bone defects
  JOURNAL   Patent: US 6478825-A 386 12-NOV-2002;
FEATURES             Location/Qualifiers
     source          1. .1346
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:                9.02e-114      Length:          1346
Score:                    1102.00        Matches:         212
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       6              Gaps:            0

US-09-989-724-387 (1-212) x AR252633 (1-1346)

Qy          1 MetLeuTrpLeuLeuPhePheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20
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Db          7 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 66

Qy         21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
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Db         67 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 126

Qy         41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
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Db        127 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 186

Qy         61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80
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Db        187 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 246

Qy         81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
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Db        247 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 306

Qy        101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120
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Db        307 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 366

Qy        121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140
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Db        367 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 426

Qy        141 ProIleTrpIleIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 486

Qy        161 LeuIleLeuSerGlyIleTrpGlnArgArgArgLysAsnLysGluProSerGluValAsp 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 546

Qy        181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200
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Db        547 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 606

Qy        201 LeuAspMetLysGlyGlyIleLeuMetMetProSer 212
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Db        607 CTGGACATGAAGGGGGGCATATTAATGATGCCTTCA 642
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RESULT 2
AR528692
LOCUS AR528692 1346 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 481 from patent US 6725730.
ACCESSION AR528692
VERSION AR528692.1 GI:53916770
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1346)
AUTHORS Bollinger,C.L. Jr.
TITLE Crane test weight assembly and method
JOURNAL Patent: US 6725730-A 481 27-APR-2004;
FEATURES Location/Qualifiers
source 1. .1346
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Alignment Scores:

Pred. No.:	9.02e-114	Length:	1346
Score:	1102.00	Matches:	212
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-09-989-724-387 (1-212) x AR528692 (1-1346)

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Qy         21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
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Db         67 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 126

Qy         41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
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Db        127 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 186

Qy         61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80
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Db        187 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 246

Qy         81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
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Db        247 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 306

Qy        101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120
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Db        307 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 366

Qy        121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140
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Db        367 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 426

Qy        141 ProIleTrpIleIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 486

Qy        161 LeuIleLeuSerGlyIleTrpGlnArgArgArgLysAsnLysGluProSerGluValAsp 180
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Qy        181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200
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Db        547 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 606

Qy        201 LeuAspMetLysGlyGlyIleLeuMetMetProSer 212
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Db        607 CTGGACATGAAGGGGGGCATATTAATGATGCCTTCA 642
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RESULT 3
AX403499
LOCUS AX403499 1346 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 386 from Patent WO0073454.
ACCESSION AX403499
VERSION AX403499.1 GI:21436987
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ashkenazi,A.J., Baker,K.P., Botstein,D., Desnoyers,L., Eaton,D.,
Ferrara,N., Gerber,H., Gerritsen,M., Goddard,A., Godowski,P.,
Grimaldi,C.J., Gurney,A.L., Kljavin,I., Napier,M.A., Pan,J.,
Paoni,N.F., Roy,M., Stewart,T.A., Tumas,D., Watanabe,C.K.,
Williams,P., Wood,W.I. and Zhang,Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0073454-A 386 07-DEC-2000;
Genentech Inc. (US)
FEATURES Location/Qualifiers
source 1. .1346
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN

Alignment Scores:

Pred. No.:	9.02e-114	Length:	1346

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Score:                  1102.00         Matches:        212
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

US-09-989-724-387 (1-212) x AX403499 (1-1346)

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Db          7 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 66

Qy         21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 126

Qy         41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
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Db        127 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 186

Qy         61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 246

Qy         81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
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Db        247 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 306

Qy        101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120
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Db        307 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 366

Qy        121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140
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Db        367 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 426

Qy        141 ProIleTrpIleIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 486

Qy        161 LeuIleLeuSerGlyIleTrpGlnArgArgArgLysAsnLysGluProSerGluValAsp 180
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Db        487 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 546

Qy        181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200
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Db        547 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 606

Qy        201 LeuAspMetLysGlyGlyIleLeuMetMetProSer 212
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Db        607 CTGGACATGAAGGGGGGCATATTAATGATGCCTTCA 642

RESULT 4
AX464348
LOCUS       AX464348               1346 bp    DNA     linear   PAT 16-JUL-2002
DEFINITION  Sequence 481 from Patent WO0140466.
ACCESSION   AX464348
VERSION     AX464348.1  GI:21899190
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Baker,K.P., Beresini,M., Deforge,L., Desnoyers,L., Filvaroff,E.,
            Gao,W.Q., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L.,
            Sherwood,S., Smith,V., Stewart,T.A., Tumas,D., Watanabe,C.K.,
            Wood,W.L. and Zhang,Z.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
            same
  JOURNAL   Patent: WO 0140466-A 481 07-JUN-2001;
            Genentech Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1346
                     /organism="Homo sapiens"
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ORIGIN

Alignment Scores:
Pred. No.:              9.02e-114       Length:         1346
Score:                  1102.00         Matches:        212
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

US-09-989-724-387 (1-212) x AX464348 (1-1346)

Qy          1 MetLeuTrpLeuLeuPhePheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20
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Qy         21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
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Db         67 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 126

Qy         41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
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Db        127 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 186

Qy         61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80
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Db        187 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 246

Qy         81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 306

Qy        101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120
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Qy        121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140
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Db        367 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 426

Qy        141 ProIleTrpIleIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 486

Qy        161 LeuIleLeuSerGlyIleTrpGlnArgArgArgLysAsnLysGluProSerGluValAsp 180
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Db        487 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 546

Qy        181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 606

Qy        201 LeuAspMetLysGlyGlyIleLeuMetMetProSer 212
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Db        607 CTGGACATGAAGGGGGGCATATTAATGATGCCTTCA 642

RESULT 5
AY359060
LOCUS       AY359060               1346 bp    mRNA    linear   PRI 03-OCT-2003
DEFINITION  Homo sapiens clone DNA61873 NX-17 (UNQ678) mRNA, complete cds.
ACCESSION   AY359060
VERSION     AY359060.1  GI:37183237
KEYWORDS    FLI_CDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1346)
  AUTHORS   Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
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          Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
          Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
          Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
          Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,
          Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,
          Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K.,
          Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
          Goddard,A., Wood,W.I. and Godowski,P.
  TITLE   The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
          Effort to Identify Novel Human Secreted and Transmembrane Proteins:
          A Bioinformatics Assessment
  JOURNAL Genome Res. 13 (10), 2265-2270 (2003)
   PUBMED 12975309
REFERENCE 2  (bases 1 to 1346)
  AUTHORS Clark,H.F.
  TITLE   Direct Submission
  JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
          Inc., 1 DNA Way, South San Francisco, CA 94080, USA
FEATURES             Location/Qualifiers
     source          1. .1346
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="DNA61873"
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                     /note="PRO1312"
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ORIGIN

Alignment Scores:
Pred. No.:                9.02e-114      Length:          1346
Score:                    1102.00        Matches:         212
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       9              Gaps:            0

US-09-989-724-387 (1-212) x AY359060 (1-1346)

Qy          1 MetLeuTrpLeuLeuPhePheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20
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Db          7 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 66

Qy         21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 126

Qy         41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 186

Qy         61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 246

Qy         81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
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Db        247 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 306

Qy        101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120
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Db        307 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 366

Qy        121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140
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Db        367 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 426

Qy        141 ProIleTrpIleIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 486

Qy        161 LeuIleLeuSerGlyIleTrpGlnArgArgArgLysAsnLysGluProSerGluValAsp 180
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Db        487 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 546

Qy        181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200
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Db        547 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 606

Qy        201 LeuAspMetLysGlyGlyIleLeuMetMetProSer 212
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Db        607 CTGGACATGAAGGGGGGCATATTAATGATGCCTTCA 642

RESULT 6
AX083382
LOCUS       AX083382                 666 bp    DNA     linear   PAT 28-FEB-2001
DEFINITION  Sequence 74 from Patent WO0112660.
ACCESSION   AX083382
VERSION     AX083382.1  GI:13185219
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kato,S. and Kimura,T.
  TITLE     Human proteins having hydrophobic domains and dnas encoding these
            proteins
  JOURNAL   Patent: WO 0112660-A 74 22-FEB-2001;
            SAGAMI CHEMICAL RESEARCH CENTER (JP) ; Protegene Inc. (JP)
FEATURES             Location/Qualifiers
     source          1. .666
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
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ORIGIN

Alignment Scores:
Pred. No.:                1.11e-112      Length:          666
Score:                    1089.00        Matches:         212
Percent Similarity:       99.53%         Conservative:    0
Best Local Similarity:    99.53%         Mismatches:      0
Query Match:              98.82%         Indels:          1
DB:                       6              Gaps:            0

US-09-989-724-387 (1-212) x AX083382 (1-666)

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Db          1 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 60

Qy         21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
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Db         61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120

Qy         41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
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Db        121 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 180

Qy         61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80
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Qy         81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
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Qy        101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120
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Db        301 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 360

Qy        121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140
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Db        361 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 420

Qy        141 ProIleTrpIleIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160
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Db        421 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480

Qy        161 LeuIleLeuSerGlyIleTrpGlnArgArgArgLysAsnLysGluProSerGluValAsp 180
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Db        481 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 540

Qy        181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200
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Qy        201 LeuAspMetLysGly-GlyIleLeuMetMetProSer 212
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Db        601 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCA 637

RESULT 7
AF229179
LOCUS       AF229179               1345 bp    mRNA    linear   PRI 05-APR-2002
DEFINITION  Homo sapiens collectrin mRNA, complete cds.
ACCESSION   AF229179
VERSION     AF229179.1  GI:9957753
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1345)
  AUTHORS   Zhang,H., Wada,J., Hida,K., Tsuchiyama,Y., Hiragushi,K.,
            Shikata,K., Wang,H., Lin,S., Kanwar,Y.S. and Makino,H.
  TITLE     Collectrin, a collecting duct-specific transmembrane glycoprotein,
            is a novel homolog of ACE2 and is developmentally regulated in
            embryonic kidneys
  JOURNAL   J. Biol. Chem. 276 (20), 17132-17139 (2001)
  MEDLINE   21264468
   PUBMED   11278314
REFERENCE   2  (bases 1 to 1345)
  AUTHORS   Zhang,H., Wada,J. and Makino,H.
  TITLE     Human kidney specific membrane protein (NX-17)
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 1345)
  AUTHORS   Zhang,H., Wada,J. and Makino,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-JAN-2000) Department of Medicine III, Okayama
            University Medical School, 2-5-1 Shikata-cho, Okayama 700-8558,
            Japan
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
     CDS             24. .692
                     /note="kidney-specific membrane protein NX-17; similar to
                     the Mus musculus and Rattus norvegicus products encoded by
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                     /codon_start=1
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                     LTPL"
ORIGIN

Alignment Scores:
Pred. No.:              2.6e-112        Length:         1345
Score:                  1089.00         Matches:        212
Percent Similarity:     99.53%          Conservative:   0
Best Local Similarity:  99.53%          Mismatches:     0
Query Match:            98.82%          Indels:         1
DB:                     9               Gaps:           0

US-09-989-724-387 (1-212) x AF229179 (1-1345)

Qy          1 MetLeuTrpLeuLeuPhePheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20
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Db         24 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 83

Qy         21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 143

Qy         41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
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Db        144 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 203

Qy         61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80
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Db        204 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 263

Qy         81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
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Db        264 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAA 323

Qy        101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120
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Db        324 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 383

Qy        121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140
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Db        384 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 443

Qy        141 ProIleTrpIleIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160
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Db        444 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 503

Qy        161 LeuIleLeuSerGlyIleTrpGlnArgArgArgLysAsnLysGluProSerGluValAsp 180
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Qy        181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200
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Db        564 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 623

Qy        201 LeuAspMetLysGly-GlyIleLeuMetMetProSer 212
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Db        624 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCA 660

RESULT 8
AX083392
LOCUS       AX083392               1347 bp    DNA     linear   PAT 28-FEB-2001
DEFINITION  Sequence 84 from Patent WO0112660.
ACCESSION   AX083392
VERSION     AX083392.1  GI:13185232
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kato,S. and Kimura,T.
  TITLE     Human proteins having hydrophobic domains and dnas encoding these
            proteins
  JOURNAL   Patent: WO 0112660-A 84 22-FEB-2001;
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            SAGAMI CHEMICAL RESEARCH CENTER (JP) ; Protegene Inc. (JP)
FEATURES             Location/Qualifiers
     source          1. .1347
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
     CDS             26. .694
                     /note="unnamed protein product"
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                     /protein_id="CAC33295.1"
                     /db_xref="GI:13185233"
                     /translation="MLWLLFFLVTAIHAELCQPGAENAFKVRLSIRTALGDKAYAWDT
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                     LILSGIWQRRRKNKEPSEVDDAEDKCENMITIENGIPSDPLDMKGGHINDAFMTEDER
                     LTPL"
ORIGIN

Alignment Scores:
Pred. No.:                2.61e-112      Length:          1347
Score:                    1089.00        Matches:         212
Percent Similarity:       99.53%         Conservative:    0
Best Local Similarity:    99.53%         Mismatches:      0
Query Match:              98.82%         Indels:          1
DB:                       6              Gaps:            0

US-09-989-724-387 (1-212) x AX083392 (1-1347)

Qy          1 MetLeuTrpLeuLeuPhePheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20
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Db         26 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 85

Qy         21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
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Db         86 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 145

Qy         41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
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Db        146 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 205

Qy         61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80
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Db        206 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 265

Qy         81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
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Db        266 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 325

Qy        101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120
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Db        326 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 385

Qy        121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140
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Db        386 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 445

Qy        141 ProIleTrpIleIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160
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Db        446 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 505

Qy        161 LeuIleLeuSerGlyIleTrpGlnArgArgArgLysAsnLysGluProSerGluValAsp 180
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Db        506 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 565

Qy        181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        566 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 625

Qy        201 LeuAspMetLysGly-GlyIleLeuMetMetProSer 212
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RESULT 9
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BC050606
LOCUS       BC050606                1377 bp    mRNA    linear   PRI 30-JUN-2004
DEFINITION  Homo sapiens transmembrane protein 27, mRNA (cDNA clone MGC:60059
            IMAGE:5183554), complete cds.
ACCESSION   BC050606
VERSION     BC050606.1  GI:30047080
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1377)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
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            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1377)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-APR-2003) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA  94305
            Web site:       http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 110 Row: c Column: 4
            This clone was selected for full length sequencing because it
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                     /lab_host="DH10B"
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                     /db_xref="LocusID:57393"
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                     LILSGIWQRRRKNKEPSEVDDAEDKCENMITIENGIPSDPLDMKGGHINDAFMTEDER
                     LTPL"
ORIGIN

Alignment Scores:
Pred. No.:              2.68e-112       Length:         1377
Score:                  1089.00         Matches:        212
Percent Similarity:     99.53%          Conservative:   0
Best Local Similarity:  99.53%          Mismatches:     0
Query Match:            98.82%          Indels:         1
DB:                     9               Gaps:           0

US-09-989-724-387 (1-212) x BC050606 (1-1377)

Qy          1 MetLeuTrpLeuLeuPhePheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20
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Db          9 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 68

Qy         21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
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Db         69 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 128

Qy         41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
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Db        129 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 188

Qy         61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80
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Db        189 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 248

Qy         81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
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Qy        101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120
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Db        309 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 368

Qy        121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140
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Db        369 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 428

Qy        141 ProIleTrpIleIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160
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Db        429 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 488

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Qy        181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200
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Qy        201 LeuAspMetLysGly-GlyIleLeuMetMetProSer 212
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Db        609 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCA 645

RESULT 10
BC015099
LOCUS       BC015099               1440 bp    mRNA    linear   PRI 29-JUN-2004
DEFINITION  Homo sapiens transmembrane protein 27, mRNA (cDNA clone MGC:22827
            IMAGE:3829035), complete cds.

ACCESSION   BC015099
VERSION     BC015099.1  GI:15929328
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1440)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
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            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
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            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
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            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1440)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-OCT-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: CLONTECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Institute for Systems Biology
            http://www.systemsbiology.org
            contact: amadan@systemsbiology.org
            Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
            Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 31 Row: d Column: 11
            This clone was selected for full length sequencing because it
            passed the following selection criteria: GenomeScan gene
            prediction, Similarity but not identity to protein.
FEATURES             Location/Qualifiers
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     gene            1. .1440
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                     /note="synonyms: NX-17, NX17"
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                     LTPL"
ORIGIN

Alignment Scores:
Pred. No.:              2.83e-112       Length:         1440
Score:                  1089.00         Matches:        212
Percent Similarity:     99.53%          Conservative:   0
Best Local Similarity:  99.53%          Mismatches:     0
Query Match:            98.82%          Indels:         1
DB:                     9               Gaps:           0

US-09-989-724-387 (1-212) x BC015099 (1-1440)

Qy          1 MetLeuTrpLeuLeuPhePheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20
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Qy         21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
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Qy         41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
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Qy         61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80
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Db        269 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 328

Qy         81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
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Qy        101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120
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Db        389 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 448

Qy        121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140
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Db        449 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 508

Qy        141 ProIleTrpIleIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160
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Db        509 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 568

Qy        161 LeuIleLeuSerGlyIleTrpGlnArgArgArgLysAsnLysGluProSerGluValAsp 180
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Db        569 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 628

Qy        181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200
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Db        629 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 688

Qy        201 LeuAspMetLysGly-GlyIleLeuMetMetProSer 212
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Db        689 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCA 725

RESULT 11
BC014317
LOCUS       BC014317                1605 bp    mRNA    linear   PRI 29-JUN-2004
DEFINITION  Homo sapiens transmembrane protein 27, mRNA (cDNA clone MGC:22707
            IMAGE:4048217), complete cds.
ACCESSION   BC014317
VERSION     BC014317.1  GI:15680012
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1605)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1605)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-SEP-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: CLONTECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Institute for Systems Biology
            http://www.systemsbiology.org
            contact: amadan@systemsbiology.org
            Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
            Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 31 Row: n Column: 3
            This clone was selected for full length sequencing because it
            passed the following selection criteria: Hexamer frequency ORF
            analysis, Similarity but not identity to protein.
FEATURES             Location/Qualifiers
     source          1. .1605
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                     /tissue_type="Bone marrow, chronic myelogenous leukemia"
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                     /note="synonyms: NX-17, NX17"
                     /db_xref="LocusID:57393"
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                     /product="transmembrane protein 27"
                     /protein_id="AAH14317.1"
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LTPL"

ORIGIN

Alignment Scores:

Pred. No.:	3.22e-112	Length:	1605
Score:	1089.00	Matches:	212
Percent Similarity:	99.53%	Conservative:	0
Best Local Similarity:	99.53%	Mismatches:	0
Query Match:	98.82%	Indels:	1
DB:	9	Gaps:	0

US-09-989-724-387 (1-212) x BC014317 (1-1605)

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Db        261 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 320

Qy         21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
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Db        321 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 380

Qy         41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
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Db        381 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 440

Qy         61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80
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Db        441 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 500

Qy         81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
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Db        501 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 560

Qy        101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120
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Db        561 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 620

Qy        121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140
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Db        621 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 680

Qy        141 ProIleTrpIleIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160
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Db        681 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 740

Qy        161 LeuIleLeuSerGlyIleTrpGlnArgArgArgLysAsnLysGluProSerGluValAsp 180
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Db        741 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 800

Qy        181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200
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Db        801 GACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 860

Qy        201 LeuAspMetLysGly-GlyIleLeuMetMetProSer 212
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Db        861 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCA 897
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RESULT 12
BD083420

LOCUS	BD083420 1401 bp DNA linear PAT 27-AUG-2002
DEFINITION	Secreted proteins and polynucleotides encoding them.
ACCESSION	BD083420
VERSION	BD083420.1 GI:22629030
KEYWORDS	JP 2001523950-A/2.
SOURCE	synthetic construct
ORGANISM	synthetic construct other sequences; artificial sequences.
REFERENCE	1 (bases 1 to 1401)
AUTHORS	Jacobs,K., Mccoy,J.M., Lavallie,E.R., Racie,L.A., Merberg,D., Treacy,M., Spaulding,V. and Agostino,M.J.
TITLE	Secreted proteins and polynucleotides encoding them
JOURNAL	Patent: JP 2001523950-A 2 27-NOV-2001; GENETICS INSTITUTE INC
COMMENT	PN JP 2001523950-A/2 PD 27-NOV-2001 PF 23-JAN-1998 JP 1998532177 PR 24-JAN-1997 US 08/788789 PI KENNETH JACOBS,JOHN M MCCOY,EDWARD R LAVALLIE,LISA A RACIE, PI DAVID MERBERG, PI MAURICE TREACY,VIKKI SPAULDING,MICHAEL J AGOSTINO PC C12N15/12,C12N5/10,C07K14/47,C12Q1/68,A61K38/17 CC Strandedness: Double; CC Topology: Linear; FH Key Location/Qualifiers.

FEATURES Location/Qualifiers

source	1. .1401 /organism="synthetic construct" /mol_type="genomic DNA" /db_xref="taxon:32630"

ORIGIN

Alignment Scores:

Pred. No.:	5.94e-112	Length:	1401
Score:	1086.00	Matches:	211
Percent Similarity:	99.53%	Conservative:	1
Best Local Similarity:	99.06%	Mismatches:	0
Query Match:	98.55%	Indels:	1
DB:	6	Gaps:	0

US-09-989-724-387 (1-212) x BD083420 (1-1401)

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Db         71 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 130

Qy         21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
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Db        131 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 190

Qy         41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
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Db        191 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 250

Qy         61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80
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Db        251 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 310

Qy         81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
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Db        311 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 370

Qy        101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120
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Db        371 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTGTAAATGAC 430

Qy        121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140
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Db        431 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 490

Qy        141 ProIleTrpIleIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160
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Db        491 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 550

Qy        161 LeuIleLeuSerGlyIleTrpGlnArgArgArgLysAsnLysGluProSerGluValAsp 180
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Qy        181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200
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Qy        201 LeuAspMetLysGly-GlyIleLeuMetMetProSer 212
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Db        671 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCA 707

RESULT 13
BD205644
LOCUS       BD205644                1447 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  97 human secreted proteins.
ACCESSION   BD205644
VERSION     BD205644.1  GI:33015414
KEYWORDS    JP 2002533058-A/21.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1447)
  AUTHORS   Ruben,S.M., Florence,K., Ni,J., Rosen,C.A., Carter,K.C.,
            Moore,P.A., Olsen,H.S., Shi,Y., Young,P.E., Wei,F.F., Brewer,L.A.,
            Soppet,D.R., Lafleur,D.W., Endress,G.A. and Ebner,R.
  TITLE     97 human secreted proteins
  JOURNAL   Patent: JP 2002533058-A 21 08-OCT-2002;
            HUMAN GENOME SCIENCES INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002533058-A/21
            PD   08-OCT-2002
            PF   06-MAY-1999 JP 2000548451
            PR   12-MAY-1998 US    60/085093,12-MAY-1998 US    60/085094 PR
            12-MAY-1998 US    60/085105,12-MAY-1998 US    60/085180 PR
            18-MAY-1998 US    60/085927,18-MAY-1998 US    60/085906 PR
            18-MAY-1998 US    60/085924,18-MAY-1998 US    60/085922 PR
            18-MAY-1998 US    60/085923,18-MAY-1998 US    60/085921 PR
            18-MAY-1998 US    60/085925,18-MAY-1998 US    60/085928 PR
            18-MAY-1998 US    60/085920
            PI   STEVEN M RUBEN,KIMBERLY FLORENCE,JIAN NI,CRAIG A ROSEN,KENNETH

            PI   C CARTER,
            PI   PAUL A MOORE,HENRIK S OLSEN,YANGGU SHI,PAUL E YOUNG,FING FEI
            PI   WEI,
            PI   LAURIE A BREWER,DANIEL R SOPPET,DAVID W LAFLEUR,GREGORY A  PI
             ENDRESS,
            PI   REINHARD EBNER
            PC   C12N15/09,C07K14/00,C07K14/435,C07K16/18,C12N1/15,C12N1/19, PC
              C12N1/21,
            PC   C12N5/10,C12P21/02,C12N15/00,C12N5/00
            CC   97 human secreted proteins.
            FH   Key             Location/Qualifiers
            FT   source          1. .1447
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .1447
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ORIGIN

Alignment Scores:
Pred. No.:              1.74e-111      Length:         1447
Score:                  1082.00        Matches:        211
Percent Similarity:     99.06%         Conservative:   0
Best Local Similarity:  99.06%         Mismatches:     1
Query Match:            98.19%         Indels:         1
DB:                     6              Gaps:           0

US-09-989-724-387 (1-212) x BD205644 (1-1447)

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Qy         21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
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Db        137 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 196

Qy         41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
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Db        197 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 256

Qy         61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80
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Qy         81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
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Qy        121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140
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Db        437 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 496

Qy        141 ProIleTrpIleIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160
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Qy        161 LeuIleLeuSerGlyIleTrpGlnArgArgArgLysAsnLysGluProSerGluValAsp 180
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Db        557 CTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGAT 616

Qy        181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200
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Qy        201 LeuAspMetLysGly-GlyIleLeuMetMetProSer 212
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Db        677 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCA 713

RESULT 14
AR177334
LOCUS       AR177334                848 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 27 from patent US 6312922.
ACCESSION   AR177334
VERSION     AR177334.1  GI:17919689
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 848)
  AUTHORS   Edwards,J.-B.Dumas.Milne., Duclert,A. and Bougueleret,L.
  TITLE     Complementary DNAs
  JOURNAL   Patent: US 6312922-A 27 06-NOV-2001;
FEATURES             Location/Qualifiers
     source          1. .848
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ORIGIN

Alignment Scores:
Pred. No.:              9.55e-110      Length:         848
Score:                  1064.00        Matches:        208
Percent Similarity:     97.65%         Conservative:   0
Best Local Similarity:  97.65%         Mismatches:     4
Query Match:            96.55%         Indels:         1
DB:                     6              Gaps:           0

US-09-989-724-387 (1-212) x AR177334 (1-848)

Qy          1 MetLeuTrpLeuLeuPhePheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20
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Db         32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91

Qy         21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
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Db         92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy         41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
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Qy         61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80
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Db        212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 271

Qy         81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
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Db        272 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 331

Qy        101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120
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Db        332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy        121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140
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Db        392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 451

Qy        141 ProIleTrpIleIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160
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Db        452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy        161 LeuIleLeuSerGlyIleTrpGlnArgArgArgLysAsnLysGluProSerGluValAsp 180
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Db        512 CTGATTTTATCAGGGATCTGGCAACGTADAARAAAGAACAAAGAACCATCTGAAGTGGAT 571

Qy        181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200
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Db        572 GACGCTGAARATAAKTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 631

Qy        201 LeuAspMetLysGly-GlyIleLeuMetMetProSer 212
                 ||||||||||||||||||||||||||||||||||||
Db        632 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCA 668

RESULT 15
BD139270
LOCUS       BD139270                 848 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Extended cDNA of secretory protein.
ACCESSION   BD139270
VERSION     BD139270.1  GI:23234215
KEYWORDS    JP 2002508182-A/22.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 848)
  AUTHORS   Bougueleret,L., Duclert,A. and Edwards,J.B.D.M.
  TITLE     Extended cDNA of secretory protein
  JOURNAL   Patent: JP 2002508182-A 22 19-MAR-2002;
            GENSET
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002508182-A/22
            PD   19-MAR-2002
            PF   17-DEC-1998 JP 2000539136
            PR   17-DEC-1997 US    60/069957,09-FEB-1998 US    60/074121 PR
            13-APR-1998 US    60/081563,10-AUG-1998 US    60/096116 PI   LYDIE
            BOUGUELERET,AYMERIC DUCLERT,JEAN BAPTISTE DUMAS MILNE  PI   EDWARDS
            PC   C12N15/09,C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19, PC
             C12N1/21,
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            Von Heijne matrix
            FH   Key             Location/Qualifiers
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FEATURES              Location/Qualifiers
     source           1. .848
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                      /mol_type="genomic DNA"
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ORIGIN

Alignment Scores:
Pred. No.:              9.55e-110      Length:        848
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Best Local Similarity:  97.65%         Mismatches:    4
Query Match:            96.55%         Indels:        1
DB:                     6              Gaps:          0

US-09-989-724-387 (1-212) x BD139270 (1-848)

Qy          1 MetLeuTrpLeuLeuPhePheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91

Qy         21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
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Db         92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy         41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
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Db        152 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy         61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 271

Qy         81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 331

Qy        101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy        121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140
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Db        392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 451

Qy        141 ProIleTrpIleIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160
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Db        452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy        161 LeuIleLeuSerGlyIleTrpGlnArgArgArgLysAsnLysGluProSerGluValAsp 180
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Qy        181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200
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Db        572 GACGCTGAARATAAKTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 631

Qy        201 LeuAspMetLysGly-GlyIleLeuMetMetProSer 212
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Db        632 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCA 668

Search completed: February 25, 2005, 03:07:45
Job time : 3160 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
OM protein - nucleic search, using frame_plus_p2n model
Run on: February 25, 2005, 01:20:49 ; Search time 426 Seconds
(without alignments)
2945.975 Million cell updates/sec
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Perfect score: 1102
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0
Searched: 4390206 seqs, 2959870667 residues
Total number of hits satisfying chosen parameters: 8780412
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries
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-LIST=1500 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=1500
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description

RESULT 1
ID AAZ65097 standard; cDNA; 1346 BP.
DE Membrane-bound protein PRO1312 encoding cDNA.
PN WO9963088-A2.
PD 09-DEC-1999.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 2
ID AAC58612 standard; cDNA; 1346 BP.
DE Human PRO1312 protein UNQ678 encoding cDNA SEQ ID NO:160.
PN WO200053758-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 3
ID AAA77680 standard; cDNA; 1346 BP.
DE Human PRO1312 cDNA sequence SEQ ID NO:213.
PN WO200032221-A2.
PD 08-JUN-2000.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 4
ID AAS21484 standard; cDNA; 1346 BP.
DE Human cDNA sequence encoding for PRO1312 polypeptide.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 5
ID AAF44243 standard; cDNA; 1346 BP.
DE Human PRO1312 (UNQ678) nucleotide sequence SEQ ID NO:386.
PN WO200073454-A1.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 6
ID ACA64416 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 7
ID ACA03843 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 8
ID ABX89381 standard; cDNA; 1346 BP.
DE DNA encoding novel secreted and transmembrane protein PRO1312.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 9
ID ABX80875 standard; cDNA; 1346 BP.
DE Human secreted/transmembrane protein cDNA, #157.
PN US2003027162-A1.
PD 06-FEB-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 10
ID ACD44384 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO1312 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 11
ID ACD42035 standard; cDNA; 1346 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #241.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 12
ID ABX79555 standard; cDNA; 1346 BP.
DE Human sectreted/transmembrane protein cDNA, #157.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 13
ID ACA93576 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003022187-A1.
PD 30-JAN-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 14
ID ABX81258 standard; DNA; 1346 BP.
DE Novel human secreted or transmembrane protein PRO1192 DNA.
PN US2003027985-A1.
PD 06-FEB-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 15
ID ACA04264 standard; cDNA; 1346 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 481.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 16
ID ACA93074 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003017476-A1.
PD 23-JAN-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 17
ID ABX17158 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 18
ID ACA68013 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 19
ID ACA88462 standard; cDNA; 1346 BP.
DE Human secreted and transmembrane polypeptide PRO1312 cDNA.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 20
ID ACD81969 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO1312 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 21
ID ADA46000 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 22
ID ADA76431 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 23
ID ADA19081 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 24
ID ADA61704 standard; cDNA; 1346 BP.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 25
ID ADB19489 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 26
ID ADB28030 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 27
ID ADA86509 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 28
ID ADB16073 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.

PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 29
ID ADA37897 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1312.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 30
ID ADA47859 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 31
ID ADA21583 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO1312.
PN US2003054404-A1.
PD 20-MAR-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 32
ID ADA10370 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1312.
PN US2003059831-A1.
PD 27-MAR-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 33
ID ADA67654 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 34
ID ADB30661 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 35
ID ADA85957 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 36
ID ADA17914 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO1312 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 37
ID ADA97169 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 38
ID ADA79473 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 39
ID ADA87612 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 40
ID ADB16814 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 41
ID ADA28022 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1312.
PN US2003054359-A1.
PD 20-MAR-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 42
ID ADA91906 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 43
ID ADB14969 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 44
ID ADB18930 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

RESULT 45
ID ADA94145 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 46
ID ADB20041 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 47
ID ADB13353 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 48
ID ACD98664 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 49
ID ADA94602 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1312.
PN US2003059832-A1.
PD 27-MAR-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 50
ID ADA74607 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 51
ID ADB24840 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide SEQ ID NO 481.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 52
ID ADA82364 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 53
ID ADA75327 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 54
ID ADA85405 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 55
ID ADA84853 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 56
ID ADB30109 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 57
ID ADA80637 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 58
ID ADA75879 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 59
ID ADA38827 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1312.
PN US2003059780-A1.
PD 27-MAR-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 60
ID ADA47104 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 61
ID ADB25400 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide SEQ ID NO 481.
PN US2003077715-A1.

PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 62
ID ADA93576 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 63
ID ADB26926 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 64
ID ADB31213 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 65
ID ADA92948 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1312.
PN US2003060407-A1.
PD 27-MAR-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 66
ID ADA61141 standard; cDNA; 1346 BP.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 67
ID ADB24288 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide SEQ ID NO 481.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 68
ID ADA96617 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 69
ID ADA81189 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 70
ID ADA96065 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 71
ID ADB26374 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 72
ID ADB21859 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 73
ID ADA77638 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 74
ID ADB18378 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 75
ID ADA87061 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 76
ID ADA88164 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 77
ID ADA46552 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 78
ID ADB28582 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 79
ID ADB29134 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 80
ID ACH65530 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1312.
PN US2003044806-A1.
PD 06-MAR-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 81
ID ADA77086 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 82
ID ADA22509 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO1312.
PN US2003040473-A1.
PD 27-FEB-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 83
ID ADA88716 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 84
ID ADA97721 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 85
ID ADB27478 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003022239-A1.
PD 30-JAN-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 86
ID ADB22411 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087344-A1.
PD 08-MAY-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 87
ID ACD39520 standard; cDNA; 1346 BP.
DE Human cDNA encoding PRO1192.
PN US2003017982-A1.
PD 23-JAN-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 88
ID ADA06675 standard; cDNA; 1346 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #121.
PN US2003049638-A1.
PD 13-MAR-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 89
ID ADA39368 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1312.
PN US2003059782-A1.
PD 27-MAR-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 90
ID ADA67102 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 91
ID ADB22963 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 92
ID ADB23736 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide SEQ ID NO 481.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 93
ID ADA92458 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 94
ID ADB15521 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 95
ID ADB38773 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 96
ID ADB96394 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2003054403-A1.
PD 20-MAR-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 97
ID ADB38221 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 98
ID ADB66693 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 99
ID ADB89773 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 100
ID ADB90505 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 101
ID ADB39606 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 102
ID ADB47229 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 103
ID ADB86836 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 104
ID ADB77441 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 105
ID ADB34598 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide SEQ ID NO 481.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 106
ID ADB35702 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide SEQ ID NO 481.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 107
ID ADB34046 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide SEQ ID NO 481.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 108
ID ADB35150 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide SEQ ID NO 481.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 109
ID ADB36254 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide SEQ ID NO 481.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 110
ID ADB46649 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 111

ID ADC57866 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2003027754-A1.
PD 06-FEB-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 112
ID ADC55230 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2003045463-A1.
PD 06-MAR-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 113
ID ADC12097 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1312.
PN US2003049681-A1.
PD 13-MAR-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 114
ID ADC56519 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2003064375-A1.
PD 03-APR-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 115
ID ADC07574 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1312.
PN US2003068647-A1.
PD 10-APR-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 116
ID ADC11564 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1312.
PN US2003069403-A1.
PD 10-APR-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 117
ID ADC50522 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 118
ID ADC72069 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 119
ID ADC60048 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 120
ID ADC53055 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID481.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 121
ID ADC57409 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID481.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 122
ID ADC60600 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 123
ID ADC51075 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 124
ID ADC65602 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 125
ID ADC54700 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID481.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 126
ID ADC53661 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID481.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 127
ID ADC59184 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID481.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

RESULT 128
ID ADC56062 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID481.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 129
ID ADC58632 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID481.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 130
ID ADC14686 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082546-A1.
PD 01-MAY-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 131
ID ADD08218 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003068623-A1.
PD 10-APR-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 132
ID ADD03306 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 133
ID ADC90298 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 134
ID ADC82043 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2003083461-A1.
PD 01-MAY-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 135
ID ADC69717 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 136
ID ADC48606 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 137
ID ADD10135 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 138
ID ADD07685 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 139
ID ADD04710 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 140
ID ADC82576 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2003059833-A1.
PD 27-MAR-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 141
ID ADC80666 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 142
ID ADD11173 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 143
ID ADC48054 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 144
ID ADD08756 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003073090-A1.
PD 17-APR-2003.
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 145
ID ADC80114 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 146
ID ADD07005 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 147
ID ADD09583 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 148
ID ADC83252 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2003059783-A1.
PD 27-MAR-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 149
ID ADD41296 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 150
ID ADD52435 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 151
ID ADD53175 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 152
ID ADD53727 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 153
ID ADD55359 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2003077593-A1.
PD 24-APR-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 154
ID ADD56317 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2003077594-A1.
PD 24-APR-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 155
ID ADD51883 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 156
ID ADD02682 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 157
ID ADD02116 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 158
ID ADD54298 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 159
ID ADD54755 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 160
ID ADD92615 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 161
ID ADD91511 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.

PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 162
ID ADE04125 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 163
ID ADE26909 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087304-A1.
PD 08-MAY-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 164
ID ADE32422 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 165
ID ADE22354 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 166
ID ADD79578 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 167
ID ADE42114 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 168
ID ADE17931 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 169
ID ADD92063 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 170
ID ADE33526 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 171
ID ADE34078 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 172
ID ADD80130 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 173
ID ADD93167 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 174
ID ADE19587 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 175
ID ADE19035 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 176
ID ADE43231 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 177
ID ADD96020 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 178
ID ADE22906 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 179
ID ADD79024 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 180
ID ADE26376 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087305-A1.
PD 08-MAY-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 181
ID ADE32974 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 182
ID ADE42666 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 183
ID ADD80682 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 184
ID ADD89710 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 185
ID ADE40994 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 186
ID ADE04793 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 187
ID ADE92922 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 188
ID ADF67313 standard; cDNA; 1346 BP.
DE Human PRO1312 nucleotide sequence SEQ ID NO:386.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 189
ID ADG21631 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 190
ID ADG23272 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 191
ID ADF97607 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 192
ID ADG80671 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 193
ID ADG80119 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

RESULT 194
ID ADH55411 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 195
ID ADH55963 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 196
ID ADI35567 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2003050457-A1.
PD 13-MAR-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 197
ID ADI64182 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 198
ID ADI65131 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 199
ID ADI63630 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 200
ID ADH82044 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 201
ID ADI00060 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003049682-A1.
PD 13-MAR-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 202
ID ADH81492 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 203
ID ABX77959 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2003027163-A1.
PD 06-FEB-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 204
ID ABX80371 standard; DNA; 1346 BP.
DE Novel human secreted or transmembrane protein PRO1192 DNA.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 205
ID ACA69277 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1312.
PN US2003032023-A1.
PD 13-FEB-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 206
ID ACD24093 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 207
ID ABX90348 standard; cDNA; 1346 BP.
DE Human secreted/transmembrane protein cDNA, #157.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 208
ID ABX64194 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO1312 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 209
ID ACA67234 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 210
ID ADM82661 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 211
ID ADN16060 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 212
ID ADN16689 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 213
ID ADN15508 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 214
ID ADN14956 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 215
ID ADC81218 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 216
ID ADD76666 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 217
ID ADD88030 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 218
ID ADD86434 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 219
ID ADE75882 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 220
ID ADE23458 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 221
ID ADE24010 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 222
ID ADE24653 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 223
ID ADD87478 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 224
ID ADE89344 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 225
ID ADE18483 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 226
ID ADE88792 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0
RESULT 227
ID ADE94812 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 228
ID ADE91223 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 229
ID ADF35512 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO1312 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 230
ID ADE95364 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 231
ID ADE93474 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 232
ID ADF35055 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 233
ID ADE92370 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 234
ID ADE90671 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 235
ID ADE91818 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 236
ID ADG11762 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO1312 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 237
ID ADG02397 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 238
ID ADG22183 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 239
ID ADG20253 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 240
ID ADF98159 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 241
ID ADG24376 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 242
ID ADF98730 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 243
ID ADG03561 standard; cDNA; 1346 BP.

DE Human PRO polynucleotide #241.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 244
ID ADF99282 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 245
ID ADG16867 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 246
ID ADG05326 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 247
ID ADG19593 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 248
ID ADG13430 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 249
ID ADG08487 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 250
ID ADG15657 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 251
ID ADF97055 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 252
ID ADG06240 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 253
ID ADG23824 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 254
ID ADG04113 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 255
ID ADG25014 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 256
ID ADG07311 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 257
ID ADG07863 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 258
ID ADG55358 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 259
ID ADG61022 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207390-A1.

PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 260
ID ADG62126 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 261
ID ADG82327 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 262
ID ADG57566 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 263
ID ADG57014 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 264
ID ADG55910 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 265
ID ADG58670 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 266
ID ADG71036 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 267
ID ADG58118 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 268
ID ADG53702 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 269
ID ADG71588 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 270
ID ADG81775 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003207805-A1.
PD 06-NOV-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 271
ID ADH19632 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1312.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 272
ID ADH30737 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 273
ID ADH12104 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 274
ID ADG52526 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 275
ID ADG54254 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

RESULT 276
ID ADG81223 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

RESULT 277
ID ADG56462 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

RESULT 278
ID ADH12728 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

RESULT 279
ID ADH21125 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1312.
PN US2003224358-A1.
PD 04-DEC-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

RESULT 280
ID ADG61574 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

RESULT 281
ID ADH20165 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1312.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

RESULT 282
ID ADH28661 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

RESULT 283
ID ADG54806 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

RESULT 284
ID ADG59846 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

RESULT 285
ID ADI81270 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

RESULT 286
ID ADG10013 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

RESULT 287
ID ADI15484 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

RESULT 288
ID ADG09361 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

RESULT 289
ID ADI14816 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

RESULT 290
ID ADI18411 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

RESULT 291
ID ADJ63692 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

RESULT 292

ID ADJ77587 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 293
ID ADJ65709 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 294
ID ADM27845 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 295
ID ADM42569 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 296
ID ADM28431 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 297
ID ADI95913 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 298
ID ADI96465 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 299
ID ADT94383 standard; cDNA; 1346 BP.
DE Human PRO1312 cDNA sequence.
PN AU2003259607-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 300
ID AAF94460 standard; cDNA; 666 BP.
DE Human hydrophobic domain containing protein clone HP10720 cDNA #74.
PN WO200112660-A2.
PD 22-FEB-2001.
PA (SAGA) SAGAMI CHEM RES CENT.
PA (PROT-) PROTEGENE INC.
Percent Similarity: 99.53% Conservative: 0
Best Local Similarity: 99.53% Mismatches: 0
Query Match: 98.82% Indels: 1
RESULT 301
ID ADI02664 standard; cDNA; 1312 BP.
DE Human cDNA differentially expressed in the vascular endothelium #205.
PN US2003166903-A1.
PD 04-SEP-2003.
PA (ASTR/) ASTROMOFF A.
PA (BAND/) BANDMAN O.
PA (COCK/) COCKS B G.
Percent Similarity: 99.53% Conservative: 0
Best Local Similarity: 99.53% Mismatches: 0
Query Match: 98.82% Indels: 1
RESULT 302
ID ABZ78127 standard; cDNA; 1345 BP.
DE Human cancer-related coding sequence, 156P1D4.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Percent Similarity: 99.53% Conservative: 0
Best Local Similarity: 99.53% Mismatches: 0
Query Match: 98.82% Indels: 1
RESULT 303
ID AAF94470 standard; cDNA; 1347 BP.
DE Human hydrophobic domain containing protein clone HP10720 cDNA #84.
PN WO200112660-A2.
PD 22-FEB-2001.
PA (SAGA) SAGAMI CHEM RES CENT.
PA (PROT-) PROTEGENE INC.
Percent Similarity: 99.53% Conservative: 0
Best Local Similarity: 99.53% Mismatches: 0
Query Match: 98.82% Indels: 1
RESULT 304
ID ADA39900 standard; cDNA; 1432 BP.
DE Human secreted protein encoding cDNA.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 99.53% Conservative: 0
Best Local Similarity: 99.53% Mismatches: 0
Query Match: 98.82% Indels: 1
RESULT 305
ID ADA11489 standard; DNA; 1432 BP.
DE Human cDNA encoding a novel secreted protein, SEQ ID NO 17.
PN US2003055236-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 99.53% Conservative: 0
Best Local Similarity: 99.53% Mismatches: 0
Query Match: 98.82% Indels: 1
RESULT 306
ID ADD37613 standard; cDNA; 1432 BP.
DE Human secreted protein encoding sequence #95.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 99.53% Conservative: 0
Best Local Similarity: 99.53% Mismatches: 0
Query Match: 98.82% Indels: 1
RESULT 307
ID ADA56090 standard; DNA; 1432 BP.
DE Gene encoding human secreted protein #269.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 99.53% Conservative: 0
Best Local Similarity: 99.53% Mismatches: 0

Query Match: 98.82% Indels: 1
RESULT 308
ID AAV40540 standard; cDNA; 1401 BP.
DE Homo sapiens secreted protein clone AM42_3.
PN WO9832853-A2.
PD 30-JUL-1998.
PA (GEMY) GENETICS INST INC.
Percent Similarity: 99.53% Conservative: 1
Best Local Similarity: 99.06% Mismatches: 0
Query Match: 98.55% Indels: 1
RESULT 309
ID AAZ65261 standard; DNA; 1447 BP.
DE Human secreted protein gene 12.
PN WO9958660-A1.
PD 18-NOV-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 99.06% Conservative: 0
Best Local Similarity: 99.06% Mismatches: 1
Query Match: 98.19% Indels: 1
RESULT 310
ID ADE11650 standard; cDNA; 1447 BP.
DE Human secreted polypeptide cDNA #12.
PN US2003100051-A1.
PD 29-MAY-2003.
PA (RUBE/) RUBEN S M.
PA (FLOR/) FLORENCE K A.
PA (NIJJ/) NI J.
PA (ROSE/) ROSEN C A.
PA (CART/) CARTER K C.
PA (MOOR/) MOORE P A.
PA (OLSE/) OLSEN H S.
PA (SHIY/) SHI Y.
PA (YOUN/) YOUNG P E.
PA (WEIY/) WEI Y.
PA (BREW/) BREWER L A.
PA (SOPP/) SOPPET D R.
PA (LAFL/) LAFLEUR D W.
PA (ENDR/) ENDRESS G A.
PA (EBNE/) EBNER R.
PA (BIRS/) BIRSE C E.
Percent Similarity: 99.06% Conservative: 0
Best Local Similarity: 99.06% Mismatches: 1
Query Match: 98.19% Indels: 1
RESULT 311
ID AAH98224 standard; cDNA; 1365 BP.
DE Human EST-derived coding sequence SEQ ID NO: 81.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 99.07% Conservative: 1
Best Local Similarity: 98.60% Mismatches: 0
Query Match: 97.28% Indels: 2
RESULT 312
ID AAX19983 standard; cDNA; 848 BP.
DE Human secreted protein 5' EST SEQ ID NO:27.
PN WO9906439-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Percent Similarity: 97.65% Conservative: 0
Best Local Similarity: 97.65% Mismatches: 4
Query Match: 96.55% Indels: 1
RESULT 313
ID AAX39430 standard; DNA; 848 BP.
DE Human secreted protein 5' EST SEQ ID NO: 27.
PN WO9906551-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Percent Similarity: 97.65% Conservative: 0
Best Local Similarity: 97.65% Mismatches: 4
Query Match: 96.55% Indels: 1
RESULT 314
ID AAX41369 standard; cDNA; 848 BP.
DE Extended cDNA obtained from 5' EST, SEQ ID NO: 27 from WO 9906553.
PN WO9906553-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Percent Similarity: 97.65% Conservative: 0
Best Local Similarity: 97.65% Mismatches: 4
Query Match: 96.55% Indels: 1
RESULT 315
ID AAX97564 standard; DNA; 848 BP.
DE Extended human secreted protein coding sequence, SEQ ID NO. 27.
PN WO9931236-A2.
PD 24-JUN-1999.
PA (GEST) GENSET.
Percent Similarity: 97.65% Conservative: 0
Best Local Similarity: 97.65% Mismatches: 4
Query Match: 96.55% Indels: 1
RESULT 316
ID AAZ40770 standard; DNA; 848 BP.
DE Secreted protein extended EST coding sequence #6.
PN WO9940189-A2.
PD 12-AUG-1999.
PA (GEST) GENSET.
Percent Similarity: 97.65% Conservative: 0
Best Local Similarity: 97.65% Mismatches: 4
Query Match: 96.55% Indels: 1
RESULT 317
ID AAX26672 standard; RNA; 848 BP.
DE Extended cDNA derived from a 5' EST encoding a secreted protien.
PN WO9906554-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Percent Similarity: 97.65% Conservative: 0
Best Local Similarity: 97.65% Mismatches: 4
Query Match: 96.55% Indels: 1
RESULT 318
ID AAX51777 standard; cDNA; 848 BP.
DE Human secreted protein 5' EST clone 58-35-2-F10-FL2.
PN WO9906552-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Percent Similarity: 97.65% Conservative: 0
Best Local Similarity: 97.65% Mismatches: 4
Query Match: 96.55% Indels: 1
RESULT 319
ID AAX88191 standard; cDNA; 848 BP.
DE Human secreted protein 6 extended cDNA.
PN WO9925825-A2.
PD 27-MAY-1999.
PA (GEST) GENSET.
Percent Similarity: 97.65% Conservative: 0
Best Local Similarity: 97.65% Mismatches: 4
Query Match: 96.55% Indels: 1
RESULT 320
ID AAX51449 standard; DNA; 848 BP.
DE Human secreted protein 5' EST SEQ ID NO. 27.
PN WO9906549-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Percent Similarity: 97.65% Conservative: 0
Best Local Similarity: 97.65% Mismatches: 4
Query Match: 96.55% Indels: 1
RESULT 321
ID AAX40428 standard; cDNA; 848 BP.
DE Extended cDNA derived from 5' EST.
PN WO9906550-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Percent Similarity: 97.65% Conservative: 0
Best Local Similarity: 97.65% Mismatches: 4
Query Match: 96.55% Indels: 1
RESULT 322
ID AAZ42251 standard; cDNA; 848 BP.
DE Human full length cDNA 58-35-2-F10-FL2.
PN WO9953051-A2.

PD 21-OCT-1999.
PA (GEST) GENSET.
Percent Similarity: 97.65% Conservative: 0
Best Local Similarity: 97.65% Mismatches: 4
Query Match: 96.55% Indels: 1
RESULT 323
ID AAC00012 standard; cDNA; 848 BP.
DE Human secreted protein cDNA sequence #3.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Percent Similarity: 97.65% Conservative: 0
Best Local Similarity: 97.65% Mismatches: 4
Query Match: 96.55% Indels: 1
RESULT 324
ID ADJ45874 standard; cDNA; 848 BP.
DE Novel human secreted protein-related cDNA sequence SeqID27.
PN US2003144490-A1.
PD 31-JUL-2003.
PA (EDWA/) EDWARDS J D M.
PA (DUCL/) DUCLERT A.
PA (BOUG/) BOUGUELERET L.
Percent Similarity: 97.65% Conservative: 0
Best Local Similarity: 97.65% Mismatches: 4
Query Match: 96.55% Indels: 1
RESULT 325
ID ADM77746 standard; cDNA; 848 BP.
DE EST encoding signal sequence #6.
PN US2003162176-A1.
PD 28-AUG-2003.
PA (EDWA/) EDWARDS J D M.
PA (DUCL/) DUCLERT A.
PA (BOUG/) BOUGUELERET L.
Percent Similarity: 97.65% Conservative: 0
Best Local Similarity: 97.65% Mismatches: 4
Query Match: 96.55% Indels: 1
RESULT 326
ID AAX97957 standard; DNA; 1356 BP.
DE Human secreted protein gene 42.
PN WO9931117-A1.
PD 24-JUN-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 99.06% Conservative: 0
Best Local Similarity: 99.06% Mismatches: 1
Query Match: 96.37% Indels: 2
RESULT 327
ID ADA40381 standard; cDNA; 1356 BP.
DE Human secreted protein encoding cDNA.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 99.06% Conservative: 0
Best Local Similarity: 99.06% Mismatches: 1
Query Match: 96.37% Indels: 2
RESULT 328
ID ADA11594 standard; DNA; 1356 BP.
DE Human cDNA encoding a novel secreted protein, SEQ ID NO 122.
PN US2003055236-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 99.06% Conservative: 0
Best Local Similarity: 99.06% Mismatches: 1
Query Match: 96.37% Indels: 2
RESULT 329
ID ADD37752 standard; cDNA; 1356 BP.
DE Human secreted protein encoding sequence #234.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 99.06% Conservative: 0
Best Local Similarity: 99.06% Mismatches: 1
Query Match: 96.37% Indels: 2
RESULT 330
ID ADA56545 standard; DNA; 1356 BP.
DE Gene encoding human secreted protein #269.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 99.06% Conservative: 0
Best Local Similarity: 99.06% Mismatches: 1
Query Match: 96.37% Indels: 2
RESULT 331
ID AAX30083 standard; cDNA; 847 BP.
DE Human secreted protein 5' EST SEQ ID NO:27.
PN WO9906548-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Percent Similarity: 97.18% Conservative: 0
Best Local Similarity: 97.18% Mismatches: 5
Query Match: 95.83% Indels: 1
RESULT 332
ID ADO07092 standard; cDNA; 774 BP.
DE Human protein modification and maintenance molecule 26 (PMMM-26) cDNA.
PN WO2004033636-A2.
PD 22-APR-2004.
PA (INCY-) INCYTE CORP.
Percent Similarity: 87.19% Conservative: 0
Best Local Similarity: 87.19% Mismatches: 1
Query Match: 94.46% Indels: 31
RESULT 333
ID ABT42042 standard; DNA; 1181 BP.
DE Toxicity modelling related rat gene SEQ ID No 1744.
PN WO200295000-A2.
PD 28-NOV-2002.
PA (GENE-) GENE LOGIC INC.
Percent Similarity: 89.67% Conservative: 13
Best Local Similarity: 83.57% Mismatches: 21
Query Match: 83.85% Indels: 1
RESULT 334
ID AAX40832 standard; cDNA; 439 BP.
DE Human secreted protein 5' EST SEQ ID NO: 44.
PN WO9906554-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 62.98% Indels: 0
RESULT 335
ID AAV86301 standard; cDNA; 462 BP.
DE EST clone AM42.
PN WO9845435-A2.
PD 15-OCT-1998.
PA (GEMY) GENETICS INST INC.
Percent Similarity: 97.08% Conservative: 3
Best Local Similarity: 94.89% Mismatches: 4
Query Match: 61.16% Indels: 0
RESULT 336
ID ABS69507 standard; DNA; 532 BP.
DE Novel murine polynucleotide isolated using gene trap technology #570.
PN US2002102543-A1.
PD 01-AUG-2002.
PA (FRIE/) FRIEDRICH G.
PA (ZAMB/) ZAMBROWICZ B.
PA (SAND/) SANDS A T.
Percent Similarity: 88.15% Conservative: 6
Best Local Similarity: 83.70% Mismatches: 16
Query Match: 54.17% Indels: 0
RESULT 337
ID ADN43035 standard; cDNA; 379 BP.
DE Human secreted protein SECP-21 cDNA.
PN WO2004037987-A2.
PD 06-MAY-2004.
PA (INCY-) INCYTE CORP.
Percent Similarity: 51.17% Conservative: 0
Best Local Similarity: 51.17% Mismatches: 0
Query Match: 44.96% Indels: 104

RESULT 338
ID ABL78658 standard; cDNA; 355 BP.
DE Human ovarian cancer related cDNA clone SEQ ID NO:1636.
PN WO200192581-A2.
PD 06-DEC-2001.
PA (CORI-) CORIXA CORP.
Percent Similarity: 88.24% Conservative: 8
Best Local Similarity: 81.51% Mismatches: 10
Query Match: 42.01% Indels: 4
RESULT 339
ID ADL95396 standard; cDNA; 2415 BP.
DE Angiotensin converting enzyme-2 (ACE-2) coding sequence.
PN US6610497-B1.
PD 26-AUG-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Percent Similarity: 67.27% Conservative: 32
Best Local Similarity: 47.88% Mismatches: 48
Query Match: 34.12% Indels: 6
RESULT 340
ID AAZ59465 standard; DNA; 2418 BP.
DE Human MPROT15 coding sequence #1.
PN JP11318472-A.
PD 24-NOV-1999.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Percent Similarity: 67.27% Conservative: 32
Best Local Similarity: 47.88% Mismatches: 48
Query Match: 34.12% Indels: 6
RESULT 341
ID ACN43792 standard; cDNA; 3064 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2667.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Percent Similarity: 67.27% Conservative: 32
Best Local Similarity: 47.88% Mismatches: 48
Query Match: 34.12% Indels: 6
RESULT 342
ID ACH03967 standard; cDNA; 3324 BP.
DE Human cDNA differentially expressed in lung cancer #172.
PN US2003065157-A1.
PD 03-APR-2003.
PA (LASE/) LASEK A W.
Percent Similarity: 67.27% Conservative: 32
Best Local Similarity: 47.88% Mismatches: 48
Query Match: 34.12% Indels: 6
RESULT 343
ID ADC38727 standard; cDNA; 3325 BP.
DE Human cDNA encoding a secreted protein #41.
PN US2002193567-A1.
PD 19-DEC-2002.
PA (GEMY) GENETICS INST INC.
Percent Similarity: 67.27% Conservative: 32
Best Local Similarity: 47.88% Mismatches: 48
Query Match: 34.12% Indels: 6
RESULT 344
ID AAC84366 standard; cDNA; 3334 BP.
DE Human Zace2 protein encoding cDNA.
PN WO200070032-A1.
PD 23-NOV-2000.
PA (ZYMO) ZYMOGENETICS INC.
Percent Similarity: 67.27% Conservative: 32
Best Local Similarity: 47.88% Mismatches: 48
Query Match: 34.12% Indels: 6
RESULT 345
ID ABX93333 standard; cDNA; 3334 BP.
DE cDNA encoding human zinc metallopeptidase Zace2.
PN US2002177211-A1.
PD 28-NOV-2002.
PA (ZYMO) ZYMOGENETICS INC.
Percent Similarity: 67.27% Conservative: 32
Best Local Similarity: 47.88% Mismatches: 48
Query Match: 34.12% Indels: 6
RESULT 346
ID AAA12764 standard; cDNA; 3396 BP.
DE cDNA encoding a human angiotensin converting enzyme-2 (ACE-2).
PN WO200018899-A2.
PD 06-APR-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Percent Similarity: 67.27% Conservative: 32
Best Local Similarity: 47.88% Mismatches: 48
Query Match: 34.12% Indels: 6
RESULT 347
ID AAD02758 standard; cDNA; 3396 BP.
DE Human angiotensin converting enzyme-2 (ACE-2) cDNA.
PN US6194556-B1.
PD 27-FEB-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Percent Similarity: 67.27% Conservative: 32
Best Local Similarity: 47.88% Mismatches: 48
Query Match: 34.12% Indels: 6
RESULT 348
ID AAD32586 standard; cDNA; 3396 BP.
DE Human ACE-2 full-length cDNA.
PN WO200212471-A2.
PD 14-FEB-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Percent Similarity: 67.27% Conservative: 32
Best Local Similarity: 47.88% Mismatches: 48
Query Match: 34.12% Indels: 6
RESULT 349
ID ABK87623 standard; cDNA; 3396 BP.
DE cDNA encoding human angiotensin converting enzyme-2 (ACE-2) protein.
PN WO200239997-A2.
PD 23-MAY-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Percent Similarity: 67.27% Conservative: 32
Best Local Similarity: 47.88% Mismatches: 48
Query Match: 34.12% Indels: 6
RESULT 350
ID ADA03343 standard; DNA; 3396 BP.
DE Human angiotensin converting enzyme 2-like protein gene.
PN WO200298448-A1.
PD 12-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 67.27% Conservative: 32
Best Local Similarity: 47.88% Mismatches: 48
Query Match: 34.12% Indels: 6
RESULT 351
ID ACC79022 standard; cDNA; 3396 BP.
DE Human ACE-2 protein encoding cDNA SEQ ID NO:141.
PN WO200298906-A1.
PD 12-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 67.27% Conservative: 32
Best Local Similarity: 47.88% Mismatches: 48
Query Match: 34.12% Indels: 6
RESULT 352
ID ADL95394 standard; cDNA; 3396 BP.
DE Human angiotensin converting enzyme-2 (ACE-2) cDNA.
PN US6610497-B1.
PD 26-AUG-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Percent Similarity: 67.27% Conservative: 32
Best Local Similarity: 47.88% Mismatches: 48
Query Match: 34.12% Indels: 6
RESULT 353
ID ADH51356 standard; DNA; 3404 BP.
DE Human angiotensin-converting enzyme homologue ACE2 DNA.
PN WO2004000367-A1.
PD 31-DEC-2003.
PA (UYHE-) UNIV HEALTH NETWORK.
Percent Similarity: 67.27% Conservative: 32
Best Local Similarity: 47.88% Mismatches: 48
Query Match: 34.12% Indels: 6
RESULT 354
ID ABS60632 standard; cDNA; 3405 BP.

DE Human cDNA encoding angiotensin converting enzyme 2 variant #1.
PN WO200261131-A2.
PD 08-AUG-2002.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
PA (TSUC/) TSUCHIHASHI Z.
PA (HUIL/) HUI L.
Percent Similarity: 67.27% Conservative: 32
Best Local Similarity: 47.88% Mismatches: 48
Query Match: 34.12% Indels: 6
RESULT 355
ID ABS60371 standard; cDNA; 3405 BP.
DE Human cDNA encoding angiotensin converting enzyme 2.
PN WO200261131-A2.
PD 08-AUG-2002.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
PA (TSUC/) TSUCHIHASHI Z.
PA (HUIL/) HUI L.
Percent Similarity: 67.27% Conservative: 32
Best Local Similarity: 47.88% Mismatches: 48
Query Match: 34.12% Indels: 6
RESULT 356
ID AAS21279 standard; cDNA; 3732 BP.
DE Human cDNA sequence encoding for PRO1885 polypeptide.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 357
ID ACA03638 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 358
ID ABX89176 standard; cDNA; 3732 BP.
DE DNA encoding novel secreted and transmembrane protein PRO1885.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 359
ID ACD41830 standard; cDNA; 3732 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #36.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 360
ID ACA04059 standard; cDNA; 3732 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 71.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 361
ID ADA45590 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 362
ID ADA76021 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 363
ID ADA18671 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 364
ID ADA61294 standard; cDNA; 3732 BP.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 365
ID ADB19079 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 366
ID ADB27620 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 367
ID ADA86099 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 368
ID ADB15663 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 369
ID ADA47449 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12

RESULT 370
ID ADA67244 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 371
ID ADB30251 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 372
ID ADA85547 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 373
ID ADA96759 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 374
ID ADA79063 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 375
ID ADA87202 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 376
ID ADB16404 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 377
ID ADA91496 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 378
ID ADB14559 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 379
ID ADB18520 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 380
ID ADA93735 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 381
ID ADB19631 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 382
ID ADB12943 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 383
ID ACD98459 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 384
ID ADA74197 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 385
ID ADB24430 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide SEQ ID NO 71.
PN US2003077713-A1,
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 386
ID ADA81954 standard; cDNA; 3732 BP.

DE Human PRO polynucleotide #36.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 387
ID ADA74917 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 388
ID ADA84995 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 389
ID ADA84443 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 390
ID ADB29699 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 391
ID ADA80227 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 392
ID ADA75469 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 393
ID ADA46694 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 394
ID ADB24990 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide SEQ ID NO 71.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 395
ID ADA93166 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 396
ID ADB26516 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 397
ID ADB30803 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 398
ID ADA60731 standard; cDNA; 3732 BP.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 399
ID ADB23878 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide SEQ ID NO 71.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 400
ID ADA96207 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 401
ID ADA80779 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 402
ID ADA95655 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003082759-A1.

PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 403
ID ADB25964 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 404
ID ADB21449 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 405
ID ADA77228 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 406
ID ADB17968 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 407
ID ADA86651 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 408
ID ADA87754 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 409
ID ADA46142 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 410
ID ADB28172 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 411
ID ADB28724 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 412
ID ADA76676 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 413
ID ADA88306 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 414
ID ADA97311 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 415
ID ADB27068 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003022239-A1.
PD 30-JAN-2003.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 416
ID ADB22001 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003087344-A1.
PD 08-MAY-2003.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 417
ID ADA66692 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 418
ID ADB22553 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50

Query Match: 33.48% Indels: 12
RESULT 419
ID ADB23326 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide SEQ ID NO 71.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 420
ID ADA92048 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 421
ID ADB15111 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 422
ID ADB38363 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 423
ID ADB37811 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 424
ID ADB66283 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 425
ID ADB89363 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 426
ID ADB90095 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 427
ID ADB39196 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 428
ID ADB46819 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 429
ID ADB86426 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 430
ID ADB77031 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 431
ID ADB34188 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide SEQ ID NO 71.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 432
ID ADB35292 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide SEQ ID NO 71.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 433
ID ADB33636 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide SEQ ID NO 71.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 434
ID ADB34740 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide SEQ ID NO 71.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 435

ID ADB35844 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide SEQ ID NO 71.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 436
ID ADB46239 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 437
ID ADC50112 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 438
ID ADC71659 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 439
ID ADC59638 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 440
ID ADC52645 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID71.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 441
ID ADC56999 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID71.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 442
ID ADC60190 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 443
ID ADC50665 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 444
ID ADC65192 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 445
ID ADC54290 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID71.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 446
ID ADC53251 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID71.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 447
ID ADC58774 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID71.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 448
ID ADC55652 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID71.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 449
ID ADC58222 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID71.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 450
ID ADD02896 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 451
ID ADC89888 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.

PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 452
ID ADC69307 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 453
ID ADC48196 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 454
ID ADD09725 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 455
ID ADD04300 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 456
ID ADC80256 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 457
ID ADD10763 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 458
ID ADC47644 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 459
ID ADC79704 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 460
ID ADD09173 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 461
ID ADD40886 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 462
ID ADD52025 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 463
ID ADD52765 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 464
ID ADD53317 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 465
ID ADD51473 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 466
ID ADD02272 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 467
ID ADD01706 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003203430-A1.
PD 30-OCT-2003.

PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 468
ID ADD53888 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 469
ID ADD92205 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 470
ID ADD91101 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 471
ID ADE03715 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 472
ID ADE32012 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 473
ID ADE21944 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 474
ID ADD79168 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 475
ID ADE41704 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 476
ID ADE17521 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 477
ID ADD91653 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 478
ID ADE33116 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 479
ID ADE33668 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 480
ID ADD79720 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 481
ID ADD92757 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 482
ID ADE19177 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 483
ID ADE18625 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33

Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 484
ID ADE42821 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 485
ID ADD95610 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 486
ID ADE22496 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 487
ID ADD78614 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 488
ID ADE32564 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 489
ID ADE42256 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 490
ID ADD80272 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 491
ID ADD89300 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 492
ID ADE40584 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 493
ID ADE04383 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 494
ID ADE92512 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 495
ID ADG21221 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 496
ID ADG22862 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 497
ID ADF97197 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 498
ID ADG80261 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 499
ID ADG79709 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12

RESULT 500
ID ADH55001 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 501
ID ADH55553 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 502
ID ADI64721 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 503
ID ADH81634 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 504
ID ADH81082 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 505
ID ACD23888 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 506
ID ACA67029 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 507
ID ADM82251 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 508
ID ADN15650 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 509
ID ADN16279 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 510
ID ADN15098 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 511
ID ADN14546 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 512
ID ADI63772 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 513
ID ADI63220 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 514
ID ADC80808 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 515
ID ADD76256 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 516
ID ADD87620 standard; cDNA; 3732 BP.

DE Human PRO polynucleotide #36.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 517
ID ADD86024 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 518
ID ADE75472 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 519
ID ADE23048 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 520
ID ADE23600 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 521
ID ADE24243 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 522
ID ADD87068 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 523
ID ADE88934 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 524
ID ADE18073 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 525
ID ADE88382 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 526
ID ADE94402 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 527
ID ADE90813 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 528
ID ADE94954 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 529
ID ADE93064 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 530
ID ADF34645 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 531
ID ADE91960 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 532
ID ADE90261 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199063-A1.

PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 533
ID ADE91408 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 534
ID ADG01987 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 535
ID ADG21773 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 536
ID ADG19843 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 537
ID ADF97749 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 538
ID ADG23966 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 539
ID ADF98320 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 540
ID ADG03151 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 541
ID ADF98872 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 542
ID ADG16457 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 543
ID ADG04916 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 544
ID ADG19183 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 545
ID ADG13020 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 546
ID ADG08077 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 547
ID ADG15247 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 548
ID ADF96645 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 549
ID ADG05830 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 550
ID ADG23414 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 551
ID ADG03703 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 552
ID ADG24604 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 553
ID ADG06901 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 554
ID ADG07453 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 555
ID ADG54948 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 556
ID ADG60612 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 557
ID ADG61716 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 558
ID ADG81917 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 559
ID ADG57156 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 560
ID ADG56604 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 561
ID ADG55500 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 562
ID ADG58260 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 563
ID ADG70626 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 564
ID ADG57708 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50

Query Match: 33.48% Indels: 12
RESULT 565
ID ADG53292 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 566
ID ADG71178 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 567
ID ADG81365 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003207805-A1.
PD 06-NOV-2003.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 568
ID ADH30327 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 569
ID ADH11694 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 570
ID ADG52116 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 571
ID ADG53844 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 572
ID ADG80813 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 573
ID ADG56052 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 574
ID ADH12318 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 575
ID ADG61164 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 576
ID ADH28251 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 577
ID ADG54396 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 578
ID ADG59436 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 579
ID ADI80860 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 580
ID ADG09603 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 581
ID ADI15074 standard; cDNA; 3732 BP.

DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 582
ID ADG08951 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 583
ID ADI14406 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 584
ID ADI18001 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 585
ID ADJ63282 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 586
ID ADJ77177 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 587
ID ADJ65299 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 588
ID ADM27435 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 589
ID ADM42159 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 590
ID ADM28021 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 591
ID ADI95503 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 592
ID ADI96055 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 64.37% Conservative: 33
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 593
ID AAC84368 standard; cDNA; 2638 BP.
DE Mouse Zace2-5 protein encoding cDNA.
PN WO200070032-A1.
PD 23-NOV-2000.
PA (ZYMO) ZYMOGENETICS INC.
Percent Similarity: 58.59% Conservative: 35
Best Local Similarity: 40.91% Mismatches: 52
Query Match: 32.76% Indels: 30
RESULT 594
ID AAC84370 standard; cDNA; 2638 BP.
DE Mouse Zace2-10 protein encoding cDNA.
PN WO200070032-A1.
PD 23-NOV-2000.
PA (ZYMO) ZYMOGENETICS INC.
Percent Similarity: 58.59% Conservative: 35
Best Local Similarity: 40.91% Mismatches: 52
Query Match: 32.76% Indels: 30
RESULT 595
ID ABX93337 standard; cDNA; 2638 BP.
DE cDNA encoding mouse zinc metallopeptidase mZace-10.
PN US2002177211-A1.
PD 28-NOV-2002.
PA (ZYMO) ZYMOGENETICS INC.
Percent Similarity: 58.59% Conservative: 35
Best Local Similarity: 40.91% Mismatches: 52
Query Match: 32.76% Indels: 30
RESULT 596
ID ABX93335 standard; cDNA; 2638 BP.
DE cDNA encoding mouse zinc metallopeptidase mZace-5.
PN US2002177211-A1.
PD 28-NOV-2002.
PA (ZYMO) ZYMOGENETICS INC.
Percent Similarity: 58.59% Conservative: 35
Best Local Similarity: 40.91% Mismatches: 52
Query Match: 32.76% Indels: 30
RESULT 597
ID ADH51358 standard; DNA; 2739 BP.
DE Mouse angiotensin-converting enzyme homologue ACE2 DNA.
PN WO2004000367-A1.

PD 31-DEC-2003.
PA (UYHE-) UNIV HEALTH NETWORK.
Percent Similarity: 58.59% Conservative: 35
Best Local Similarity: 40.91% Mismatches: 52
Query Match: 32.76% Indels: 30
RESULT 598
ID AAS14890 standard; cDNA; 2911 BP.
DE Human cDNA encoding novel human protein NHP #11.
PN WO200174896-A1.
PD 11-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 67.30% Conservative: 32
Best Local Similarity: 47.17% Mismatches: 46
Query Match: 32.58% Indels: 6
RESULT 599
ID AAS14880 standard; cDNA; 2920 BP.
DE Human cDNA encoding novel human protein NHP #1.
PN WO200174896-A1.
PD 11-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 67.30% Conservative: 32
Best Local Similarity: 47.17% Mismatches: 46
Query Match: 32.58% Indels: 6
RESULT 600
ID ADA03339 standard; DNA; 2920 BP.
DE Human angiotensin converting enzyme 2 gene.
PN WO200298448-A1.
PD 12-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 67.30% Conservative: 32
Best Local Similarity: 47.17% Mismatches: 46
Query Match: 32.58% Indels: 6
RESULT 601
ID ACC79021 standard; cDNA; 2920 BP.
DE Human ACE-2 protein encoding cDNA SEQ ID NO:137.
PN WO200298906-A1.
PD 12-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 67.30% Conservative: 32
Best Local Similarity: 47.17% Mismatches: 46
Query Match: 32.58% Indels: 6
RESULT 602
ID ABA71751 standard; DNA; 213 BP.
DE Human foetal liver single exon nucleic acid probe #20056.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 30.40% Indels: 0
RESULT 603
ID AAI52077 standard; DNA; 213 BP.
DE Probe #20763 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 30.40% Indels: 0
RESULT 604
ID ABA37840 standard; DNA; 213 BP.
DE Probe #16306 for gene expression analysis in human heart cell sample.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 30.40% Indels: 0
RESULT 605
ID AAK46169 standard; DNA; 213 BP.
DE Human bone marrow expressed single exon probe SEQ ID NO: 20726.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 30.40% Indels: 0
RESULT 606
ID AAK20115 standard; DNA; 213 BP.
DE Human brain expressed single exon probe SEQ ID NO: 20106.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 30.40% Indels: 0
RESULT 607
ID ABS45886 standard; DNA; 213 BP.
DE Human liver single exon probe, SEQ ID No 20876.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 30.40% Indels: 0
RESULT 608
ID ABS20478 standard; DNA; 213 BP.
DE Human genome-derived single exon probe ORF from lung SEQ ID No 20469.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 30.40% Indels: 0
RESULT 609
ID ABA59231 standard; DNA; 464 BP.
DE Human foetal liver single exon nucleic acid probe #7536.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 29.40% Indels: 0
RESULT 610
ID AAI39012 standard; DNA; 464 BP.
DE Probe #7698 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 29.40% Indels: 0
RESULT 611
ID ABA27979 standard; DNA; 464 BP.
DE Probe #6445 for gene expression analysis in human heart cell sample.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 29.40% Indels: 0
RESULT 612
ID AAK33216 standard; DNA; 464 BP.
DE Human bone marrow expressed single exon probe SEQ ID NO: 7773.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 29.40% Indels: 0
RESULT 613
ID AAK07438 standard; DNA; 464 BP.
DE Human brain expressed single exon probe SEQ ID NO: 7429.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 29.40% Indels: 0
RESULT 614
ID ABS32964 standard; DNA; 464 BP.
DE Human liver single exon probe, SEQ ID No 7954.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 29.40% Indels: 0
RESULT 615
ID ABS08046 standard; DNA; 464 BP.
DE Human genome-derived single exon probe from lung SEQ ID No 8037.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 29.40% Indels: 0
RESULT 616
ID ACN43791 standard; cDNA; 3072 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2666.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Percent Similarity: 56.25% Conservative: 26
Best Local Similarity: 40.00% Mismatches: 40
Query Match: 25.77% Indels: 31
RESULT 617
ID AAC66136 standard; DNA; 862 BP.
DE Human kidney disease associated gene SEQ ID 6.
PN WO200061622-A2.
PD 19-OCT-2000.
PA (INCY-) INCYTE PHARM INC.
Percent Similarity: 98.28% Conservative: 0
Best Local Similarity: 98.28% Mismatches: 0
Query Match: 25.50% Indels: 1
RESULT 618
ID AAC84367 standard; DNA; 2415 BP.
DE Human Zace2 protein encoding degenerate sequence.
PN WO200070032-A1.
PD 23-NOV-2000.
PA (ZYMO) ZYMOGENETICS INC.
Percent Similarity: 52.15% Conservative: 20
Best Local Similarity: 39.88% Mismatches: 70
Query Match: 25.23% Indels: 8
RESULT 619
ID ABX93334 standard; DNA; 2415 BP.
DE Degenerate DNA sequence encoding human zinc metallopeptidase Zace2.
PN US2002177211-A1.
PD 28-NOV-2002.
PA (ZYMO) ZYMOGENETICS INC.
Percent Similarity: 52.15% Conservative: 20
Best Local Similarity: 39.88% Mismatches: 70
Query Match: 25.23% Indels: 8
RESULT 620
ID AAZ59466 standard; DNA; 2262 BP.
DE Human MPROT15 coding sequence #2.
PN JP11318472-A.
PD 24-NOV-1999.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Percent Similarity: 53.04% Conservative: 31
Best Local Similarity: 35.91% Mismatches: 53
Query Match: 23.77% Indels: 32
RESULT 621
ID ABQ57861 standard; cDNA; 561 BP.
DE Human colon cancer related nucleotide sequence SEQ ID NO:1556.
PN WO200229086-A2.
PD 11-APR-2002.
PA (FARB) BAYER CORP.
Percent Similarity: 68.22% Conservative: 20
Best Local Similarity: 49.53% Mismatches: 33
Query Match: 23.73% Indels: 1
RESULT 622
ID AAC84369 standard; DNA; 2415 BP.
DE Mouse Zace2-5 protein encoding degenerate sequence.
PN WO200070032-A1.
PD 23-NOV-2000.
PA (ZYMO) ZYMOGENETICS INC.
Percent Similarity: 44.95% Conservative: 23
Best Local Similarity: 33.33% Mismatches: 79
Query Match: 23.50% Indels: 30
RESULT 623
ID ABX93336 standard; DNA; 2415 BP.
DE Degenerate DNA sequence encoding mouse zinc metallopeptidase mZace-5.
PN US2002177211-A1.
PD 28-NOV-2002.
PA (ZYMO) ZYMOGENETICS INC.
Percent Similarity: 44.95% Conservative: 23
Best Local Similarity: 33.33% Mismatches: 79
Query Match: 23.50% Indels: 30
RESULT 624
ID AAS42515 standard; cDNA; 3474 BP.
DE Human cDNA encoding an mddt protein, clone LI:347572.1:2000MAY01.
PN WO200162922-A2.
PD 30-AUG-2001.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 59.78% Conservative: 32
Best Local Similarity: 42.39% Mismatches: 50
Query Match: 21.60% Indels: 26
RESULT 625
ID ABK30270 standard; cDNA; 2350 BP.
DE Human G-protein-coupled protease #40.
PN US6331427-B1.
PD 18-DEC-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Percent Similarity: 62.86% Conservative: 27
Best Local Similarity: 43.57% Mismatches: 37
Query Match: 21.19% Indels: 16
RESULT 626
ID ABS51330 standard; cDNA; 3666 BP.
DE cDNA encoding human secretory protein #28.
PN WO200257304-A2.
PD 25-JUL-2002.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 47.22% Conservative: 44
Best Local Similarity: 29.76% Mismatches: 63
Query Match: 9.66% Indels: 70
RESULT 627
ID ABN36017 standard; DNA; 60 BP.
DE Human spliced transcript detection oligonucleotide SEQ ID NO:8765.
PN WO200210449-A2.
PD 07-FEB-2002.
PA (COMP-) COMPUGEN INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.26% Indels: 0
RESULT 628
ID ADL45106 standard; DNA; 531 BP.
DE Human ovarian cancer DNA marker #18996.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Percent Similarity: 80.00% Conservative: 7
Best Local Similarity: 56.67% Mismatches: 6
Query Match: 8.89% Indels: 0
RESULT 629
ID ABA18993 standard; DNA; 4069 BP.
DE Human nervous system related polynucleotide SEQ ID NO 11324.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 39.72% Conservative: 32
Best Local Similarity: 24.77% Mismatches: 87

Query Match: 8.53% Indels: 42
RESULT 630
ID ABL55857 standard; DNA; 34337 BP.
DE Human GABA transporter protein gene.
PN US2002031800-A1.
PD 14-MAR-2002.
PA (LIZZ/) LI Z.
PA (CHAT/) CHATURVEDI K.
PA (ZHUS/) ZHU S.
PA (WOOD/) WOODAGE T.
PA (GUEG/) GUEGLER K.
PA (WEBS/) WEBSTER M.
PA (DFRA/) DI FRANCESCO V.
PA (BEAS/) BEASLEY E M.
Percent Similarity: 39.72% Conservative: 32
Best Local Similarity: 24.77% Mismatches: 87
Query Match: 8.53% Indels: 42
RESULT 631
ID ADG88376 standard; DNA; 34337 BP.
DE Human transporter gene.
PN US2003157649-A1.
PD 21-AUG-2003.
PA (APPL-) APPLERA CORP.
Percent Similarity: 39.72% Conservative: 32
Best Local Similarity: 24.77% Mismatches: 87
Query Match: 8.53% Indels: 42
RESULT 632
ID ABL28081 standard; DNA; 2790 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 35716.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 41.76% Conservative: 22
Best Local Similarity: 28.82% Mismatches: 66
Query Match: 8.48% Indels: 33
RESULT 633
ID ADP24566 standard; cDNA; 3857 BP.
DE PRO polypeptide encoding cDNA SEQ ID NO:1744.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 40.10% Conservative: 37
Best Local Similarity: 21.32% Mismatches: 64
Query Match: 8.44% Indels: 54
RESULT 634
ID ABL34973 standard; cDNA; 3134 BP.
DE Murine cDNA isolated from skin cells SEQ ID NO: 478.
PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Percent Similarity: 38.35% Conservative: 37
Best Local Similarity: 20.39% Mismatches: 70
Query Match: 8.30% Indels: 57
RESULT 635
ID ABL34985 standard; cDNA; 3380 BP.
DE Rat cDNA isolated from skin cells SEQ ID NO: 514.
PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Percent Similarity: 38.35% Conservative: 37
Best Local Similarity: 20.39% Mismatches: 70
Query Match: 8.30% Indels: 57
RESULT 636
ID AAC91905 standard; cDNA; 3567 BP.
DE Murine A259 ORF.
PN WO200073339-A1.
PD 07-DEC-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Percent Similarity: 38.05% Conservative: 36
Best Local Similarity: 20.49% Mismatches: 70
Query Match: 8.30% Indels: 57
RESULT 637
ID AAC91904 standard; cDNA; 4858 BP.
DE Murine A259 coding sequence.
PN WO200073339-A1.
PD 07-DEC-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Percent Similarity: 38.05% Conservative: 36
Best Local Similarity: 20.49% Mismatches: 70
Query Match: 8.30% Indels: 57
RESULT 638
ID AAS16874 standard; cDNA; 4858 BP.
DE Murine A259 cDNA.
PN WO200181414-A2.
PD 01-NOV-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Percent Similarity: 38.05% Conservative: 36
Best Local Similarity: 20.49% Mismatches: 70
Query Match: 8.30% Indels: 57
RESULT 639
ID ACA39448 standard; DNA; 2421 BP.
DE Prokaryotic essential gene #21105.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 43.52% Conservative: 31
Best Local Similarity: 27.46% Mismatches: 60
Query Match: 8.26% Indels: 50
RESULT 640
ID ABL06502 standard; cDNA; 5149 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 13988.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 36.74% Conservative: 50
Best Local Similarity: 17.80% Mismatches: 83
Query Match: 8.26% Indels: 85
RESULT 641
ID AAD63505 standard; DNA; 38459 BP.
DE Mycoplasma genitalium gene involved in translation-part I.
PN US2003138777-A1.
PD 24-JUL-2003.
PA (EVAN/) EVANS G A.
Percent Similarity: 43.52% Conservative: 31
Best Local Similarity: 27.46% Mismatches: 60
Query Match: 8.26% Indels: 50
RESULT 642
ID ACC69135 standard; DNA; 38459 BP.
DE M. genitalium translation part 1 gene cassette DNA SEQ ID NO:3.
PN WO2003025145-A2.
PD 27-MAR-2003.
PA (EGEA-) EGEA BIOSCIENCES INC.
Percent Similarity: 43.52% Conservative: 31
Best Local Similarity: 27.46% Mismatches: 60
Query Match: 8.26% Indels: 50
RESULT 643
ID ADN48940 standard; DNA; 38459 BP.
DE Mycoplasma genitalium functional gene fragment #3.
PN US2004063097-A1.
PD 01-APR-2004.
PA (EVAN/) EVANS G A.
Percent Similarity: 43.52% Conservative: 31
Best Local Similarity: 27.46% Mismatches: 60
Query Match: 8.26% Indels: 50
RESULT 644
Percent Similarity: 43.52% Conservative: 31
Best Local Similarity: 27.46% Mismatches: 60
Query Match: 8.26% Indels: 50
RESULT 645
ID ADB52297 standard; DNA; 492 BP.
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:2839.
PN WO2003065993-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Percent Similarity: 38.93% Conservative: 27
Best Local Similarity: 20.81% Mismatches: 37

Query Match: 8.17% Indels: 54
RESULT 646
ID AAT85406 standard; cDNA; 3136 BP.
DE Rat full length cadherin-8 coding sequence.
PN US5646250-A.
PD 08-JUL-1997.
PA (DOHE-) DOHENY EYE INST.
Percent Similarity: 35.39% Conservative: 34
Best Local Similarity: 21.40% Mismatches: 91
Query Match: 8.17% Indels: 66
RESULT 647
ID AAT61917 standard; cDNA; 3136 BP.
DE Full length rat cadherin-8 cDNA.
PN US5597725-A.
PD 28-JAN-1997.
PA (DOHE-) DOHENY EYE INST.
Percent Similarity: 35.39% Conservative: 34
Best Local Similarity: 21.40% Mismatches: 91
Query Match: 8.17% Indels: 66
RESULT 648
ID ADP26917 standard; cDNA; 2545 BP.
DE Human cadherin 8 encoding cDNA SEQ ID NO:18.
PN EP1428893-A2.
PD 16-JUN-2004.
PA (SPRE/) SPRECHER E.
PA (BERG/) BERGMAN R.
Percent Similarity: 34.98% Conservative: 35
Best Local Similarity: 20.58% Mismatches: 93
Query Match: 8.12% Indels: 65
RESULT 649
ID AAT85402 standard; cDNA; 2550 BP.
DE Human cadherin-8 coding sequence.
PN US5646250-A.
PD 08-JUL-1997.
PA (DOHE-) DOHENY EYE INST.
Percent Similarity: 34.98% Conservative: 35
Best Local Similarity: 20.58% Mismatches: 93
Query Match: 8.12% Indels: 65
RESULT 650
ID AAT61923 standard; cDNA; 2550 BP.
DE Full length human cadherin-8 cDNA.
PN US5597725-A.
PD 28-JAN-1997.
PA (DOHE-) DOHENY EYE INST.
Percent Similarity: 34.98% Conservative: 35
Best Local Similarity: 20.58% Mismatches: 93
Query Match: 8.12% Indels: 65
RESULT 651
ID AAI58397 standard; cDNA; 3146 BP.
DE Human polynucleotide SEQ ID NO 600.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 41.07% Conservative: 35
Best Local Similarity: 20.24% Mismatches: 40
Query Match: 8.12% Indels: 59
RESULT 652
ID ADQ98607 standard; cDNA; 3146 BP.
DE DNA encoding human GPCR-like protein seqid 277.
PN US6569662-B1.
PD 27-MAY-2003.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 41.07% Conservative: 35
Best Local Similarity: 20.24% Mismatches: 40
Query Match: 8.12% Indels: 59
RESULT 653
ID ADB48367 standard; cDNA; 3146 BP.
DE Novel human cDNA SEQ ID NO 277.
PN US2003104529-A1.
PD 05-JUN-2003.
PA (ZHOU/) ZHOU P.
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (ASUN/) ASUNDI V.
PA (DRMA/) DRMANAC R T.
Percent Similarity: 41.07% Conservative: 35
Best Local Similarity: 20.24% Mismatches: 40
Query Match: 8.12% Indels: 59
RESULT 654
ID ABL65914 standard; DNA; 3150 BP.
DE Lung cancer related gene sequence SEQ ID NO:4251.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Percent Similarity: 41.07% Conservative: 35
Best Local Similarity: 20.24% Mismatches: 40
Query Match: 8.12% Indels: 59
RESULT 655
ID ABL69587 standard; DNA; 3150 BP.
DE Prostate cancer related gene sequence SEQ ID NO:7924.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Percent Similarity: 41.07% Conservative: 35
Best Local Similarity: 20.24% Mismatches: 40
Query Match: 8.12% Indels: 59
RESULT 656
ID ABL64453 standard; DNA; 3150 BP.
DE Stomach cancer related gene sequence SEQ ID NO:2790.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Percent Similarity: 41.07% Conservative: 35
Best Local Similarity: 20.24% Mismatches: 40
Query Match: 8.12% Indels: 59
RESULT 657
ID AAI60183 standard; cDNA; 3196 BP.
DE Human polynucleotide SEQ ID NO 4172.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 41.07% Conservative: 35
Best Local Similarity: 20.24% Mismatches: 40
Query Match: 8.12% Indels: 59
RESULT 658
ID ABT16049 standard; DNA; 3617 BP.
DE NOVX related polynucleotide SEQ ID No 65.
PN WO200299062-A2.
PD 12-DEC-2002.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 41.07% Conservative: 35
Best Local Similarity: 20.24% Mismatches: 40
Query Match: 8.12% Indels: 59
RESULT 659
ID ADO41699 standard; cDNA; 3617 BP.
DE Novel human polypeptide NOV24b cDNA.
PN US2004018555-A1.
PD 29-JAN-2004.
PA (ANDE/) ANDERSON D W.
PA (ZERH/) ZERHUSEN B D.
PA (LILL/) LI L.
PA (ZHON/) ZHONG M.
PA (CASM/) CASMAN S J.
PA (GERL/) GERLACH V.
PA (SHIM/) SHIMKETS R A.
PA (GORM/) GORMAN L.
PA (PENA/) PENA C E A.
PA (KEKU/) KEKUDA R.
PA (PATT/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (LEIT/) LEITE M W.
PA (RAST/) RASTELLI L.
PA (MACD/) MACDOUGALL J R.
PA (TAUP/) TAUPIER R J.
PA (GUOX/) GUO X S.
PA (MILL/) MILLER C E.

PA (SHEN/) SHENOY S G.
PA (HJAL/) HJALT T.
PA (VOSS/) VOSS E Z.
PA (BOLD/) BOLDOG F L.
PA (MALY/) MALYANKAR U M.
PA (PADI/) PADIGARU M.
PA (JIWW/) JI W.
PA (SMIT/) SMITHSON G.
PA (EDIN/) EDINGER S R.
PA (MILL/) MILLET I.
PA (ELLE/) ELLERMAN K.
Percent Similarity: 41.07% Conservative: 35
Best Local Similarity: 20.24% Mismatches: 40
Query Match: 8.12% Indels: 59
RESULT 660
ID AAD33323 standard; cDNA; 3868 BP.
DE Human INTG-1 protein encoding cDNA.
PN WO200212339-A2.
PD 14-FEB-2002.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 41.07% Conservative: 35
Best Local Similarity: 20.24% Mismatches: 40
Query Match: 8.12% Indels: 59
RESULT 661
ID ADG42064 standard; DNA; 2929 BP.
DE Human CDH8 nucleic acid sequence.
PN WO2003087408-A2.
PD 23-OCT-2003.
PA (UYED-) UNIV EDINBURGH.
Percent Similarity: 35.39% Conservative: 34
Best Local Similarity: 21.40% Mismatches: 91
Query Match: 8.08% Indels: 66
RESULT 662
ID ADR41320 standard; cDNA; 5427 BP.
DE Human CD-like molecule HFOYM21 cDNA, SEQ ID NO:119.
PN WO200226930-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 42.22% Conservative: 35
Best Local Similarity: 22.78% Mismatches: 68
Query Match: 8.08% Indels: 36
RESULT 663
ID ABT16048 standard; DNA; 3617 BP.
DE NOVX related polynucleotide SEQ ID No 63.
PN WO200299062-A2.
PD 12-DEC-2002.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 41.07% Conservative: 35
Best Local Similarity: 20.24% Mismatches: 40
Query Match: 8.03% Indels: 59
RESULT 664
ID ADO41697 standard; cDNA; 3617 BP.
DE Novel human polypeptide NOV24a cDNA.
PN US2004018555-A1.
PD 29-JAN-2004.
PA (ANDE/) ANDERSON D W.
PA (ZERH/) ZERHUSEN B D.
PA (LILL/) LI L.
PA (ZHON/) ZHONG M.
PA (CASM/) CASMAN S J.
PA (GERL/) GERLACH V.
PA (SHIM/) SHIMKETS R A.
PA (GORM/) GORMAN L.
PA (PENA/) PENA C E A.
PA (KEKU/) KEKUDA R.
PA (PATT/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (LEIT/) LEITE M W.
PA (RAST/) RASTELLI L.
PA (MACD/) MACDOUGALL J R.
PA (TAUP/) TAUPIER R J.
PA (GUOX/) GUO X S.
PA (MILL/) MILLER C E.

PA (SHEN/) SHENOY S G.
PA (HJAL/) HJALT T.
PA (VOSS/) VOSS E Z.
PA (BOLD/) BOLDOG F L.
PA (MALY/) MALYANKAR U M.
PA (PADI/) PADIGARU M.
PA (JIWW/) JI W.
PA (SMIT/) SMITHSON G.
PA (EDIN/) EDINGER S R.
PA (MILL/) MILLET I.
PA (ELLE/) ELLERMAN K.
Percent Similarity: 41.07% Conservative: 35
Best Local Similarity: 20.24% Mismatches: 40
Query Match: 8.03% Indels: 59
RESULT 665
ID AAC86870 standard; cDNA; 3983 BP.
DE DNA encoding a human alpha11 integrin chain.
PN WO200075187-A1.
PD 14-DEC-2000.
PA (ACTI-) ACTIVE BIOTECH AB.
Percent Similarity: 42.94% Conservative: 36
Best Local Similarity: 22.60% Mismatches: 54
Query Match: 8.03% Indels: 47
RESULT 666
ID ABN86522 standard; cDNA; 1177 BP.
DE Nucleotide sequence of mouse CD44 cDNA.
PN WO200238794-A2.
PD 16-MAY-2002.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
Percent Similarity: 42.34% Conservative: 23
Best Local Similarity: 21.62% Mismatches: 30
Query Match: 7.99% Indels: 34
RESULT 667
ID ABL06503 standard; cDNA; 2908 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 13991.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 35.53% Conservative: 47
Best Local Similarity: 18.32% Mismatches: 77
Query Match: 7.94% Indels: 100
RESULT 668
ID ABN86523 standard; cDNA; 1089 BP.
DE Nucleotide sequence of hamster CD44 cDNA.
PN WO200238794-A2.
PD 16-MAY-2002.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
Percent Similarity: 42.20% Conservative: 20
Best Local Similarity: 23.85% Mismatches: 29
Query Match: 7.89% Indels: 34
RESULT 669
ID AAA80620 standard; cDNA; 4631 BP.
DE Human secreted protein gene #7 from clone HOHBY69.
PN WO200029435-A1.
PD 25-MAY-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 43.09% Conservative: 39
Best Local Similarity: 21.55% Mismatches: 65
Query Match: 7.89% Indels: 38
RESULT 670
ID ADA27044 standard; cDNA; 4631 BP.
DE Human novel secreted protein gene 7 cDNA HOHBY69 #2.
PN US2003055231-A1.
PD 20-MAR-2003.
PA (NIJJ/) NI J.
PA (YOUN/) YOUNG P E.
PA (KENN/) KENNY J J.
PA (OLSE/) OLSEN H S.
PA (MOOR/) MOORE P A.
PA (WEIY/) WEI Y.
PA (GREE/) GREENE J M.
PA (RUBE/) RUBEN S M.
PA (LIUD/) LIU D.

PA (CROC/) CROCKER P R.
Percent Similarity: 42.05% Conservative: 35
Best Local Similarity: 22.16% Mismatches: 74
Query Match: 7.89% Indels: 28
RESULT 671
ID ADE86574 standard; cDNA; 4631 BP.
DE Novel human secreted protein cDNA #15.
PN US2003129685-A1.
PD 10-JUL-2003.
PA (NIJJ/) NI J.
PA (YOUN/) YOUNG P E.
PA (KENN/) KENNY J J.
PA (OLSE/) OLSEN H S.
PA (MOOR/) MOORE P A.
PA (WEIY/) WEI Y.
PA (GREE/) GREENE J M.
PA (RUBE/) RUBEN S M.
Percent Similarity: 42.05% Conservative: 35
Best Local Similarity: 22.16% Mismatches: 74
Query Match: 7.89% Indels: 28
RESULT 672
ID ABN86507 standard; cDNA; 2747 BP.
DE Rat glycoprotein CD44 polypeptide encoding cDNA.
PN WO200238794-A2.
PD 16-MAY-2002.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
Percent Similarity: 42.34% Conservative: 24
Best Local Similarity: 20.72% Mismatches: 30
Query Match: 7.80% Indels: 34
RESULT 673
ID ABK63681 standard; cDNA; 2747 BP.
DE Rat sequence differentially expressed in response to a hepatotoxin #1588.
PN WO200210453-A2.
PD 07-FEB-2002.
PA (GENE-) GENE LOGIC INC.
Percent Similarity: 42.34% Conservative: 24
Best Local Similarity: 20.72% Mismatches: 30
Query Match: 7.80% Indels: 34
RESULT 674
ID AAQ14263 standard; cDNA; 3207 BP.
DE p-meta-1 metastasis-specific variant of CD44 glycoprotein.
PN DE4014510-A.
PD 14-NOV-1991.
PA (GESL) KERNFORSCHUNGSZENT KARLSRUHE.
PA (UYKA-) UNIV KARLSRUHE.
PA (DEKR-) DEUT KREBSFORSCHUNGSLENT.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENT.
Percent Similarity: 42.34% Conservative: 24
Best Local Similarity: 20.72% Mismatches: 30
Query Match: 7.80% Indels: 34
RESULT 675
ID AAD53012 standard; DNA; 5965 BP.
DE B4 DNA clone (CA125).
PN WO200292836-A2.
PD 21-NOV-2002.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
Percent Similarity: 33.73% Conservative: 36
Best Local Similarity: 19.28% Mismatches: 75
Query Match: 7.80% Indels: 90
RESULT 676
ID ABZ38842 standard; DNA; 1404 BP.
DE N. gonorrhoeae nucleotide sequence SEQ ID 2273.
PN WO200279243-A2.
PD 10-OCT-2002.
PA (CHIR-) CHIRON SPA.
Percent Similarity: 39.70% Conservative: 31
Best Local Similarity: 24.12% Mismatches: 77
Query Match: 7.76% Indels: 43
RESULT 677
ID ABN72972 standard; DNA; 3447 BP.
DE Truncated nucleotide sequence with homology to 0772P.
PN WO200206317-A2.
PD 24-JAN-2002.
PA (CORI-) CORIXA CORP.
Percent Similarity: 36.98% Conservative: 30
Best Local Similarity: 21.35% Mismatches: 60
Query Match: 7.76% Indels: 61
RESULT 678
ID ADA08609 standard; DNA; 3447 BP.
DE Human O772P homology protein #1 DNA.
PN US2003091580-A1.
PD 15-MAY-2003.
PA (MITC/) MITCHAM J L.
PA (KING/) KING G E.
PA (ALGA/) ALGATE P A.
PA (FLIN/) FLING S P.
PA (RETT/) RETTER M W.
PA (FANG/) FANGER G R.
PA (REED/) REED S G.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (HILL/) HILL P.
PA (ALBO/) ALBONE E.
Percent Similarity: 36.98% Conservative: 30
Best Local Similarity: 21.35% Mismatches: 60
Query Match: 7.76% Indels: 61
RESULT 679
ID ADF08952 standard; cDNA; 3447 BP.
DE cDNA encoding secreted ovarian carcinoma antigen seqid 456.
PN US2003124140-A1.
PD 03-JUL-2003.
PA (CORI-) CORIXA CORP.
Percent Similarity: 36.98% Conservative: 30
Best Local Similarity: 21.35% Mismatches: 60
Query Match: 7.76% Indels: 61
RESULT 680
ID ADG46239 standard; cDNA; 3447 BP.
DE Human ovarian carcinoma polynucleotide #388.
PN US2003165504-A1.
PD 04-SEP-2003.
PA (RETT/) RETTER M W.
PA (FANG/) FANGER G R.
Percent Similarity: 36.98% Conservative: 30
Best Local Similarity: 21.35% Mismatches: 60
Query Match: 7.76% Indels: 61
RESULT 681
ID AAH18639 standard; cDNA; 3557 BP.
DE Human cDNA sequence SEQ ID NO:18864.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Percent Similarity: 36.98% Conservative: 30
Best Local Similarity: 21.35% Mismatches: 60
Query Match: 7.76% Indels: 61
RESULT 682
ID ABA83109 standard; DNA; 3557 BP.
DE HOST-1 ovarian tumour marker gene, SEQ ID NO:55.
PN WO200175177-A2.
PD 11-OCT-2001.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Percent Similarity: 36.98% Conservative: 30
Best Local Similarity: 21.35% Mismatches: 60
Query Match: 7.76% Indels: 61
RESULT 683
ID ABN72973 standard; DNA; 3557 BP.
DE Full nucleotide sequence with homology to 0772P.
PN WO200206317-A2.
PD 24-JAN-2002.
PA (CORI-) CORIXA CORP.
Percent Similarity: 36.98% Conservative: 30
Best Local Similarity: 21.35% Mismatches: 60
Query Match: 7.76% Indels: 61
RESULT 684
ID ABN72975 standard; cDNA; 3557 BP.
DE cDNA sequence for clone FLJ14303.
PN WO200206317-A2.

PD 24-JAN-2002.
PA (CORI-) CORIXA CORP.
Percent Similarity: 36.98% Conservative: 30
Best Local Similarity: 21.35% Mismatches: 60
Query Match: 7.76% Indels: 61
RESULT 685
ID ACF36017 standard; DNA; 3557 BP.
DE DNA expressed by human ovarian cancer cells.
PN WO2003059256-A2.
PD 24-JUL-2003.
PA (IDEC-) IDEC PHARM CORP.
Percent Similarity: 36.98% Conservative: 30
Best Local Similarity: 21.35% Mismatches: 60
Query Match: 7.76% Indels: 61
RESULT 686
ID ADA08610 standard; DNA; 3557 BP.
DE Human O772P homology protein #2 DNA.
PN US2003091580-A1.
PD 15-MAY-2003.
PA (MITC/) MITCHAM J L.
PA (KING/) KING G E.
PA (ALGA/) ALGATE P A.
PA (FLIN/) FLING S P.
PA (RETT/) RETTER M W.
PA (FANG/) FANGER G R.
PA (REED/) REED S G.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (HILL/) HILL P.
PA (ALBO/) ALBONE E.
Percent Similarity: 36.98% Conservative: 30
Best Local Similarity: 21.35% Mismatches: 60
Query Match: 7.76% Indels: 61
RESULT 687
ID ADA08616 standard; cDNA; 3557 BP.
DE Human cDNA clone FLJ14303.
PN US2003091580-A1.
PD 15-MAY-2003.
PA (MITC/) MITCHAM J L.
PA (KING/) KING G E.
PA (ALGA/) ALGATE P A.
PA (FLIN/) FLING S P.
PA (RETT/) RETTER M W.
PA (FANG/) FANGER G R.
PA (REED/) REED S G.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (HILL/) HILL P.
PA (ALBO/) ALBONE E.
Percent Similarity: 36.98% Conservative: 30
Best Local Similarity: 21.35% Mismatches: 60
Query Match: 7.76% Indels: 61
RESULT 688
ID ADF08953 standard; cDNA; 3557 BP.
DE cDNA encoding secreted ovarian carcinoma antigen seqid 457.
PN US2003124140-A1.
PD 03-JUL-2003.
PA (CORI-) CORIXA CORP.
Percent Similarity: 36.98% Conservative: 30
Best Local Similarity: 21.35% Mismatches: 60
Query Match: 7.76% Indels: 61
RESULT 689
ID ADF08959 standard; cDNA; 3557 BP.
DE cDNA encoding secreted ovarian carcinoma antigen seqid 463.
PN US2003124140-A1.
PD 03-JUL-2003.
PA (CORI-) CORIXA CORP.
Percent Similarity: 36.98% Conservative: 30
Best Local Similarity: 21.35% Mismatches: 60
Query Match: 7.76% Indels: 61
RESULT 690
ID ADG46240 standard; cDNA; 3557 BP.
DE Human ovarian carcinoma polynucleotide #389.
PN US2003165504-A1.
PD 04-SEP-2003.
PA (RETT/) RETTER M W.
PA (FANG/) FANGER G R.
Percent Similarity: 36.98% Conservative: 30
Best Local Similarity: 21.35% Mismatches: 60
Query Match: 7.76% Indels: 61
RESULT 691
ID ADG08770 standard; cDNA; 3557 BP.
DE Human ovarian cancer related EST SEQ ID NO:11.
PN WO2003104429-A2.
PD 18-DEC-2003.
PA (IDEC-) IDEC PHARM CORP.
Percent Similarity: 36.98% Conservative: 30
Best Local Similarity: 21.35% Mismatches: 60
Query Match: 7.76% Indels: 61
RESULT 692
ID ADQ29638 standard; DNA; 3557 BP.
DE Human colorectal cancer-associated protein coding sequence #60.
PN EP1439393-A2.
PD 21-JUL-2004.
PA (FARB) BAYER HEALTHCARE LLC.
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
Percent Similarity: 36.98% Conservative: 30
Best Local Similarity: 21.35% Mismatches: 60
Query Match: 7.76% Indels: 61
RESULT 693
ID ABZ11844 standard; cDNA; 4573 BP.
DE Human polynucleotide SEQ ID NO 726.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 40.41% Conservative: 35
Best Local Similarity: 22.28% Mismatches: 66
Query Match: 7.76% Indels: 50
RESULT 694
ID ACC72807 standard; cDNA; 5264 BP.
DE Human cancer related protein encoding cDNA SEQ ID NO:145.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Percent Similarity: 40.41% Conservative: 35
Best Local Similarity: 22.28% Mismatches: 66
Query Match: 7.76% Indels: 50
RESULT 695
ID ADM44362 standard; cDNA; 5323 BP.
DE Novel human arginine-rich protein cDNA #726.
PN US2004053250-A1.
PD 18-MAR-2004.
PA (TANG/) TANG Y T.
PA (XUEA/) XUE A.
PA (DRMA/) DRMANAC R T.
Percent Similarity: 40.41% Conservative: 35
Best Local Similarity: 22.28% Mismatches: 66
Query Match: 7.76% Indels: 50
RESULT 696
ID ABX72534 standard; cDNA; 6833 BP.
DE Human cDNA encoding 13 CA125 repeats and the carboxy terminus.
PN WO200283866-A2.
PD 24-OCT-2002.
PA (UYAR-) UNIV ARKANSAS.
Percent Similarity: 36.98% Conservative: 30
Best Local Similarity: 21.35% Mismatches: 60
Query Match: 7.76% Indels: 61
RESULT 697
ID ABN80091 standard; DNA; 8186 BP.
DE Human chemically modified disease associated gene SEQ ID NO 108.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Percent Similarity: 39.08% Conservative: 29
Best Local Similarity: 22.41% Mismatches: 69
Query Match: 7.76% Indels: 37

RESULT 698
ID ADL16194 standard; DNA; 4756 BP.
DE Human protein tyrosine phosphatase gene #18.
PN WO2003068984-A2.
PD 21-AUG-2003.
PA (COLD-) COLD SPRING HARBOR LAB.
PA (CEPT-) CEPTYR INC.
Percent Similarity: 41.57% Conservative: 35
Best Local Similarity: 20.48% Mismatches: 77
Query Match: 7.71% Indels: 20
RESULT 699
ID ADI32135 standard; cDNA; 4756 BP.
DE Human cDNA #1461.
PN US6607879-B1.
PD 19-AUG-2003.
PA (INCY-) INCYTE CORP.
Percent Similarity: 41.57% Conservative: 35
Best Local Similarity: 20.48% Mismatches: 77
Query Match: 7.71% Indels: 20
RESULT 700
Percent Similarity: 37.76% Conservative: 27
Best Local Similarity: 23.98% Mismatches: 53
Query Match: 7.71% Indels: 70
RESULT 701
Percent Similarity: 37.76% Conservative: 27
Best Local Similarity: 23.98% Mismatches: 53
Query Match: 7.71% Indels: 70
RESULT 702
ID ADL85166 standard; DNA; 529 BP.
DE DNA up-regulated in murine common lymphoid myeloid cells SeqID 1559.
PN WO2003093445-A2.
PD 13-NOV-2003.
PA (STOW-) STOWERS INST MEDICAL RES.
Percent Similarity: 45.05% Conservative: 20
Best Local Similarity: 23.08% Mismatches: 31
Query Match: 7.67% Indels: 19
RESULT 703
ID ADL85165 standard; DNA; 529 BP.
DE DNA up-regulated in murine common lymphoid myeloid cells SeqID 1558.
PN WO2003093445-A2.
PD 13-NOV-2003.
PA (STOW-) STOWERS INST MEDICAL RES.
Percent Similarity: 45.05% Conservative: 20
Best Local Similarity: 23.08% Mismatches: 31
Query Match: 7.67% Indels: 19
RESULT 704
ID AAZ53929 standard; DNA; 1407 BP.
DE Neisseria meningitidis ORF 585 partial DNA sequence SEQ ID NO:1807.
PN WO9957280-A2.
PD 11-NOV-1999.
PA (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
Percent Similarity: 38.38% Conservative: 29
Best Local Similarity: 23.74% Mismatches: 81
Query Match: 7.67% Indels: 41
RESULT 705
ID AAC91902 standard; cDNA; 3567 BP.
DE Human A259 ORF.
PN WO200073339-A1.
PD 07-DEC-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Percent Similarity: 43.35% Conservative: 36
Best Local Similarity: 22.54% Mismatches: 59
Query Match: 7.67% Indels: 39
RESULT 706
ID AAS22772 standard; cDNA; 3967 BP.
DE Human cDNA encoding a novel human protein #338.
PN WO200155437-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 43.35% Conservative: 36
Best Local Similarity: 22.54% Mismatches: 59
Query Match: 7.67% Indels: 39
RESULT 707
ID ADE09822 standard; DNA; 3967 BP.
DE Novel DNA-related contig nucleotide sequence #544.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 43.35% Conservative: 36
Best Local Similarity: 22.54% Mismatches: 59
Query Match: 7.67% Indels: 39
RESULT 708
ID AAS22536 standard; cDNA; 3969 BP.
DE Human cDNA encoding a novel human protein #102.
PN WO200155437-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 43.35% Conservative: 36
Best Local Similarity: 22.54% Mismatches: 59
Query Match: 7.67% Indels: 39
RESULT 709
ID AAC91901 standard; cDNA; 5042 BP.
DE Human A259 coding sequence.
PN WO200073339-A1.
PD 07-DEC-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Percent Similarity: 43.35% Conservative: 36
Best Local Similarity: 22.54% Mismatches: 59
Query Match: 7.67% Indels: 39
RESULT 710
ID AAS16873 standard; cDNA; 5042 BP.
DE Human A259 cDNA.
PN WO200181414-A2.
PD 01-NOV-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Percent Similarity: 43.35% Conservative: 36
Best Local Similarity: 22.54% Mismatches: 59
Query Match: 7.67% Indels: 39
RESULT 711
ID ADQ24050 standard; DNA; 5117 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6870.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Percent Similarity: 43.35% Conservative: 36
Best Local Similarity: 22.54% Mismatches: 59
Query Match: 7.67% Indels: 39
RESULT 712
ID ADO05745 standard; DNA; 38306 BP.
DE Recombinant adenoviral vector polynucleotide sequence.
PN EP1418185-A1.
PD 12-MAY-2004.
PA (AVET) AVENTIS PHARMA DEUT GMBH.
Percent Similarity: 33.56% Conservative: 42
Best Local Similarity: 19.03% Mismatches: 101
Query Match: 7.67% Indels: 92
RESULT 713
ID AAT06027 standard; cDNA; 5117 BP.
DE huDEP-1 cDNA.
PN WO9530008-A1.
PD 09-NOV-1995.
PA (COLD-) COLD SPRING HARBOR LAB.
Percent Similarity: 48.35% Conservative: 20
Best Local Similarity: 26.37% Mismatches: 34
Query Match: 7.58% Indels: 13
RESULT 714
ID ADL16192 standard; DNA; 5117 BP.
DE Human protein tyrosine phosphatase gene #17.
PN WO2003068984-A2.
PD 21-AUG-2003.
PA (COLD-) COLD SPRING HARBOR LAB.
PA (CEPT-) CEPTYR INC.
Percent Similarity: 48.35% Conservative: 20
Best Local Similarity: 26.37% Mismatches: 34
Query Match: 7.58% Indels: 13

RESULT 715
ID ADP74602 standard; DNA; 5117 BP.
DE Nucleotide sequence of human DEP-1.
PN WO2004048549-A2.
PD 10-JUN-2004.
PA (COLD-) COLD SPRING HARBOR LAB.
Percent Similarity: 48.35% Conservative: 20
Best Local Similarity: 26.37% Mismatches: 34
Query Match: 7.58% Indels: 13
RESULT 716
ID ADC87424 standard; DNA; 34551 BP.
DE Human GPCR gene SEQ ID NO:1877.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Percent Similarity: 43.40% Conservative: 15
Best Local Similarity: 29.25% Mismatches: 41
Query Match: 7.58% Indels: 19
RESULT 717
ID ABK63658 standard; cDNA; 5588 BP.
DE Rat sequence differentially expressed in response to a hepatotoxin #1565.
PN WO200210453-A2.
PD 07-FEB-2002.
PA (GENE-) GENE LOGIC INC.
Percent Similarity: 42.06% Conservative: 19
Best Local Similarity: 24.30% Mismatches: 50
Query Match: 7.53% Indels: 13
RESULT 718
Percent Similarity: 39.38% Conservative: 32
Best Local Similarity: 22.80% Mismatches: 63
Query Match: 7.53% Indels: 55
RESULT 719
ID ABL65294 standard; DNA; 386 BP.
DE Lung cancer related gene sequence SEQ ID NO:3631.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Percent Similarity: 38.75% Conservative: 26
Best Local Similarity: 22.50% Mismatches: 51
Query Match: 7.49% Indels: 47
RESULT 720
ID ADK58075 standard; DNA; 551 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #5458.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
PA (DOWC) DOW AGROSCIENCES LLC.
Percent Similarity: 46.15% Conservative: 25
Best Local Similarity: 22.12% Mismatches: 37
Query Match: 7.49% Indels: 19
RESULT 721
ID AAZ53927 standard; DNA; 696 BP.
DE Neisseria gonorrheae ORF 585 partial DNA sequence SEQ ID NO:1803.
PN WO9957280-A2.
PD 11-NOV-1999.
PA (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
Percent Similarity: 40.51% Conservative: 32
Best Local Similarity: 24.10% Mismatches: 73
Query Match: 7.49% Indels: 43
RESULT 722
ID ADH84658 standard; DNA; 1590 BP.
DE Enterococcus faecalis polynucleotide #2543.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Percent Similarity: 41.18% Conservative: 28
Best Local Similarity: 24.71% Mismatches: 75
Query Match: 7.49% Indels: 25
RESULT 723
ID AAX13278 standard; DNA; 13884 BP.
DE Enterococcus faecalis genome contig SEQ ID NO:341.
PN WO9850555-A2.
PD 12-NOV-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 41.18% Conservative: 28
Best Local Similarity: 24.71% Mismatches: 75
Query Match: 7.49% Indels: 25
RESULT 724
ID ABS99073 standard; DNA; 13884 BP.
DE Enterococcus faecalis contig sequence #341.
PN US2002120116-A1.
PD 29-AUG-2002.
PA (KUNS/) KUNSCH C A.
PA (DILL/) DILLON P J.
PA (BARA/) BARASH S.
Percent Similarity: 41.18% Conservative: 28
Best Local Similarity: 24.71% Mismatches: 75
Query Match: 7.49% Indels: 25
RESULT 725
ID ACN45042 standard; DNA; 95835 BP.
DE Human genomic sequence hCG37223.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Percent Similarity: 39.13% Conservative: 32
Best Local Similarity: 19.25% Mismatches: 51
Query Match: 7.49% Indels: 47
RESULT 726
ID ACA31993 standard; DNA; 1401 BP.
DE Prokaryotic essential gene #13650.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 37.31% Conservative: 25
Best Local Similarity: 24.35% Mismatches: 67
Query Match: 7.44% Indels: 54
RESULT 727
ID AAH33739 standard; cDNA; 1929 BP.
DE Human colon cancer antigen encoding cDNA SEQ ID NO:795.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 36.18% Conservative: 32
Best Local Similarity: 20.10% Mismatches: 73
Query Match: 7.44% Indels: 54
RESULT 728
ID ABL09031 standard; cDNA; 2339 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 21575.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 53.73% Conservative: 16
Best Local Similarity: 29.85% Mismatches: 26
Query Match: 7.44% Indels: 5
RESULT 729
ID ACC72077 standard; DNA; 4779 BP.
DE Human NOV2b coding sequence.
PN WO2003029423-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 41.84% Conservative: 40
Best Local Similarity: 21.43% Mismatches: 74
Query Match: 7.44% Indels: 40
RESULT 730
ID ABX04161 standard; cDNA; 4986 BP.
DE Human mRNA differentially expressed in mesenchymal cells #8.
PN WO200271927-A2.
PD 19-SEP-2002.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
Percent Similarity: 41.84% Conservative: 40
Best Local Similarity: 21.43% Mismatches: 74
Query Match: 7.44% Indels: 40
RESULT 731

ID ADQ19967 standard; DNA; 4986 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2787.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Percent Similarity: 41.84% Conservative: 40
Best Local Similarity: 21.43% Mismatches: 74
Query Match: 7.44% Indels: 40
RESULT 732
ID AAA80612 standard; cDNA; 4995 BP.
DE Human ITGA11 secreted protein gene #7.
PN WO200029435-A1.
PD 25-MAY-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 41.84% Conservative: 40
Best Local Similarity: 21.43% Mismatches: 74
Query Match: 7.44% Indels: 40
RESULT 733
ID ACC72076 standard; DNA; 4995 BP.
DE Human NOV2a coding sequence.
PN WO2003029423-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 41.84% Conservative: 40
Best Local Similarity: 21.43% Mismatches: 74
Query Match: 7.44% Indels: 40
RESULT 734
ID ADA27036 standard; cDNA; 4995 BP.
DE Human novel secreted protein gene 7 cDNA HOHBY69 #1.
PN US2003055231-A1.
PD 20-MAR-2003.
PA (NIJJ/) NI J.
PA (YOUN/) YOUNG P E.
PA (KENN/) KENNY J J.
PA (OLSE/) OLSEN H S.
PA (MOOR/) MOORE P A.
PA (WEIY/) WEI Y.
PA (GREE/) GREENE J M.
PA (RUBE/) RUBEN S M.
PA (LIUD/) LIU D.
PA (CROC/) CROCKER P R.
Percent Similarity: 41.84% Conservative: 40
Best Local Similarity: 21.43% Mismatches: 74
Query Match: 7.44% Indels: 40
RESULT 735
ID ADE86566 standard; cDNA; 4995 BP.
DE Novel human secreted protein cDNA #7.
PN US2003129685-A1.
PD 10-JUL-2003.
PA (NIJJ/) NI J.
PA (YOUN/) YOUNG P E.
PA (KENN/) KENNY J J.
PA (OLSE/) OLSEN H S.
PA (MOOR/) MOORE P A.
PA (WEIY/) WEI Y.
PA (GREE/) GREENE J M.
PA (RUBE/) RUBEN S M.
Percent Similarity: 41.84% Conservative: 40
Best Local Similarity: 21.43% Mismatches: 74
Query Match: 7.44% Indels: 40
RESULT 736
ID ABL09030 standard; cDNA; 5820 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 21572.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 53.73% Conservative: 16
Best Local Similarity: 29.85% Mismatches: 26
Query Match: 7.44% Indels: 5
RESULT 737
ID ADL16199 standard; DNA; 6314 BP.
DE Rat protein tyrosine phosphatase gene #4.
PN WO2003068984-A2.
PD 21-AUG-2003.
PA (COLD-) COLD SPRING HARBOR LAB.
PA (CEPT-) CEPTYR INC.
Percent Similarity: 48.89% Conservative: 20
Best Local Similarity: 26.67% Mismatches: 36
Query Match: 7.44% Indels: 10
RESULT 738
ID AAZ91916 standard; cDNA; 8827 BP.
DE Wild type (C57BL/6J) murine mahogany protein coding sequence.
PN WO200005373-A2.
PD 03-FEB-2000.
PA (MILL-) MILLENIUM PHARM INC.
Percent Similarity: 32.08% Conservative: 29
Best Local Similarity: 20.00% Mismatches: 111
Query Match: 7.44% Indels: 52
RESULT 739
ID ABV94618 standard; cDNA; 910 BP.
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:258.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 38.36% Conservative: 23
Best Local Similarity: 23.90% Mismatches: 63
Query Match: 7.40% Indels: 35
RESULT 740
ID ADM18893 standard; cDNA; 910 BP.
DE Human co-stimulatory molecule encoding cDNA SEQ ID NO:258.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 38.36% Conservative: 23
Best Local Similarity: 23.90% Mismatches: 63
Query Match: 7.40% Indels: 35
RESULT 741
ID ACF71663 standard; DNA; 1092 BP.
DE Photorhabdus luminescens nucleotide sequence #10130.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Percent Similarity: 37.77% Conservative: 24
Best Local Similarity: 25.00% Mismatches: 54
Query Match: 7.40% Indels: 63
RESULT 742
ID ABV78128 standard; DNA; 3147 BP.
DE Human alpha V integrin DNA SEQ ID NO 12.
PN WO200255693-A2.
PD 18-JUL-2002.
PA (RIBO-) RIBOPHARMA AG.
Percent Similarity: 40.62% Conservative: 38
Best Local Similarity: 23.66% Mismatches: 82
Query Match: 7.40% Indels: 51
RESULT 743
ID ABZ35704 standard; DNA; 3147 BP.
DE Human alpha V integrin encoding polynucleotide SEQ ID NO 12.
PN DE10100588-A1.
PD 18-JUL-2002.
PA (RIBO-) RIBOPHARMA AG.
Percent Similarity: 40.62% Conservative: 38
Best Local Similarity: 23.66% Mismatches: 82
Query Match: 7.40% Indels: 51
RESULT 744
ID ABX09947 standard; DNA; 3147 BP.
DE Human alpha v integrin DNA fragment SEQ ID 12.
PN DE10100587-C1.
PD 21-NOV-2002.
PA (RIBO-) RIBOPHARMA AG.
Percent Similarity: 40.62% Conservative: 38
Best Local Similarity: 23.66% Mismatches: 82
Query Match: 7.40% Indels: 51
RESULT 745
ID ABL91669 standard; DNA; 3147 BP.
DE Human polynucleotide SEQ ID NO 12.

PN DE10100586-C1.
PD 11-APR-2002.
PA (RIBO-) RIBOPHARMA AG.
Percent Similarity: 40.62% Conservative: 38
Best Local Similarity: 23.66% Mismatches: 82
Query Match: 7.40% Indels: 51
RESULT 746
ID ABL69959 standard; DNA; 3269 BP.
DE Pancreas cancer related gene sequence SEQ ID NO:8296.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Percent Similarity: 40.10% Conservative: 36
Best Local Similarity: 21.83% Mismatches: 64
Query Match: 7.40% Indels: 54
RESULT 747
ID ADP24568 standard; cDNA; 3269 BP.
DE PRO polypeptide encoding cDNA SEQ ID NO:1746.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 40.10% Conservative: 36
Best Local Similarity: 21.83% Mismatches: 64
Query Match: 7.40% Indels: 54
RESULT 748
ID AAS83082 standard; cDNA; 5717 BP.
DE DNA encoding novel human diagnostic protein #18886.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 40.62% Conservative: 38
Best Local Similarity: 23.66% Mismatches: 82
Query Match: 7.40% Indels: 51
RESULT 749
ID ABX08833 standard; cDNA; 5717 BP.
DE Angiogenesis-associated human polynucleotide sequence #95.
PN WO200279492-A2.
PD 10-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Percent Similarity: 40.62% Conservative: 38
Best Local Similarity: 23.66% Mismatches: 82
Query Match: 7.40% Indels: 51
RESULT 750
ID ADI32007 standard; cDNA; 5717 BP.
DE Human cDNA #1333.
PN US6607879-B1.
PD 19-AUG-2003.
PA (INCY-) INCYTE CORP.
Percent Similarity: 40.62% Conservative: 38
Best Local Similarity: 23.66% Mismatches: 82
Query Match: 7.40% Indels: 51
RESULT 751
ID ADM99592 standard; cDNA; 5717 BP.
DE Human integrin alphaV subunit precursor cDNA.
PN WO2004007530-A2.
PD 22-JAN-2004.
PA (BLOO-) CENT BLOOD RES INC.
Percent Similarity: 40.62% Conservative: 38
Best Local Similarity: 23.66% Mismatches: 82
Query Match: 7.40% Indels: 51
RESULT 752
ID AAL62048 standard; cDNA; 6871 BP.
DE Human cell adhesion and extracellular matrix protein (CADECM)-36 cDNA.
PN WO2003047526-A2.
PD 12-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 40.62% Conservative: 38
Best Local Similarity: 23.66% Mismatches: 82
Query Match: 7.40% Indels: 51
RESULT 753
ID ABV25831 standard; cDNA; 6952 BP.
DE Human prostate expression marker cDNA 25822.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Percent Similarity: 40.62% Conservative: 38
Best Local Similarity: 23.66% Mismatches: 82
Query Match: 7.40% Indels: 51
RESULT 754
ID ADL45678 standard; DNA; 6954 BP.
DE Human ovarian cancer DNA marker #19568.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Percent Similarity: 40.62% Conservative: 38
Best Local Similarity: 23.66% Mismatches: 82
Query Match: 7.40% Indels: 51
RESULT 755
ID ACF65372 standard; DNA; 21520 BP.
DE Photorhabdus luminescens nucleotide sequence #25.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Percent Similarity: 37.77% Conservative: 24
Best Local Similarity: 25.00% Mismatches: 54
Query Match: 7.40% Indels: 63
RESULT 756
Percent Similarity: 37.77% Conservative: 24
Best Local Similarity: 25.00% Mismatches: 54
Query Match: 7.40% Indels: 63
RESULT 757
ID ACN45170 standard; DNA; 133955 BP.
DE Human genomic sequence hCG23504.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Percent Similarity: 38.92% Conservative: 29
Best Local Similarity: 21.56% Mismatches: 65
Query Match: 7.40% Indels: 37
RESULT 758
ID AAS71946 standard; cDNA; 853 BP.
DE DNA encoding novel human diagnostic protein #7750.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 43.40% Conservative: 29
Best Local Similarity: 25.16% Mismatches: 62
Query Match: 7.35% Indels: 28
RESULT 759
ID ADK53982 standard; DNA; 484 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #1365.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
PA (DOWC) DOW AGROSCIENCES LLC.
Percent Similarity: 46.15% Conservative: 25
Best Local Similarity: 22.12% Mismatches: 37
Query Match: 7.30% Indels: 19
RESULT 760
ID ABX72616 standard; cDNA; 1422 BP.
DE Human cDNA encoding the CA125 protein carboxy terminus.
PN WO200283866-A2.
PD 24-OCT-2002.
PA (UYAR-) UNIV ARKANSAS.
Percent Similarity: 36.71% Conservative: 33
Best Local Similarity: 20.77% Mismatches: 68
Query Match: 7.30% Indels: 63
RESULT 761
ID ABN72979 standard; cDNA; 1636 BP.
DE Clone 0772P partial cDNA sequence #4.
PN WO200206317-A2.
PD 24-JAN-2002.
PA (CORI-) CORIXA CORP.
Percent Similarity: 36.71% Conservative: 33
Best Local Similarity: 20.77% Mismatches: 68

Query Match: 7.30% Indels: 63
RESULT 762
ID ADA08620 standard; cDNA; 1636 BP.
DE Human O772P partial cDNA clone #4.
PN US2003091580-A1.
PD 15-MAY-2003.
PA (MITC/) MITCHAM J L.
PA (KING/) KING G E.
PA (ALGA/) ALGATE P A.
PA (FLIN/) FLING S P.
PA (RETT/) RETTER M W.
PA (FANG/) FANGER G R.
PA (REED/) REED S G.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (HILL/) HILL P.
PA (ALBO/) ALBONE E.
Percent Similarity: 36.71% Conservative: 33
Best Local Similarity: 20.77% Mismatches: 68
Query Match: 7.30% Indels: 63
RESULT 763
ID ADF08963 standard; cDNA; 1636 BP.
DE cDNA encoding secreted ovarian carcinoma antigen seqid 467.
PN US2003124140-A1.
PD 03-JUL-2003.
PA (CORI-) CORIXA CORP.
Percent Similarity: 36.71% Conservative: 33
Best Local Similarity: 20.77% Mismatches: 68
Query Match: 7.30% Indels: 63
RESULT 764
ID AAD20618 standard; cDNA; 1704 BP.
DE Human ovarian cancer antigen-encoding gene 1 cDNA clone HIPAZ30.
PN WO200170804-A1.
PD 27-SEP-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 36.71% Conservative: 33
Best Local Similarity: 20.77% Mismatches: 68
Query Match: 7.30% Indels: 63
RESULT 765
ID ADH41325 standard; DNA; 1721 BP.
DE Human ovarian specific gene (OSG) sequence #1.
PN US2003096238-A1.
PD 22-MAY-2003.
PA (SALC/) SALCEDA S.
PA (CAFF/) CAFFERKEY R.
Percent Similarity: 36.71% Conservative: 33
Best Local Similarity: 20.77% Mismatches: 68
Query Match: 7.30% Indels: 63
RESULT 766
ID ABZ35214 standard; cDNA; 2166 BP.
DE Human gene expression profile polynucleotide SEQ ID NO 326.
PN WO200274979-A2.
PD 26-SEP-2002.
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
Percent Similarity: 34.85% Conservative: 42
Best Local Similarity: 18.94% Mismatches: 68
Query Match: 7.30% Indels: 104
RESULT 767
ID ABX05223 standard; cDNA; 3546 BP.
DE Human novel polynucleotide #238.
PN WO200274961-A1.
PD 26-SEP-2002.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 36.71% Conservative: 33
Best Local Similarity: 20.77% Mismatches: 68
Query Match: 7.30% Indels: 63
RESULT 768
ID ADR08401 standard; cDNA; 3613 BP.
DE Full length human cDNA useful for treating neurological disease Seq 1907.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity: 36.71% Conservative: 33
Best Local Similarity: 20.77% Mismatches: 68
Query Match: 7.30% Indels: 63
RESULT 769
ID ADR08234 standard; cDNA; 4184 BP.
DE Full length human cDNA useful for treating neurological disease Seq 1740.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity: 36.71% Conservative: 33
Best Local Similarity: 20.77% Mismatches: 68
Query Match: 7.30% Indels: 63
RESULT 770
ID ADH41327 standard; DNA; 4494 BP.
DE Human ovarian specific gene (OSG) sequence #2.
PN US2003096238-A1.
PD 22-MAY-2003.
PA (SALC/) SALCEDA S.
PA (CAFF/) CAFFERKEY R.
Percent Similarity: 36.71% Conservative: 33
Best Local Similarity: 20.77% Mismatches: 68
Query Match: 7.30% Indels: 63
RESULT 771
ID AAZ22904 standard; DNA; 15893 BP.
DE Nucleotide sequence of wild type measles virus Montefiore strain.
PN WO9949017-A2.
PD 30-SEP-1999.
PA (AMCY) AMERICAN CYANAMID CO.
Percent Similarity: 34.88% Conservative: 17
Best Local Similarity: 25.00% Mismatches: 55
Query Match: 7.30% Indels: 57
RESULT 772
ID AAV18267 standard; DNA; 15894 BP.
DE Measles virus Montefiore isolate wild-type L protein genomic DNA.
PN WO9813501-A2.
PD 02-APR-1998.
PA (AMCY) AMERICAN CYANAMID CO.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Percent Similarity: 34.88% Conservative: 17
Best Local Similarity: 25.00% Mismatches: 55
Query Match: 7.30% Indels: 57
RESULT 773
ID AAV18266 standard; DNA; 15894 BP.
DE Measles virus 1983 isolate wild-type L protein genomic DNA.
PN WO9813501-A2.
PD 02-APR-1998.
PA (AMCY) AMERICAN CYANAMID CO.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Percent Similarity: 34.88% Conservative: 16
Best Local Similarity: 25.58% Mismatches: 55
Query Match: 7.30% Indels: 57
RESULT 774
ID AAZ22903 standard; DNA; 15894 BP.
DE Nucleotide sequence of wild type measles virus 1983 strain.
PN WO9949017-A2.
PD 30-SEP-1999.
PA (AMCY) AMERICAN CYANAMID CO.
Percent Similarity: 34.88% Conservative: 16
Best Local Similarity: 25.58% Mismatches: 55
Query Match: 7.30% Indels: 57
RESULT 775
ID ADP84154 standard; cDNA; 66765 BP.
DE Human CA125 cDNA SeqID 4.
PN WO2004045553-A2.
PD 03-JUN-2004.
PA (UYAR-) UNIV ARKANSAS.
Percent Similarity: 36.71% Conservative: 33
Best Local Similarity: 20.77% Mismatches: 68
Query Match: 7.30% Indels: 63
RESULT 776
ID ADR72872 standard; DNA; 66765 BP.
DE Human ovarian cancer-related tumour marker CA125 DNA.
PN WO2004075713-A2.
PD 10-SEP-2004.

PA (MOUN) MOUNT SINAI HOSPITAL.
Percent Similarity: 36.71% Conservative: 33
Best Local Similarity: 20.77% Mismatches: 68
Query Match: 7.30% Indels: 63
RESULT 777
ID ADG34281 standard; DNA; 762 BP.
DE Neurokinin B antibody encoding DNA SEQ ID NO:4.
PN WO2003102136-A2.
PD 11-DEC-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 36.99% Conservative: 29
Best Local Similarity: 20.23% Mismatches: 56
Query Match: 7.26% Indels: 53
RESULT 778
ID ABL04091 standard; cDNA; 1349 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 6755.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 48.86% Conservative: 16
Best Local Similarity: 30.68% Mismatches: 36
Query Match: 7.26% Indels: 9
RESULT 779
ID AAC46959 standard; DNA; 2219 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 52039.
PN EP1033405-A2.
PD 06-SEP-2000.
Percent Similarity: 42.61% Conservative: 35
Best Local Similarity: 22.73% Mismatches: 69
Query Match: 7.26% Indels: 32
RESULT 780
ID ADT05389 standard; DNA; 3711 BP.
DE Haemophilus influenzae (NTHi) contig DNA sequence - SEQ ID 425.
PN WO2004078949-A2.
PD 16-SEP-2004.
PA (CHIL-) CHILDRENS HOSPITAL INC.
Percent Similarity: 38.78% Conservative: 33
Best Local Similarity: 21.94% Mismatches: 60
Query Match: 7.26% Indels: 61
RESULT 781
ID ADC00087 standard; DNA; 86248 BP.
DE Enterohaemorragic E. coli 0157:H7-specific nucleic acid SEQ ID NO: 132.
PN JP2002355074-A.
PD 10-DEC-2002.
PA (UYTS-) UNIV TSUKUBA.
Percent Similarity: 38.46% Conservative: 32
Best Local Similarity: 22.05% Mismatches: 88
Query Match: 7.26% Indels: 32
RESULT 782
ID ACD19044 standard; DNA; 87563 BP.
DE E. coli 0157 unique DNA sequence OZID_57.
PN US2003023075-A1.
PD 30-JAN-2003.
PA (BLAT/) BLATTNER F R.
PA (BURL/) BURLAND V D.
PA (PERN/) PERNA N T.
PA (PLUN/) PLUNKETT G.
PA (WELC/) WELCH R.
Percent Similarity: 38.46% Conservative: 32
Best Local Similarity: 22.05% Mismatches: 88
Query Match: 7.26% Indels: 32
RESULT 783
ID ADN12161 standard; DNA; 172281 BP.
DE Epstein-Barr virus genome B95-8.
PN WO2004027036-A2.
PD 01-APR-2004.
PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
Percent Similarity: 38.93% Conservative: 19
Best Local Similarity: 26.17% Mismatches: 59
Query Match: 7.26% Indels: 32
RESULT 784
ID ADT05738 standard; DNA; 308766 BP.
DE Haemophilus influenzae (NTHi) DNA sequence - SEQ ID 774.
PN WO2004078949-A2.
PD 16-SEP-2004.
PA (CHIL-) CHILDRENS HOSPITAL INC.
Percent Similarity: 38.78% Conservative: 33
Best Local Similarity: 21.94% Mismatches: 60
Query Match: 7.26% Indels: 61
RESULT 785
ID AAS83081 standard; cDNA; 649 BP.
DE DNA encoding novel human diagnostic protein #18885.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 36.68% Conservative: 29
Best Local Similarity: 22.11% Mismatches: 69
Query Match: 7.21% Indels: 57
RESULT 786
ID ABV94552 standard; cDNA; 906 BP.
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:113.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 36.50% Conservative: 23
Best Local Similarity: 25.00% Mismatches: 59
Query Match: 7.21% Indels: 68
RESULT 787
ID ADM18748 standard; cDNA; 906 BP.
DE Human co-stimulatory molecule encoding cDNA SEQ ID NO:113.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 36.50% Conservative: 23
Best Local Similarity: 25.00% Mismatches: 59
Query Match: 7.21% Indels: 68
RESULT 788
ID ADS45602 standard; cDNA; 1065 BP.
DE Bacterial polynucleotide #345.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Percent Similarity: 36.76% Conservative: 25
Best Local Similarity: 23.24% Mismatches: 54
Query Match: 7.21% Indels: 63
RESULT 789
ID ACA36349 standard; DNA; 2292 BP.
DE Prokaryotic essential gene #18006.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 48.45% Conservative: 17
Best Local Similarity: 30.93% Mismatches: 31
Query Match: 7.21% Indels: 20
RESULT 790
ID ADF85455 standard; cDNA; 2306 BP.
DE Human adenoma marker cDNA, SEQ ID NO:20.
PN WO2003025214-A1.
PD 27-MAR-2003.
PA (MEDI-) MEDIMOLECULAR PTY LTD.
Percent Similarity: 36.36% Conservative: 35
Best Local Similarity: 18.69% Mismatches: 47
Query Match: 7.21% Indels: 79
RESULT 791
ID ADM30753 standard; DNA; 3559 BP.
DE Human cancer linked gene referred to as H53701_T_1 SeqID 1.
PN WO2003075854-A2.
PD 18-SEP-2003.
PA (AVAL-) AVALON PHARM.
Percent Similarity: 36.46% Conservative: 30
Best Local Similarity: 20.83% Mismatches: 61
Query Match: 7.21% Indels: 61

RESULT 792
ID ADN96165 standard; cDNA; 3879 BP.
DE Human NOVX polynucleotide #110.
PN US2004067490-A1.
PD 08-APR-2004.
PA (ZHON/) ZHONG M.
PA (LILL/) LI L.
PA (GORM/) GORMAN L.
PA (SPYT/) SPYTEK K A.
PA (KEKU/) KEKUDA R.
PA (TAUP/) TAUPIER R J.
PA (ANDE/) ANDERSON D W.
PA (VERN/) VERNET C A M.
PA (CATT/) CATTERTON E.
PA (MILL/) MILLER C E.
PA (SHEN/) SHENOY S G.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (TCHE/) TCHERNEV V T.
PA (PADI/) PADIGARU M.
PA (GUSE/) GUSEV V Y.
PA (MALY/) MALYANKAR U M.
PA (BURG/) BURGESS C E.
PA (GERL/) GERLACH V.
PA (CASM/) CASMAN S J.
PA (RIEG/) RIEGER D K.
PA (GROS/) GROSSE W M.
PA (SMIT/) SMITHSON G.
PA (PEYM/) PEYMAN J A.
PA (STAR/) STARLING G.
PA (ROTH/) ROTHENBERG M E.
PA (LARO/) LAROCHELLE W J.
PA (SHIM/) SHIMKETS R A.
PA (CRAB/) CRABTREE J.
PA (RAST/) RASTELLI L.
PA (VOSS/) VOSS E Z.
PA (BOLD/) BOLDOG F L.
PA (EDIN/) EDINGER S R.
PA (MILL/) MILLET I.
PA (MACD/) MACDOUGALL J R.
PA (ELLE/) ELLERMAN K.
PA (CHAP/) CHAPOVAL A.
Percent Similarity: 51.14% Conservative: 17
Best Local Similarity: 31.82% Mismatches: 24
Query Match: 7.21% Indels: 19
RESULT 793
ID ABS76477 standard; cDNA; 5797 BP.
DE cDNA encoding human ovarian cancer markers M461 and M612.
PN WO200271928-A2.
PD 19-SEP-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Percent Similarity: 36.46% Conservative: 30
Best Local Similarity: 20.83% Mismatches: 61
Query Match: 7.21% Indels: 61
RESULT 794
Percent Similarity: 48.45% Conservative: 17
Best Local Similarity: 30.93% Mismatches: 31
Query Match: 7.21% Indels: 20
RESULT 795
ID ADL08116 standard; DNA; 160361 BP.
DE Human gene associated with low HDL-C FABP-3.
PN US2004043389-A1.
PD 04-MAR-2004.
PA (VITI-) VITIVITY INC.
Percent Similarity: 49.02% Conservative: 24
Best Local Similarity: 25.49% Mismatches: 33
Query Match: 7.21% Indels: 19
RESULT 796
ID ABN53251 standard; DNA; 65 BP.
DE Mouse spliced transcript detection oligonucleotide SEQ ID NO:25999.
PN WO200210449-A2.
PD 07-FEB-2002.
PA (COMP-) COMPUGEN INC.
Percent Similarity: 80.00% Conservative: 1
Best Local Similarity: 75.00% Mismatches: 4
Query Match: 7.17% Indels: 0
RESULT 797
ID ABK74900 standard; DNA; 1512 BP.
DE Bacillus licheniformis genomic sequence tag (GST) #2191.
PN WO200229113-A2.
PD 11-APR-2002.
PA (NOVO) NOVOZYMES BIOTECH INC.
PA (NOVO) NOVOZYMES AS.
Percent Similarity: 39.72% Conservative: 21
Best Local Similarity: 24.82% Mismatches: 45
Query Match: 7.17% Indels: 40
RESULT 798
ID ABL02681 standard; cDNA; 1695 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 2525.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 38.67% Conservative: 20
Best Local Similarity: 25.33% Mismatches: 72
Query Match: 7.17% Indels: 20
RESULT 799
ID AAS60896 standard; cDNA; 2664 BP.
DE Human cancer agent-resistance marker #555.
PN WO200179556-A2.
PD 25-OCT-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Percent Similarity: 38.81% Conservative: 34
Best Local Similarity: 21.89% Mismatches: 78
Query Match: 7.17% Indels: 45
RESULT 800
ID AAH17743 standard; cDNA; 2932 BP.
DE Human cDNA sequence SEQ ID NO:17362.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Percent Similarity: 38.81% Conservative: 34
Best Local Similarity: 21.89% Mismatches: 78
Query Match: 7.17% Indels: 45
RESULT 801
ID ABL02680 standard; cDNA; 3750 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 2522.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 38.67% Conservative: 20
Best Local Similarity: 25.33% Mismatches: 72
Query Match: 7.17% Indels: 20
RESULT 802
ID AAS77136 standard; cDNA; 3900 BP.
DE DNA encoding novel human diagnostic protein #12940.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 42.53% Conservative: 36
Best Local Similarity: 21.84% Mismatches: 60
Query Match: 7.17% Indels: 40
RESULT 803
ID ACC47353 standard; cDNA; 4603 BP.
DE Human prostate selective polynucleotide Pr498.
PN WO2003014298-A2.
PD 20-FEB-2003.
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
Percent Similarity: 38.81% Conservative: 34
Best Local Similarity: 21.89% Mismatches: 78
Query Match: 7.17% Indels: 45
RESULT 804
ID AAD35224 standard; cDNA; 5205 BP.
DE Human TRNFR-9 cDNA.
PN WO200226950-A2.
PD 04-APR-2002.
PA (INCY-) INCYTE GENOMICS INC.

Percent Similarity: 38.81% Conservative: 34
Best Local Similarity: 21.89% Mismatches: 78
Query Match: 7.17% Indels: 45
RESULT 805
ID ABL30223 standard; DNA; 7630 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 42142.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 43.40% Conservative: 20
Best Local Similarity: 24.53% Mismatches: 30
Query Match: 7.17% Indels: 30
RESULT 806
Percent Similarity: 35.59% Conservative: 27
Best Local Similarity: 20.34% Mismatches: 68
Query Match: 7.17% Indels: 46
RESULT 807
Percent Similarity: 36.80% Conservative: 38
Best Local Similarity: 20.35% Mismatches: 79
Query Match: 7.17% Indels: 67
RESULT 808
Percent Similarity: 36.80% Conservative: 38
Best Local Similarity: 20.35% Mismatches: 79
Query Match: 7.17% Indels: 67
RESULT 809
ID ACN43996 standard; DNA; 254087 BP.
DE Mouse genomic sequence mCG12572.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Percent Similarity: 42.86% Conservative: 28
Best Local Similarity: 22.86% Mismatches: 46
Query Match: 7.17% Indels: 34
RESULT 810
ID ABL89941 standard; cDNA; 809 BP.
DE Human polynucleotide SEQ ID NO 503.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 38.07% Conservative: 33
Best Local Similarity: 21.32% Mismatches: 54
Query Match: 7.12% Indels: 68
RESULT 811
ID ABN73046 standard; cDNA; 1060 BP.
DE cDNA sequence for the 3' constant region of 0772P.
PN WO200206317-A2.
PD 24-JAN-2002.
PA (CORI-) CORIXA CORP.
Percent Similarity: 36.46% Conservative: 30
Best Local Similarity: 20.83% Mismatches: 61
Query Match: 7.12% Indels: 61
RESULT 812
ID ADA08721 standard; cDNA; 1060 BP.
DE Human O772P variable region repeat cDNA #57.
PN US2003091580-A1.
PD 15-MAY-2003.
PA (MITC/) MITCHAM J L.
PA (KING/) KING G E.
PA (ALGA/) ALGATE P A.
PA (FLIN/) FLING S P.
PA (RETT/) RETTER M W.
PA (FANG/) FANGER G R.
PA (REED/) REED S G.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (HILL/) HILL P.
PA (ALBO/) ALBONE E.
Percent Similarity: 36.46% Conservative: 30
Best Local Similarity: 20.83% Mismatches: 61
Query Match: 7.12% Indels: 61
RESULT 813
ID ADF09064 standard; cDNA; 1060 BP.
DE cDNA encoding secreted ovarian carcinoma antigen seqid 568.
PN US2003124140-A1.
PD 03-JUL-2003.
PA (CORI-) CORIXA CORP.
Percent Similarity: 36.46% Conservative: 30
Best Local Similarity: 20.83% Mismatches: 61
Query Match: 7.12% Indels: 61
RESULT 814
ID ADN74328 standard; cDNA; 1173 BP.
DE Thale cress cDNA repressed in E2Fa/Dpa expressing plants SeqID 2223.
PN WO2004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPDESIGN NV.
Percent Similarity: 48.11% Conservative: 16
Best Local Similarity: 33.02% Mismatches: 19
Query Match: 7.12% Indels: 36
RESULT 815
ID AAC76608 standard; cDNA; 1405 BP.
DE Human ORFX ORF2163 polynucleotide sequence SEQ ID NO:4325.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 37.42% Conservative: 25
Best Local Similarity: 22.09% Mismatches: 41
Query Match: 7.12% Indels: 61
RESULT 816
ID AAA70076 standard; cDNA; 1761 BP.
DE Human ovarian carcinoma antigen O772P polynucleotide SEQ ID NO:387.
PN WO200036107-A2.
PD 22-JUN-2000.
PA (CORI-) CORIXA CORP.
Percent Similarity: 38.50% Conservative: 34
Best Local Similarity: 21.50% Mismatches: 74
Query Match: 7.12% Indels: 49
RESULT 817
ID ABN72970 standard; cDNA; 1761 BP.
DE cDNA sequence of 0772P clone, 21008.
PN WO200206317-A2.
PD 24-JAN-2002.
PA (CORI-) CORIXA CORP.
Percent Similarity: 38.50% Conservative: 34
Best Local Similarity: 21.50% Mismatches: 74
Query Match: 7.12% Indels: 49
RESULT 818
ID ADA08540 standard; cDNA; 1761 BP.
DE Human ovarian carcinoma antigen polynucleotide O772P cDNA #3.
PN US2003091580-A1.
PD 15-MAY-2003.
PA (MITC/) MITCHAM J L.
PA (KING/) KING G E.
PA (ALGA/) ALGATE P A.
PA (FLIN/) FLING S P.
PA (RETT/) RETTER M W.
PA (FANG/) FANGER G R.
PA (REED/) REED S G.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (HILL/) HILL P.
PA (ALBO/) ALBONE E.
Percent Similarity: 38.50% Conservative: 34
Best Local Similarity: 21.50% Mismatches: 74
Query Match: 7.12% Indels: 49
RESULT 819
ID ADF08883 standard; cDNA; 1761 BP.
DE cDNA encoding secreted ovarian carcinoma antigen seqid 387.
PN US2003124140-A1.
PD 03-JUL-2003.
PA (CORI-) CORIXA CORP.
Percent Similarity: 38.50% Conservative: 34
Best Local Similarity: 21.50% Mismatches: 74
Query Match: 7.12% Indels: 49
RESULT 820
ID ADG46170 standard; cDNA; 1761 BP.
DE Human ovarian carcinoma polynucleotide #386.

PN US2003165504-A1.
PD 04-SEP-2003.
PA (RETT/) RETTER M W.
PA (FANG/) FANGER G R.
Percent Similarity: 38.50% Conservative: 34
Best Local Similarity: 21.50% Mismatches: 74
Query Match: 7.12% Indels: 49
RESULT 821
ID ADI57681 standard; cDNA; 2094 BP.
DE Human breast specific nucleic acid (BSNA) #52.
PN WO2003106648-A2.
PD 24-DEC-2003.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 39.64% Conservative: 18
Best Local Similarity: 23.42% Mismatches: 56
Query Match: 7.12% Indels: 11
RESULT 822
ID ABL34974 standard; cDNA; 2100 BP.
DE Rat cDNA isolated from skin cells SEQ ID NO: 479.
PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Percent Similarity: 38.35% Conservative: 37
Best Local Similarity: 20.39% Mismatches: 70
Query Match: 7.12% Indels: 58
RESULT 823
ID ADI57683 standard; cDNA; 2194 BP.
DE Human breast specific nucleic acid (BSNA) #54.
PN WO2003106648-A2.
PD 24-DEC-2003.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 39.64% Conservative: 18
Best Local Similarity: 23.42% Mismatches: 56
Query Match: 7.12% Indels: 11
RESULT 824
ID AAA70075 standard; cDNA; 2608 BP.
DE Human ovarian carcinoma antigen O772P polynucleotide SEQ ID NO:386.
PN WO200036107-A2.
PD 22-JUN-2000.
PA (CORI-) CORIXA CORP.
Percent Similarity: 38.50% Conservative: 34
Best Local Similarity: 21.50% Mismatches: 74
Query Match: 7.12% Indels: 49
RESULT 825
ID ABN72969 standard; cDNA; 2608 BP.
DE cDNA sequence of 0772P clone, 21003.
PN WO200206317-A2.
PD 24-JAN-2002.
PA (CORI-) CORIXA CORP.
Percent Similarity: 38.50% Conservative: 34
Best Local Similarity: 21.50% Mismatches: 74
Query Match: 7.12% Indels: 49
RESULT 826
ID ADA08539 standard; cDNA; 2608 BP.
DE Human ovarian carcinoma antigen polynucleotide O772P cDNA #2.
PN US2003091580-A1.
PD 15-MAY-2003.
PA (MITC/) MITCHAM J L.
PA (KING/) KING G E.
PA (ALGA/) ALGATE P A.
PA (FLIN/) FLING S P.
PA (RETT/) RETTER M W.
PA (FANG/) FANGER G R.
PA (REED/) REED S G.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (HILL/) HILL P.
PA (ALBO/) ALBONE E.
Percent Similarity: 38.50% Conservative: 34
Best Local Similarity: 21.50% Mismatches: 74
Query Match: 7.12% Indels: 49
RESULT 827
ID ADF08882 standard; cDNA; 2608 BP.
DE cDNA encoding secreted ovarian carcinoma antigen seqid 386.
PN US2003124140-A1.
PD 03-JUL-2003.
PA (CORI-) CORIXA CORP.
Percent Similarity: 38.50% Conservative: 34
Best Local Similarity: 21.50% Mismatches: 74
Query Match: 7.12% Indels: 49
RESULT 828
ID ADG46169 standard; cDNA; 2608 BP.
DE Human ovarian carcinoma polynucleotide #385.
PN US2003165504-A1.
PD 04-SEP-2003.
PA (RETT/) RETTER M W.
PA (FANG/) FANGER G R.
Percent Similarity: 38.50% Conservative: 34
Best Local Similarity: 21.50% Mismatches: 74
Query Match: 7.12% Indels: 49
RESULT 829
ID AAA70001 standard; cDNA; 2996 BP.
DE Human ovarian carcinoma antigen O772P polynucleotide SEQ ID NO:311.
PN WO200036107-A2.
PD 22-JUN-2000.
PA (CORI-) CORIXA CORP.
Percent Similarity: 38.50% Conservative: 34
Best Local Similarity: 21.50% Mismatches: 74
Query Match: 7.12% Indels: 49
RESULT 830
ID AAH55680 standard; DNA; 2996 BP.
DE Human ovarian tumour-derived antigen O772P DNA sequence.
PN WO200140269-A2.
PD 07-JUN-2001.
PA (CORI-) CORIXA CORP.
Percent Similarity: 38.50% Conservative: 34
Best Local Similarity: 21.50% Mismatches: 74
Query Match: 7.12% Indels: 49
RESULT 831
ID ABN72895 standard; DNA; 2996 BP.
DE Full length sequence of ovarian carcinoma polynucleotide 0772P.
PN WO200206317-A2.
PD 24-JAN-2002.
PA (CORI-) CORIXA CORP.
Percent Similarity: 38.50% Conservative: 34
Best Local Similarity: 21.50% Mismatches: 74
Query Match: 7.12% Indels: 49
RESULT 832
ID ABN72974 standard; DNA; 2996 BP.
DE Hypothetical nucleotide sequence for clone 0772P.
PN WO200206317-A2.
PD 24-JAN-2002.
PA (CORI-) CORIXA CORP.
Percent Similarity: 38.50% Conservative: 34
Best Local Similarity: 21.50% Mismatches: 74
Query Match: 7.12% Indels: 49
RESULT 833
ID ADA09060 standard; DNA; 2996 BP.
DE Human ovarian carcinoma antigen polynucleotide O772P.
PN US2003091580-A1.
PD 15-MAY-2003.
PA (MITC/) MITCHAM J L.
PA (KING/) KING G E.
PA (ALGA/) ALGATE P A.
PA (FLIN/) FLING S P.
PA (RETT/) RETTER M W.
PA (FANG/) FANGER G R.
PA (REED/) REED S G.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (HILL/) HILL P.
PA (ALBO/) ALBONE E.
Percent Similarity: 38.50% Conservative: 34
Best Local Similarity: 21.50% Mismatches: 74
Query Match: 7.12% Indels: 49
RESULT 834

ID ADA08615 standard; cDNA; 2996 BP.
DE Human O772P hypothetical cDNA sequence.
PN US2003091580-A1.
PD 15-MAY-2003.
PA (MITC/) MITCHAM J L.
PA (KING/) KING G E.
PA (ALGA/) ALGATE P A.
PA (FLIN/) FLING S P.
PA (RETT/) RETTER M W.
PA (FANG/) FANGER G R.
PA (REED/) REED S G.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (HILL/) HILL P.
PA (ALBO/) ALBONE E.
Percent Similarity: 38.50% Conservative: 34
Best Local Similarity: 21.50% Mismatches: 74
Query Match: 7.12% Indels: 49
RESULT 835
ID ADF08807 standard; cDNA; 2996 BP.
DE cDNA encoding secreted ovarian carcinoma antigen seqid 311.
PN US2003124140-A1.
PD 03-JUL-2003.
PA (CORI-) CORIXA CORP.
Percent Similarity: 38.50% Conservative: 34
Best Local Similarity: 21.50% Mismatches: 74
Query Match: 7.12% Indels: 49
RESULT 836
ID ADF08958 standard; cDNA; 2996 BP.
DE cDNA encoding secreted ovarian carcinoma antigen seqid 462.
PN US2003124140-A1.
PD 03-JUL-2003.
PA (CORI-) CORIXA CORP.
Percent Similarity: 38.50% Conservative: 34
Best Local Similarity: 21.50% Mismatches: 74
Query Match: 7.12% Indels: 49
RESULT 837
ID ADG46555 standard; cDNA; 2996 BP.
DE Human ovarian carcinoma polynucleotide #311.
PN US2003165504-A1.
PD 04-SEP-2003.
PA (RETT/) RETTER M W.
PA (FANG/) FANGER G R.
Percent Similarity: 38.50% Conservative: 34
Best Local Similarity: 21.50% Mismatches: 74
Query Match: 7.12% Indels: 49
RESULT 838
ID ADN40450 standard; cDNA; 2996 BP.
DE Human breast cancer associated cDNA sequence #202.
PN US2004101899-A1.
PD 27-MAY-2004.
PA (CORI-) CORIXA CORP.
Percent Similarity: 38.50% Conservative: 34
Best Local Similarity: 21.50% Mismatches: 74
Query Match: 7.12% Indels: 49
RESULT 839
ID AAF59534 standard; cDNA; 3489 BP.
DE cDNA encoding a mouse PrP-binding protein, OB-cadherin-1.
PN WO200100235-A1.
PD 04-JAN-2001.
PA (UYMC-) UNIV MCGILL.
PA (CAPR-) CAPRION PHARM INC.
Percent Similarity: 39.36% Conservative: 32
Best Local Similarity: 22.34% Mismatches: 63
Query Match: 7.12% Indels: 51
RESULT 840
ID AAQ44391 standard; cDNA to mRNA; 3581 BP.
DE Sequence of murine OSF-4 cDNA.
PN EP585801-A2.
PD 09-MAR-1994.
PA (FARH) HOECHST JAPAN LTD.
Percent Similarity: 39.36% Conservative: 32
Best Local Similarity: 22.34% Mismatches: 63
Query Match: 7.12% Indels: 51
RESULT 841
ID ABL23088 standard; DNA; 3755 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 20737.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 36.28% Conservative: 27
Best Local Similarity: 23.72% Mismatches: 77
Query Match: 7.12% Indels: 60
RESULT 842
ID ABL03155 standard; cDNA; 3862 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 3947.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 39.42% Conservative: 31
Best Local Similarity: 24.52% Mismatches: 77
Query Match: 7.12% Indels: 49
RESULT 843
ID ABI99752 standard; cDNA; 4127 BP.
DE Mouse ischaemic condition related cDNA sequence SEQ ID NO:825.
PN WO200188188-A2.
PD 22-NOV-2001.
PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
Percent Similarity: 39.36% Conservative: 32
Best Local Similarity: 22.34% Mismatches: 63
Query Match: 7.12% Indels: 51
RESULT 844
ID ADA08722 standard; cDNA; 10620 BP.
DE Human O772P variable region repeat cDNA #58.
PN US2003091580-A1.
PD 15-MAY-2003.
PA (MITC/) MITCHAM J L.
PA (KING/) KING G E.
PA (ALGA/) ALGATE P A.
PA (FLIN/) FLING S P.
PA (RETT/) RETTER M W.
PA (FANG/) FANGER G R.
PA (REED/) REED S G.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (HILL/) HILL P.
PA (ALBO/) ALBONE E.
Percent Similarity: 36.46% Conservative: 30
Best Local Similarity: 20.83% Mismatches: 61
Query Match: 7.12% Indels: 61
RESULT 845
ID ABN73047 standard; cDNA; 10622 BP.
DE cDNA sequence of 0772P and 3' constant and untranslated region.
PN WO200206317-A2.
PD 24-JAN-2002.
PA (CORI-) CORIXA CORP.
Percent Similarity: 36.46% Conservative: 30
Best Local Similarity: 20.83% Mismatches: 61
Query Match: 7.12% Indels: 61
RESULT 846
ID ADF09065 standard; cDNA; 10622 BP.
DE cDNA encoding secreted ovarian carcinoma antigen seqid 569.
PN US2003124140-A1.
PD 03-JUL-2003.
PA (CORI-) CORIXA CORP.
Percent Similarity: 36.46% Conservative: 30
Best Local Similarity: 20.83% Mismatches: 61
Query Match: 7.12% Indels: 61
RESULT 847
ID AAQ90512 standard; DNA; 11288 BP.
DE CEA clone HindIII-Sau3A fragment.
PN WO9514100-A2.
PD 26-MAY-1995.
PA (WELL) WELLCOME FOUND LTD.
Percent Similarity: 55.00% Conservative: 7
Best Local Similarity: 43.33% Mismatches: 27

Query Match: 7.12% Indels: 2
RESULT 848
ID AAS14778 standard; DNA; 11288 BP.
DE Human carcinoembryonic antigen (CEA) genomic DNA.
PN WO200174861-A2.
PD 11-OCT-2001.
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
Percent Similarity: 55.00% Conservative: 7
Best Local Similarity: 43.33% Mismatches: 27
Query Match: 7.12% Indels: 2
RESULT 849
ID ABL15248 standard; cDNA; 11743 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 40226.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 36.88% Conservative: 17
Best Local Similarity: 26.25% Mismatches: 68
Query Match: 7.12% Indels: 33
RESULT 850
ID ABL16702 standard; DNA; 12216 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 1579.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 35.00% Conservative: 17
Best Local Similarity: 22.86% Mismatches: 58
Query Match: 7.12% Indels: 33
RESULT 851
ID ADL27165 standard; cDNA; 14450 BP.
DE Human cDNA sequence for hCG23764.
PN US2003216558-A1.
PD 20-NOV-2003.
PA (MORR/) MORRIS D W.
PA (ENGE/) ENGELHARD E K.
Percent Similarity: 38.50% Conservative: 28
Best Local Similarity: 23.53% Mismatches: 64
Query Match: 7.12% Indels: 51
RESULT 852
ID AAV52967 standard; DNA; 15056 BP.
DE Carcinoembryonic antigen gene 5' flanking region.
PN WO9839467-A2.
PD 11-SEP-1998.
PA (CALY-) CALYDON INC.
Percent Similarity: 55.00% Conservative: 7
Best Local Similarity: 43.33% Mismatches: 27
Query Match: 7.12% Indels: 2
RESULT 853
ID AAZ99933 standard; DNA; 15056 BP.
DE DNA sequence of comprising a carcinoembryonic antigen TRE.
PN WO200015820-A1.
PD 23-MAR-2000.
PA (CALY-) CALYDON INC.
Percent Similarity: 55.00% Conservative: 7
Best Local Similarity: 43.33% Mismatches: 27
Query Match: 7.12% Indels: 2
RESULT 854
ID AAA46851 standard; DNA; 15056 BP.
DE Nucleotide sequence of a CEA-TRE.
PN WO200039319-A2.
PD 06-JUL-2000.
PA (CALY-) CALYDON INC.
Percent Similarity: 55.00% Conservative: 7
Best Local Similarity: 43.33% Mismatches: 27
Query Match: 7.12% Indels: 2
RESULT 855
ID AAH43620 standard; cDNA; 15056 BP.
DE CEA-TRE.
PN WO200173093-A2.
PD 04-OCT-2001.
PA (CALY-) CALYDON INC.
Percent Similarity: 55.00% Conservative: 7
Best Local Similarity: 43.33% Mismatches: 27
Query Match: 7.12% Indels: 2
RESULT 856
ID AAF87238 standard; DNA; 15056 BP.
DE CEA-TRE fusion protein coding sequence.
PN WO200172341-A2.
PD 04-OCT-2001.
PA (CALY-) CALYDON INC.
Percent Similarity: 55.00% Conservative: 7
Best Local Similarity: 43.33% Mismatches: 27
Query Match: 7.12% Indels: 2
RESULT 857
ID ABK99582 standard; DNA; 15056 BP.
DE Prostate-specific antigen transcriptional regulatory elelment (TRE).
PN US2002068049-A1.
PD 06-JUN-2002.
PA (HEND/) HENDERSON D R.
PA (SCHU/) SCHUUR E R.
Percent Similarity: 55.00% Conservative: 7
Best Local Similarity: 43.33% Mismatches: 27
Query Match: 7.12% Indels: 2
RESULT 858
ID ACD07309 standard; DNA; 15056 BP.
DE Human carcinoembryonic antigen (CEA) TRE.
PN US2003044383-A1.
PD 06-MAR-2003.
PA (HEND/) HENDERSON D R.
PA (SCHU/) SCHUUR E R.
Percent Similarity: 55.00% Conservative: 7
Best Local Similarity: 43.33% Mismatches: 27
Query Match: 7.12% Indels: 2
RESULT 859
ID ACF62751 standard; DNA; 177380 BP.
DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:683.
PN WO2003013534-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Percent Similarity: 40.97% Conservative: 22
Best Local Similarity: 25.69% Mismatches: 38
Query Match: 7.12% Indels: 47
RESULT 860
ID ADB20870 standard; DNA; 177380 BP.
DE MRP1 based cancer related nucleic acid SEQ ID NO:683.
PN WO2003013533-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Percent Similarity: 40.97% Conservative: 22
Best Local Similarity: 25.69% Mismatches: 38
Query Match: 7.12% Indels: 47
RESULT 861
ID ADB87959 standard; DNA; 177380 BP.
DE Human UGT1A1 gene sequence SEQ ID NO:683.
PN WO2003013536-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Percent Similarity: 40.97% Conservative: 22
Best Local Similarity: 25.69% Mismatches: 38
Query Match: 7.12% Indels: 47
RESULT 862
ID ADB96942 standard; DNA; 177380 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:683.
PN WO2003013537-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Percent Similarity: 40.97% Conservative: 22
Best Local Similarity: 25.69% Mismatches: 38
Query Match: 7.12% Indels: 47
RESULT 863
ID ADB92133 standard; DNA; 177380 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:683.
PN WO2003013535-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Percent Similarity: 40.97% Conservative: 22

Best Local Similarity: 25.69% Mismatches: 38
Query Match: 7.12% Indels: 47
RESULT 864
ID AAT83807 standard; DNA; 825 BP.
DE DNA encoding a surfactin synthetase.
PN WO9730070-A1.
PD 21-AUG-1997.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Percent Similarity: 45.14% Conservative: 25
Best Local Similarity: 27.78% Mismatches: 56
Query Match: 7.08% Indels: 23
RESULT 865
ID ABV94556 standard; cDNA; 903 BP.
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:117.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.62% Conservative: 29
Best Local Similarity: 21.38% Mismatches: 58
Query Match: 7.08% Indels: 38
RESULT 866
ID ADM18752 standard; cDNA; 903 BP.
DE Human co-stimulatory molecule encoding cDNA SEQ ID NO:117.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.62% Conservative: 29
Best Local Similarity: 21.38% Mismatches: 58
Query Match: 7.08% Indels: 38
RESULT 867
ID AAT36760 standard; DNA; 1599 BP.
DE CD4:T-cell receptor eta chain chimaeric receptor DNA.
PN WO9625953-A1.
PD 29-AUG-1996.
PA (GEHO) GEN HOSPITAL CORP.
Percent Similarity: 41.79% Conservative: 24
Best Local Similarity: 23.88% Mismatches: 53
Query Match: 7.08% Indels: 25
RESULT 868
ID ABQ99353 standard; cDNA; 1621 BP.
DE Human coding sequence SEQ ID 86.
PN WO200259260-A2.
PD 01-AUG-2002.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 39.52% Conservative: 31
Best Local Similarity: 20.96% Mismatches: 67
Query Match: 7.08% Indels: 34
RESULT 869
ID ADQ22129 standard; DNA; 2012 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 4949.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Percent Similarity: 36.00% Conservative: 31
Best Local Similarity: 20.50% Mismatches: 73
Query Match: 7.08% Indels: 55
RESULT 870
ID ADG93388 standard; DNA; 2664 BP.
DE Maize lipoxygenase (LOX) DNA #10.
PN US2003166855-A1.
PD 04-SEP-2003.
PA (PION-) PIONEER HI-BRED INT INC.
Percent Similarity: 42.11% Conservative: 24
Best Local Similarity: 24.06% Mismatches: 53
Query Match: 7.08% Indels: 24
RESULT 871
ID ADG93386 standard; DNA; 3080 BP.
DE Maize lipoxygenase (LOX) DNA #9.
PN US2003166855-A1.
PD 04-SEP-2003.
PA (PION-) PIONEER HI-BRED INT INC.
Percent Similarity: 42.11% Conservative: 24
Best Local Similarity: 24.06% Mismatches: 53
Query Match: 7.08% Indels: 24
RESULT 872
ID ABD33601 standard; DNA; 70019 BP.
DE Murine cancer-associated (CA) gene MD07-122.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Percent Similarity: 38.10% Conservative: 11
Best Local Similarity: 27.62% Mismatches: 43
Query Match: 7.08% Indels: 22
RESULT 873
ID ACN44044 standard; DNA; 134481 BP.
DE Mouse genomic sequence mCG13084.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Percent Similarity: 41.38% Conservative: 22
Best Local Similarity: 26.21% Mismatches: 32
Query Match: 7.08% Indels: 53
RESULT 874
ID ADI42109 standard; DNA; 583 BP.
DE Plant transcription factor polynucleotide #317.
PN US2004019927-A1.
PD 29-JAN-2004.
PA (SHER/) SHERMAN B K.
PA (RIEC/) RIECHMANN J L.
PA (JIAN/) JIANG C.
PA (HEAR/) HEARD J E.
PA (HAAK/) HAAKE V.
PA (CREE/) CREELMAN R A.
PA (RATC/) RATCLIFFE O.
PA (ADAM/) ADAM L J.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J.
PA (BROU/) BROUN P E.
PA (PILG/) PILGRIM M L.
PA (DUBE/) DUBELL A N.
PA (PINE/) PINEDA O.
PA (YUGG/) YU G.
Percent Similarity: 43.01% Conservative: 16
Best Local Similarity: 25.81% Mismatches: 42
Query Match: 7.03% Indels: 11
RESULT 875
ID ADO02651 standard; cDNA; 583 BP.
DE Soybean orthologue of Thalecress transcription factor, cDNA #55.
PN US2004045049-A1.
PD 04-MAR-2004.
PA (ZHAN/) ZHANG J.
PA (FROM/) FROMM M E.
PA (HEAR/) HEARD J E.
PA (RIEC/) RIECHMANN J L.
PA (ADAM/) ADAM L J.
PA (BROU/) BROUN P E.
PA (PINE/) PINEDA O.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J S.
PA (YUGG/) YU G.
PA (JIAN/) JIANG C.
PA (SAMA/) SAMAHA R S.
PA (PILG/) PILGRIM M L.
PA (CREE/) CREELMAN R A.
PA (DUBE/) DUBELL A N.
PA (RATC/) RATCLIFFE O.
PA (KUMI/) KUMIMOTO R.
PA (SHER/) SHERMAN B K.
Percent Similarity: 43.01% Conservative: 16
Best Local Similarity: 25.81% Mismatches: 42
Query Match: 7.03% Indels: 11
RESULT 876
ID AAK51735 standard; cDNA; 888 BP.
DE Human polynucleotide SEQ ID NO 280.
PN WO200157190-A2.
PD 09-AUG-2001.

PA (HYSE-) HYSEQ INC.
Percent Similarity: 37.40% Conservative: 22
Best Local Similarity: 19.51% Mismatches: 46
Query Match: 7.03% Indels: 31
RESULT 877
ID ABZ32399 standard; DNA; 945 BP.
DE Candida albicans essential gene SEQ ID NO 6686.
PN WO200253728-A2.
PD 11-JUL-2002.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 35.38% Conservative: 30
Best Local Similarity: 20.00% Mismatches: 67
Query Match: 7.03% Indels: 59
RESULT 878
ID AAZ53928 standard; DNA; 1407 BP.
DE Neisseria meningitidis ORF 585 partial DNA sequence SEQ ID NO:1805.
PN WO9957280-A2.
PD 11-NOV-1999.
PA (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
Percent Similarity: 38.38% Conservative: 30
Best Local Similarity: 23.23% Mismatches: 81
Query Match: 7.03% Indels: 41
RESULT 879
ID ADD69651 standard; cDNA; 1480 BP.
DE Human REMAP cDNA - SEQ ID 80.
PN WO2003048305-A2.
PD 12-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 41.38% Conservative: 31
Best Local Similarity: 23.56% Mismatches: 67
Query Match: 7.03% Indels: 36
RESULT 880
ID AAZ94095 standard; cDNA; 2313 BP.
DE Haematopoietic stem cell specific nucleic acid.
PN WO200011168-A2.
PD 02-MAR-2000.
PA (UYPR-) UNIV PRINCETON.
Percent Similarity: 36.50% Conservative: 33
Best Local Similarity: 20.00% Mismatches: 49
Query Match: 7.03% Indels: 78
RESULT 881
ID AAS23202 standard; cDNA; 2653 BP.
DE DNA encoding novel bone marrow polypeptide #103.
PN WO200155442-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 34.70% Conservative: 39
Best Local Similarity: 20.15% Mismatches: 74
Query Match: 7.03% Indels: 102
RESULT 882
ID ADS11543 standard; DNA; 2653 BP.
DE Human therapeutic contig DNA - SEQ ID 1780.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Percent Similarity: 34.70% Conservative: 39
Best Local Similarity: 20.15% Mismatches: 74
Query Match: 7.03% Indels: 102
RESULT 883
ID ADS11202 standard; DNA; 2653 BP.
DE Human therapeutic contig DNA - SEQ ID 1439.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Percent Similarity: 34.70% Conservative: 39
Best Local Similarity: 20.15% Mismatches: 74
Query Match: 7.03% Indels: 102
RESULT 884
ID AAS87573 standard; cDNA; 3097 BP.
DE DNA encoding novel human diagnostic protein #23377.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 33.96% Conservative: 26
Best Local Similarity: 21.70% Mismatches: 67
Query Match: 7.03% Indels: 73
RESULT 885
ID AAS79043 standard; cDNA; 3852 BP.
DE DNA encoding novel human diagnostic protein #14847.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 38.55% Conservative: 26
Best Local Similarity: 22.89% Mismatches: 48
Query Match: 7.03% Indels: 54
RESULT 886
ID AAZ94129 standard; cDNA; 3857 BP.
DE Haematopoietic stem cell specific nucleic acid.
PN WO200011168-A2.
PD 02-MAR-2000.
PA (UYPR-) UNIV PRINCETON.
Percent Similarity: 36.50% Conservative: 33
Best Local Similarity: 20.00% Mismatches: 49
Query Match: 7.03% Indels: 78
RESULT 887
ID ADF74188 standard; cDNA; 6957 BP.
DE Human novel brain/hippocampus cDNA #6.
PN JP2003009886-A.
PD 14-JAN-2003.
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.
PA (PROT-) PROTEIN EXPRESS KK.
Percent Similarity: 47.62% Conservative: 15
Best Local Similarity: 29.76% Mismatches: 24
Query Match: 7.03% Indels: 20
RESULT 888
ID AAQ40480 standard; cDNA; 15894 BP.
DE Attenuated measles virus strain AIK-C.
PN EP540135-A2.
PD 05-MAY-1993.
PA (KITA) KITASATO INST.
Percent Similarity: 34.30% Conservative: 16
Best Local Similarity: 25.00% Mismatches: 56
Query Match: 7.03% Indels: 57
RESULT 889
ID AAV18271 standard; DNA; 15894 BP.
DE Measles virus AIK-C vaccine L protein genomic DNA.
PN WO9813501-A2.
PD 02-APR-1998.
PA (AMCY) AMERICAN CYANAMID CO.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Percent Similarity: 34.30% Conservative: 16
Best Local Similarity: 25.00% Mismatches: 56
Query Match: 7.03% Indels: 57
RESULT 890
ID AAV18268 standard; DNA; 15894 BP.
DE Measles virus Rubeovax vaccine L protein genomic DNA.
PN WO9813501-A2.
PD 02-APR-1998.
PA (AMCY) AMERICAN CYANAMID CO.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Percent Similarity: 34.30% Conservative: 16
Best Local Similarity: 25.00% Mismatches: 56
Query Match: 7.03% Indels: 57
RESULT 891
ID AAV18269 standard; DNA; 15894 BP.
DE Measles virus Moraten vaccine L protein genomic DNA.
PN WO9813501-A2.
PD 02-APR-1998.
PA (AMCY) AMERICAN CYANAMID CO.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Percent Similarity: 34.30% Conservative: 16
Best Local Similarity: 25.00% Mismatches: 56
Query Match: 7.03% Indels: 57
RESULT 892
ID AAV18270 standard; DNA; 15894 BP.

DE Measles virus Zagreb vaccine L protein genomic DNA.
PN WO9813501-A2.
PD 02-APR-1998.
PA (AMCY) AMERICAN CYANAMID CO.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Percent Similarity: 34.30% Conservative: 16
Best Local Similarity: 25.00% Mismatches: 56
Query Match: 7.03% Indels: 57
RESULT 893
ID AAV18264 standard; DNA; 15894 BP.
DE Measles virus Edmonston isolate wild-type L protein genomic DNA.
PN WO9813501-A2.
PD 02-APR-1998.
PA (AMCY) AMERICAN CYANAMID CO.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Percent Similarity: 34.30% Conservative: 16
Best Local Similarity: 25.00% Mismatches: 56
Query Match: 7.03% Indels: 57
RESULT 894
ID AAV18265 standard; DNA; 15894 BP.
DE Measles virus 1977 isolate wild-type L protein genomic DNA.
PN WO9813501-A2.
PD 02-APR-1998.
PA (AMCY) AMERICAN CYANAMID CO.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Percent Similarity: 34.30% Conservative: 16
Best Local Similarity: 25.00% Mismatches: 56
Query Match: 7.03% Indels: 57
RESULT 895
ID AAZ22907 standard; DNA; 15894 BP.
DE Nucleotide sequence of Zagreb vaccine measles virus genome.
PN WO9949017-A2.
PD 30-SEP-1999.
PA (AMCY) AMERICAN CYANAMID CO.
Percent Similarity: 34.30% Conservative: 16
Best Local Similarity: 25.00% Mismatches: 56
Query Match: 7.03% Indels: 57
RESULT 896
ID AAZ22901 standard; DNA; 15894 BP.
DE Nucleotide sequence of wild type measles virus Edmonston strain.
PN WO9949017-A2.
PD 30-SEP-1999.
PA (AMCY) AMERICAN CYANAMID CO.
Percent Similarity: 34.30% Conservative: 16
Best Local Similarity: 25.00% Mismatches: 56
Query Match: 7.03% Indels: 57
RESULT 897
ID AAZ22908 standard; DNA; 15894 BP.
DE Nucleotide sequence of AIK-C vaccine measles virus genome.
PN WO9949017-A2.
PD 30-SEP-1999.
PA (AMCY) AMERICAN CYANAMID CO.
Percent Similarity: 34.30% Conservative: 16
Best Local Similarity: 25.00% Mismatches: 56
Query Match: 7.03% Indels: 57
RESULT 898
ID AAZ22902 standard; DNA; 15894 BP.
DE Nucleotide sequence of wild type measles virus 1977 strain.
PN WO9949017-A2.
PD 30-SEP-1999.
PA (AMCY) AMERICAN CYANAMID CO.
Percent Similarity: 34.30% Conservative: 16
Best Local Similarity: 25.00% Mismatches: 56
Query Match: 7.03% Indels: 57
RESULT 899
ID AAZ22905 standard; DNA; 15894 BP.
DE Nucleotide sequence of Rubeovax vaccine measles virus genome.
PN WO9949017-A2.
PD 30-SEP-1999.
PA (AMCY) AMERICAN CYANAMID CO.
Percent Similarity: 34.30% Conservative: 16
Best Local Similarity: 25.00% Mismatches: 56
Query Match: 7.03% Indels: 57
RESULT 900
ID AAZ22906 standard; DNA; 15895 BP.
DE Nucleotide sequence of Moraten vaccine measles virus genome.
PN WO9949017-A2.
PD 30-SEP-1999.
PA (AMCY) AMERICAN CYANAMID CO.
Percent Similarity: 34.30% Conservative: 16
Best Local Similarity: 25.00% Mismatches: 56
Query Match: 7.03% Indels: 57
RESULT 901
ID ADH43072 standard; cDNA; 18967 BP.
DE Measles virus Schwarz antigenome cDNA sequence.
PN WO2004000876-A1.
PD 31-DEC-2003.
PA (INSP) INST PASTEUR.
PA (CNRS) CENT NAT RECH SCI.
Percent Similarity: 34.30% Conservative: 16
Best Local Similarity: 25.00% Mismatches: 56
Query Match: 7.03% Indels: 57
RESULT 902
ID ACA63261 standard; DNA; 18967 BP.
DE pTM-MVSchw plasmid containing measles virus Schwarz antigenome.
PN WO2004001051-A2.
PD 31-DEC-2003.
PA (INSP) INST PASTEUR.
PA (CNRS) CENT NAT RECH SCI.
Percent Similarity: 34.30% Conservative: 16
Best Local Similarity: 25.00% Mismatches: 56
Query Match: 7.03% Indels: 57
RESULT 903
ID AAL56703 standard; DNA; 36462 BP.
DE Chimpanzee adenovirus serotype Pan5 genomic DNA.
PN WO2003046124-A2.
PD 05-JUN-2003.
PA (UYPE-) UNIV PENNSYLVANIA.
Percent Similarity: 44.53% Conservative: 28
Best Local Similarity: 22.66% Mismatches: 51
Query Match: 7.03% Indels: 20
RESULT 904
ID AAA81457 standard; DNA; 49646 BP.
DE N. meningitidis partial DNA sequence gnm_5 SEQ ID NO:5.
PN WO200022430-A2.
PD 20-APR-2000.
PA (CHIR) CHIRON CORP.
Percent Similarity: 38.38% Conservative: 30
Best Local Similarity: 23.23% Mismatches: 81
Query Match: 7.03% Indels: 41
RESULT 905
Percent Similarity: 38.38% Conservative: 30
Best Local Similarity: 23.23% Mismatches: 81
Query Match: 7.03% Indels: 41
RESULT 906
ID AAF21607 standard; DNA; 349980 BP.
DE Neisseria meningitidis B nucleotide sequence SEQ ID NO:108.
PN WO200066791-A1.
PD 09-NOV-2000.
PA (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
Percent Similarity: 38.38% Conservative: 30
Best Local Similarity: 23.23% Mismatches: 81
Query Match: 7.03% Indels: 41
RESULT 907
ID AAF21608 standard; DNA; 349980 BP.
DE Neisseria meningitidis B nucleotide sequence SEQ ID NO:109.
PN WO200066791-A1.
PD 09-NOV-2000.
PA (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
Percent Similarity: 38.38% Conservative: 30
Best Local Similarity: 23.23% Mismatches: 81
Query Match: 7.03% Indels: 41
RESULT 908
ID AAH73602 standard; DNA; 2979 BP.

DE Human WT1-interacting protein coding sequence.
PN WO200153484-A1.
PD 26-JUL-2001.
PA (SUGI/) SUGIYAMA H.
Percent Similarity: 40.94% Conservative: 29
Best Local Similarity: 23.98% Mismatches: 58
Query Match: 6.99% Indels: 43
RESULT 909
ID ADC37608 standard; DNA; 2979 BP.
DE Human nucleic acid associated protein NAAP-15 coding sequence.
PN WO2003046151-A2.
PD 05-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 40.94% Conservative: 29
Best Local Similarity: 23.98% Mismatches: 58
Query Match: 6.99% Indels: 43
RESULT 910
ID ABL14505 standard; cDNA; 6030 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 37997.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 35.78% Conservative: 33
Best Local Similarity: 20.64% Mismatches: 77
Query Match: 6.99% Indels: 64
RESULT 911
Percent Similarity: 46.90% Conservative: 19
Best Local Similarity: 30.09% Mismatches: 36
Query Match: 6.99% Indels: 24
RESULT 912
Percent Similarity: 43.24% Conservative: 35
Best Local Similarity: 24.32% Mismatches: 66
Query Match: 6.99% Indels: 39
RESULT 913
ID ACN44200 standard; DNA; 211257 BP.
DE Mouse genomic sequence mCG15870.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Percent Similarity: 45.76% Conservative: 25
Best Local Similarity: 24.58% Mismatches: 52
Query Match: 6.99% Indels: 12
RESULT 914
ID ABQ81847 standard; DNA; 349980 BP.
DE Bifidobacterium longum NCC2705 related nucleotide sequence SEQ ID:1103.
PN EP1227152-A1.
PD 31-JUL-2002.
PA (NEST) SOC PROD NESTLE SA.
Percent Similarity: 53.54% Conservative: 24
Best Local Similarity: 29.29% Mismatches: 31
Query Match: 6.99% Indels: 16
RESULT 915
ID ABQ81847 standard; DNA; 349980 BP.
DE Bifidobacterium longum NCC2705 related nucleotide sequence SEQ ID:1103.
PN EP1227152-A1.
PD 31-JUL-2002.
PA (NEST) SOC PROD NESTLE SA.
Percent Similarity: 48.54% Conservative: 25
Best Local Similarity: 24.27% Mismatches: 23
Query Match: 6.99% Indels: 30
RESULT 916
ID ABQ81849 standard; DNA; 349980 BP.
DE Bifidobacterium longum NCC2705 related nucleotide sequence SEQ ID:1105.
PN EP1227152-A1.
PD 31-JUL-2002.
PA (NEST) SOC PROD NESTLE SA.
Percent Similarity: 52.05% Conservative: 18
Best Local Similarity: 27.40% Mismatches: 27
Query Match: 6.99% Indels: 8
RESULT 917
ID ABV94498 standard; cDNA; 912 BP.
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:12.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 40.25% Conservative: 28
Best Local Similarity: 22.64% Mismatches: 60
Query Match: 6.94% Indels: 35
RESULT 918
ID ADM18647 standard; cDNA; 912 BP.
DE Human co-stimulatory molecule encoding cDNA SEQ ID NO:12.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 40.25% Conservative: 28
Best Local Similarity: 22.64% Mismatches: 60
Query Match: 6.94% Indels: 35
RESULT 919
ID ADH83660 standard; DNA; 960 BP.
DE Enterococcus faecalis polynucleotide #1545.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Percent Similarity: 36.47% Conservative: 27
Best Local Similarity: 20.59% Mismatches: 55
Query Match: 6.94% Indels: 53
RESULT 920
ID ABT17379 standard; DNA; 1644 BP.
DE Human IG gene related nucleic acid SEQ ID No 5.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Percent Similarity: 40.46% Conservative: 26
Best Local Similarity: 25.43% Mismatches: 46
Query Match: 6.94% Indels: 57
RESULT 921
ID AAD37441 standard; DNA; 1650 BP.
DE Mouse nectin-3-human nectin 3alpha fusion protein encoding DNA.
PN WO200228902-A2.
PD 11-APR-2002.
PA (IMMV) IMMUNEX CORP.
Percent Similarity: 40.46% Conservative: 26
Best Local Similarity: 25.43% Mismatches: 46
Query Match: 6.94% Indels: 57
RESULT 922
ID AAD37442 standard; DNA; 1650 BP.
DE Human nectin-3alpha DNA.
PN WO200228902-A2.
PD 11-APR-2002.
PA (IMMV) IMMUNEX CORP.
Percent Similarity: 40.46% Conservative: 26
Best Local Similarity: 25.43% Mismatches: 46
Query Match: 6.94% Indels: 57
RESULT 923
ID ABT17378 standard; DNA; 1650 BP.
DE Human IG gene related nucleic acid SEQ ID No 4.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Percent Similarity: 40.46% Conservative: 26
Best Local Similarity: 25.43% Mismatches: 46
Query Match: 6.94% Indels: 57
RESULT 924
ID ADR66544 standard; DNA; 1650 BP.
DE Human prostatic carcinoma derived DNA SEQ ID 56 #3.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Percent Similarity: 40.46% Conservative: 26
Best Local Similarity: 25.43% Mismatches: 46
Query Match: 6.94% Indels: 57

RESULT 925
ID ADR66202 standard; DNA; 1650 BP.
DE Human prostatic carcinoma derived DNA SEQ ID 56 #2.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Percent Similarity: 40.46% Conservative: 26
Best Local Similarity: 25.43% Mismatches: 46
Query Match: 6.94% Indels: 57
RESULT 926
ID AAS82539 standard; cDNA; 2155 BP.
DE DNA encoding novel human diagnostic protein #18343.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 38.30% Conservative: 31
Best Local Similarity: 21.81% Mismatches: 76
Query Match: 6.94% Indels: 41
RESULT 927
ID AAD37440 standard; DNA; 3147 BP.
DE Human deleted nectin-3alpha DNA.
PN WO200228902-A2.
PD 11-APR-2002.
PA (IMMV) IMMUNEX CORP.
Percent Similarity: 40.46% Conservative: 26
Best Local Similarity: 25.43% Mismatches: 46
Query Match: 6.94% Indels: 57
RESULT 928
ID ABL03339 standard; cDNA; 3900 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 4499.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 38.22% Conservative: 33
Best Local Similarity: 23.56% Mismatches: 81
Query Match: 6.94% Indels: 59
RESULT 929
ID ADN96169 standard; cDNA; 4031 BP.
DE Human NOVX polynucleotide #112.
PN US2004067490-A1.
PD 08-APR-2004.
PA (ZHON/) ZHONG M.
PA (LILL/) LI L.
PA (GORM/) GORMAN L.
PA (SPYT/) SPYTEK K A.
PA (KEKU/) KEKUDA R.
PA (TAUP/) TAUPIER R J.
PA (ANDE/) ANDERSON D W.
PA (VERN/) VERNET C A M.
PA (CATT/) CATTERTON E.
PA (MILL/) MILLER C E.
PA (SHEN/) SHENOY S G.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (TCHE/) TCHERNEV V T.
PA (PADI/) PADIGARU M.
PA (GUSE/) GUSEV V Y.
PA (MALY/) MALYANKAR U M.
PA (BURG/) BURGESS C E.
PA (GERL/) GERLACH V.
PA (CASM/) CASMAN S J.
PA (RIEG/) RIEGER D K.
PA (GROS/) GROSSE W M.
PA (SMIT/) SMITHSON G.
PA (PEYM/) PEYMAN J A.
PA (STAR/) STARLING G.
PA (ROTH/) ROTHENBERG M E.
PA (LARO/) LAROCHELLE W J.
PA (SHIM/) SHIMKETS R A.
PA (CRAB/) CRABTREE J.
PA (RAST/) RASTELLI L.
PA (VOSS/) VOSS E Z.
PA (BOLD/) BOLDOG F L.
PA (EDIN/) EDINGER S R.
PA (MILL/) MILLET I.
PA (MACD/) MACDOUGALL J R.
PA (ELLE/) ELLERMAN K.
PA (CHAP/) CHAPOVAL A.
Percent Similarity: 40.52% Conservative: 27
Best Local Similarity: 22.88% Mismatches: 48
Query Match: 6.94% Indels: 43
RESULT 930
ID AAQ13789 standard; DNA; 5363 BP.
DE Cellulose synthase catalytic subunit gene and related protein gene.
PN WO9113988-A.
PD 19-SEP-1991.
PA (TEXA) UNIV TEXAS SYSTEM.
Percent Similarity: 36.81% Conservative: 21
Best Local Similarity: 25.27% Mismatches: 69
Query Match: 6.94% Indels: 46
RESULT 931
ID ABS76476 standard; cDNA; 5793 BP.
DE cDNA encoding human ovarian cancer marker M460.
PN WO200271928-A2.
PD 19-SEP-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Percent Similarity: 37.76% Conservative: 31
Best Local Similarity: 21.94% Mismatches: 59
Query Match: 6.94% Indels: 63
RESULT 932
ID ABZ11166 standard; cDNA; 6376 BP.
DE Human polynucleotide SEQ ID NO 48.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 43.55% Conservative: 31
Best Local Similarity: 26.88% Mismatches: 61
Query Match: 6.94% Indels: 44
RESULT 933
ID ADM43684 standard; cDNA; 6376 BP.
DE Novel human arginine-rich protein cDNA #48.
PN US2004053250-A1.
PD 18-MAR-2004.
PA (TANG/) TANG Y T.
PA (XUEA/) XUE A.
PA (DRMA/) DRMANAC R T.
Percent Similarity: 43.55% Conservative: 31
Best Local Similarity: 26.88% Mismatches: 61
Query Match: 6.94% Indels: 44
RESULT 934
ID ABL03338 standard; cDNA; 7572 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 4496.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 38.22% Conservative: 33
Best Local Similarity: 23.56% Mismatches: 81
Query Match: 6.94% Indels: 59
RESULT 935
ID AAL56705 standard; DNA; 36535 BP.
DE Chimpanzee adenovirus serotype Pan7 genomic DNA.
PN WO2003046124-A2.
PD 05-JUN-2003.
PA (UYPE-) UNIV PENNSYLVANIA.
Percent Similarity: 37.31% Conservative: 36
Best Local Similarity: 19.40% Mismatches: 75
Query Match: 6.94% Indels: 51
RESULT 936
Percent Similarity: 33.19% Conservative: 25
Best Local Similarity: 22.55% Mismatches: 70
Query Match: 6.94% Indels: 87
RESULT 937

Percent Similarity: 33.19% Conservative: 25
Best Local Similarity: 22.55% Mismatches: 70
Query Match: 6.94% Indels: 87
RESULT 938
Percent Similarity: 33.19% Conservative: 25
Best Local Similarity: 22.55% Mismatches: 70
Query Match: 6.94% Indels: 87
RESULT 939
ID ADN46845 standard; DNA; 2089378 BP.
DE Thermococcus kodakaraensis KOD1 genome DNA sequence SeqID723.
PN WO2004022736-A1.
PD 18-MAR-2004.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Percent Similarity: 33.19% Conservative: 25
Best Local Similarity: 22.55% Mismatches: 70
Query Match: 6.94% Indels: 87
RESULT 940
ID ADN46123 standard; DNA; 2089378 BP.
DE Thermococcus kodakaraensis KOD1 genome DNA sequence SeqID1.
PN WO2004022736-A1.
PD 18-MAR-2004.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Percent Similarity: 33.19% Conservative: 25
Best Local Similarity: 22.55% Mismatches: 70
Query Match: 6.94% Indels: 87
RESULT 941
ID ADN46464 standard; DNA; 2089378 BP.
DE Thermococcus kodakaraensis KOD1 DNA sequence SeqID342.
PN WO2004022736-A1.
PD 18-MAR-2004.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Percent Similarity: 33.19% Conservative: 25
Best Local Similarity: 22.55% Mismatches: 70
Query Match: 6.94% Indels: 87
RESULT 942
ID ADD16877 standard; DNA; 511 BP.
DE DNA (SeqID 945) that confers an altered visual phenotype in plants.
PN WO2003020741-A1.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
PA (DOWC) DOW AGROSCIENCES LLC.
Percent Similarity: 40.16% Conservative: 20
Best Local Similarity: 23.77% Mismatches: 43
Query Match: 6.90% Indels: 30
RESULT 943
ID AAD56953 standard; cDNA; 730 BP.
DE Human mucin 1 transmembrane variant, MUC1/X cDNA.
PN WO2003054154-A2.
PD 03-JUL-2003.
PA (ISIS-) ISIS PHARM INC.
Percent Similarity: 40.22% Conservative: 29
Best Local Similarity: 24.02% Mismatches: 90
Query Match: 6.90% Indels: 18
RESULT 944
ID AAD56949 standard; cDNA; 981 BP.
DE Human mucin 1 transmembrane variant, MUC1-V cDNA.
PN WO2003054154-A2.
PD 03-JUL-2003.
PA (ISIS-) ISIS PHARM INC.
Percent Similarity: 39.83% Conservative: 16
Best Local Similarity: 26.27% Mismatches: 63
Query Match: 6.90% Indels: 8
RESULT 945
ID ADI57684 standard; cDNA; 1183 BP.
DE Human breast specific nucleic acid (BSNA) #55.
PN WO2003106648-A2.
PD 24-DEC-2003.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 40.22% Conservative: 29
Best Local Similarity: 24.02% Mismatches: 90
Query Match: 6.90% Indels: 18
RESULT 946
ID ADI57703 standard; cDNA; 1189 BP.
DE Human breast specific nucleic acid (BSNA) #74.
PN WO2003106648-A2.
PD 24-DEC-2003.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 40.00% Conservative: 24
Best Local Similarity: 21.54% Mismatches: 64
Query Match: 6.90% Indels: 15
RESULT 947
ID AAC53420 standard; DNA; 1327 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 74462.
PN EP1033405-A2.
PD 06-SEP-2000.
Percent Similarity: 40.16% Conservative: 20
Best Local Similarity: 23.77% Mismatches: 43
Query Match: 6.90% Indels: 30
RESULT 948
ID ADI57687 standard; cDNA; 1605 BP.
DE Human breast specific nucleic acid (BSNA) #58.
PN WO2003106648-A2.
PD 24-DEC-2003.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 39.83% Conservative: 16
Best Local Similarity: 26.27% Mismatches: 63
Query Match: 6.90% Indels: 8
RESULT 949
ID ADT44101 standard; cDNA; 1608 BP.
DE Bacterial polynucleotide #18852.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Percent Similarity: 39.73% Conservative: 20
Best Local Similarity: 26.03% Mismatches: 36
Query Match: 6.90% Indels: 52
RESULT 950
ID AAS71120 standard; cDNA; 1687 BP.
DE DNA encoding novel human diagnostic protein #6924.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 39.33% Conservative: 24
Best Local Similarity: 23.33% Mismatches: 42
Query Match: 6.90% Indels: 49
RESULT 951
ID AAX99301 standard; cDNA; 1728 BP.
DE C. elegans CED-6 protein encoding nucleic acid.
PN WO9937770-A1.
PD 29-JUL-1999.
PA (COLD-) COLD SPRING HARBOR LAB.
PA (DEVG-) DEVGEN NV.
Percent Similarity: 38.31% Conservative: 19
Best Local Similarity: 25.97% Mismatches: 49
Query Match: 6.90% Indels: 46
RESULT 952
ID ABK88194 standard; DNA; 1846 BP.
DE DNA encoding human 553 amino acid transporter protein.
PN JP2002171980-A.
PD 18-JUN-2002.
PA (TOHO) UNIV TOHOKU.
Percent Similarity: 39.45% Conservative: 29
Best Local Similarity: 26.15% Mismatches: 75
Query Match: 6.90% Indels: 58
RESULT 953
ID ABV97363 standard; cDNA; 295 BP.
DE Human pancreatic cancer expressed cDNA SEQ ID NO 2771.
PN WO200260317-A2.
PD 08-AUG-2002.
PA (CORI-) CORIXA CORP.
Percent Similarity: 42.86% Conservative: 17
Best Local Similarity: 24.18% Mismatches: 51

Query Match: 6.85% Indels: 1
RESULT 954
ID ACN54849 standard; cDNA; 520 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-025-Q6-K6-F8, SEQ:9630.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Percent Similarity: 36.60% Conservative: 21
Best Local Similarity: 22.88% Mismatches: 48
Query Match: 6.85% Indels: 49
RESULT 955
ID AAI21091 standard; DNA; 570 BP.
DE Probe #11024 for gene expression analysis in human cervical cell sample.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 39.23% Conservative: 26
Best Local Similarity: 19.23% Mismatches: 50
Query Match: 6.85% Indels: 29
RESULT 956
ID ABA66169 standard; DNA; 570 BP.
DE Human foetal liver single exon nucleic acid probe #14474.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 39.23% Conservative: 26
Best Local Similarity: 19.23% Mismatches: 50
Query Match: 6.85% Indels: 29
RESULT 957
ID AAI46353 standard; DNA; 570 BP.
DE Probe #15039 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 39.23% Conservative: 26
Best Local Similarity: 19.23% Mismatches: 50
Query Match: 6.85% Indels: 29
RESULT 958
ID ABA48285 standard; DNA; 570 BP.
DE Human breast cell single exon nucleic acid probe #6980.
PN WO200157271-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 39.23% Conservative: 26
Best Local Similarity: 19.23% Mismatches: 50
Query Match: 6.85% Indels: 29
RESULT 959
ID ABA33236 standard; DNA; 570 BP.
DE Probe #11702 for gene expression analysis in human heart cell sample.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 39.23% Conservative: 26
Best Local Similarity: 19.23% Mismatches: 50
Query Match: 6.85% Indels: 29
RESULT 960
ID AAK40334 standard; DNA; 570 BP.
DE Human bone marrow expressed single exon probe SEQ ID NO: 14891.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 39.23% Conservative: 26
Best Local Similarity: 19.23% Mismatches: 50
Query Match: 6.85% Indels: 29
RESULT 961
ID AAK14588 standard; DNA; 570 BP.
DE Human brain expressed single exon probe SEQ ID NO: 14579.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 39.23% Conservative: 26
Best Local Similarity: 19.23% Mismatches: 50
Query Match: 6.85% Indels: 29
RESULT 962
ID ABS39904 standard; DNA; 570 BP.
DE Human liver single exon probe, SEQ ID No 14894.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 39.23% Conservative: 26
Best Local Similarity: 19.23% Mismatches: 50
Query Match: 6.85% Indels: 29
RESULT 963
ID AAI06811 standard; DNA; 570 BP.
DE Probe #6802 used to measure gene expression in human breast sample.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 39.23% Conservative: 26
Best Local Similarity: 19.23% Mismatches: 50
Query Match: 6.85% Indels: 29
RESULT 964
ID ABS14351 standard; DNA; 570 BP.
DE Human genome-derived single exon probe ORF from lung SEQ ID No 14342.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 39.23% Conservative: 26
Best Local Similarity: 19.23% Mismatches: 50
Query Match: 6.85% Indels: 29
RESULT 965
ID AAT10681 standard; cDNA; 723 BP.
DE Mucin-derived protein MUC1/V cDNA.
PN WO9603502-A2.
PD 08-FEB-1996.
PA (UYRA-) UNIV RAMOT APPL RES & IND DEV LTD.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 966
ID AAT10682 standard; cDNA; 750 BP.
DE Mucin-derived protein MUC1/V/alt cDNA.
PN WO9603502-A2.
PD 08-FEB-1996.
PA (UYRA-) UNIV RAMOT APPL RES & IND DEV LTD.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 967
ID AAT10679 standard; cDNA; 768 BP.
DE Mucin-derived protein MUC1/Y cDNA.
PN WO9603502-A2.
PD 08-FEB-1996.
PA (UYRA-) UNIV RAMOT APPL RES & IND DEV LTD.
Percent Similarity: 38.31% Conservative: 27
Best Local Similarity: 20.78% Mismatches: 77
Query Match: 6.85% Indels: 19
RESULT 968
ID ADA50574 standard; DNA; 768 BP.
DE Mucin 1 (MUC-1) splice variant #2 (MUC1Y) DNA, SEQ ID NO:29.
PN WO2003031569-A2.
PD 17-APR-2003.
PA (CENZ) CENTOCOR INC.
Percent Similarity: 38.31% Conservative: 27
Best Local Similarity: 20.78% Mismatches: 77
Query Match: 6.85% Indels: 19
RESULT 969
ID AAT10680 standard; cDNA; 795 BP.
DE Mucin-derived protein MUC1/Y/alt cDNA.
PN WO9603502-A2.
PD 08-FEB-1996.
PA (UYRA-) UNIV RAMOT APPL RES & IND DEV LTD.
Percent Similarity: 38.31% Conservative: 27

Best Local Similarity: 20.78% Mismatches: 77
Query Match: 6.85% Indels: 19
RESULT 970
ID AAA78516 standard; DNA; 808 BP.
DE Plant SDF polynucleotide sequence SEQ List 1 NO:290.
PN WO200040695-A2.
PD 13-JUL-2000.
PA (CERE-) CERES INC.
Percent Similarity: 45.26% Conservative: 24
Best Local Similarity: 27.74% Mismatches: 53
Query Match: 6.85% Indels: 22
RESULT 971
ID AAC48060 standard; DNA; 808 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 56120.
PN EP1033405-A2.
PD 06-SEP-2000.
Percent Similarity: 45.26% Conservative: 24
Best Local Similarity: 27.74% Mismatches: 53
Query Match: 6.85% Indels: 22
RESULT 972
ID AAT10677 standard; cDNA; 822 BP.
DE Mucin-derived protein MUC1/X cDNA.
PN WO9603502-A2.
PD 08-FEB-1996.
PA (UYRA-) UNIV RAMOT APPL RES & IND DEV LTD.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 973
ID AAT10678 standard; cDNA; 849 BP.
DE Mucin-derived protein MUC1/X/alt cDNA.
PN WO9603502-A2.
PD 08-FEB-1996.
PA (UYRA-) UNIV RAMOT APPL RES & IND DEV LTD.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 974
ID AAD57036 standard; cDNA; 859 BP.
DE Human mucin 1 transmembrane variant, MUC1/Z cDNA.
PN WO2003054154-A2.
PD 03-JUL-2003.
PA (ISIS-) ISIS PHARM INC.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 975
ID ADJ62779 standard; cDNA; 859 BP.
DE Human cDNA differentially expressed in response to docetaxel #49.
PN US2004018527-A1.
PD 29-JAN-2004.
PA (CHAN/) CHANG J C.
PA (OCON/) O'CONNELL P.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 976
ID ABV94488 standard; cDNA; 900 BP.
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:2.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.51% Conservative: 29
Best Local Similarity: 21.60% Mismatches: 57
Query Match: 6.85% Indels: 41
RESULT 977
ID ADM18637 standard; cDNA; 900 BP.
DE Human co-stimulatory molecule encoding cDNA SEQ ID NO:2.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.51% Conservative: 29
Best Local Similarity: 21.60% Mismatches: 57
Query Match: 6.85% Indels: 41
RESULT 978
ID ABV94501 standard; cDNA; 909 BP.
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:15.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.51% Conservative: 29
Best Local Similarity: 21.60% Mismatches: 57
Query Match: 6.85% Indels: 41
RESULT 979
ID ABV94573 standard; cDNA; 909 BP.
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:134.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.51% Conservative: 29
Best Local Similarity: 21.60% Mismatches: 57
Query Match: 6.85% Indels: 41
RESULT 980
ID ABV94563 standard; cDNA; 909 BP.
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:124.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.51% Conservative: 29
Best Local Similarity: 21.60% Mismatches: 57
Query Match: 6.85% Indels: 41
RESULT 981
ID ABV94540 standard; cDNA; 909 BP.
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:101.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.51% Conservative: 29
Best Local Similarity: 21.60% Mismatches: 57
Query Match: 6.85% Indels: 41
RESULT 982
ID ADM18736 standard; cDNA; 909 BP.
DE Human co-stimulatory molecule encoding cDNA SEQ ID NO:101.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.51% Conservative: 29
Best Local Similarity: 21.60% Mismatches: 57
Query Match: 6.85% Indels: 41
RESULT 983
ID ADM18650 standard; cDNA; 909 BP.
DE Human co-stimulatory molecule encoding cDNA SEQ ID NO:15.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.51% Conservative: 29
Best Local Similarity: 21.60% Mismatches: 57
Query Match: 6.85% Indels: 41
RESULT 984
ID ADM18769 standard; cDNA; 909 BP.
DE Human co-stimulatory molecule encoding cDNA SEQ ID NO:134.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.51% Conservative: 29
Best Local Similarity: 21.60% Mismatches: 57
Query Match: 6.85% Indels: 41
RESULT 985
ID ADM18759 standard; cDNA; 909 BP.
DE Human co-stimulatory molecule encoding cDNA SEQ ID NO:124.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.51% Conservative: 29
Best Local Similarity: 21.60% Mismatches: 57
Query Match: 6.85% Indels: 41

RESULT 986
ID ABV94579 standard; cDNA; 910 BP.
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:140.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.51% Conservative: 29
Best Local Similarity: 21.60% Mismatches: 57
Query Match: 6.85% Indels: 41
RESULT 987
ID ABV94555 standard; cDNA; 910 BP.
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:116.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.51% Conservative: 29
Best Local Similarity: 21.60% Mismatches: 57
Query Match: 6.85% Indels: 41
RESULT 988
ID ADM18751 standard; cDNA; 910 BP.
DE Human co-stimulatory molecule encoding cDNA SEQ ID NO:116.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.51% Conservative: 29
Best Local Similarity: 21.60% Mismatches: 57
Query Match: 6.85% Indels: 41
RESULT 989
ID ADM18775 standard; cDNA; 910 BP.
DE Human co-stimulatory molecule encoding cDNA SEQ ID NO:140.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.51% Conservative: 29
Best Local Similarity: 21.60% Mismatches: 57
Query Match: 6.85% Indels: 41
RESULT 990
ID ABV94571 standard; cDNA; 912 BP.
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:132.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.51% Conservative: 29
Best Local Similarity: 21.60% Mismatches: 57
Query Match: 6.85% Indels: 41
RESULT 991
ID ABV94564 standard; cDNA; 912 BP.
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:125.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.51% Conservative: 29
Best Local Similarity: 21.60% Mismatches: 57
Query Match: 6.85% Indels: 41
RESULT 992
ID ADM18760 standard; cDNA; 912 BP.
DE Human co-stimulatory molecule encoding cDNA SEQ ID NO:125.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.51% Conservative: 29
Best Local Similarity: 21.60% Mismatches: 57
Query Match: 6.85% Indels: 41
RESULT 993
ID ADM18767 standard; cDNA; 912 BP.
DE Human co-stimulatory molecule encoding cDNA SEQ ID NO:132.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.51% Conservative: 29
Best Local Similarity: 21.60% Mismatches: 57
Query Match: 6.85% Indels: 41
RESULT 994
ID AAI11883 standard; DNA; 962 BP.
DE Probe #1816 for gene expression analysis in human cervical cell sample.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 39.23% Conservative: 26
Best Local Similarity: 19.23% Mismatches: 50
Query Match: 6.85% Indels: 29
RESULT 995
ID ABA53584 standard; DNA; 962 BP.
DE Human foetal liver single exon nucleic acid probe #1889.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 39.23% Conservative: 26
Best Local Similarity: 19.23% Mismatches: 50
Query Match: 6.85% Indels: 29
RESULT 996
ID AAI33210 standard; DNA; 962 BP.
DE Probe #1896 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 39.23% Conservative: 26
Best Local Similarity: 19.23% Mismatches: 50
Query Match: 6.85% Indels: 29
RESULT 997
ID ABA43165 standard; DNA; 962 BP.
DE Human breast cell single exon nucleic acid probe #1860.
PN WO200157271-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 39.23% Conservative: 26
Best Local Similarity: 19.23% Mismatches: 50
Query Match: 6.85% Indels: 29
RESULT 998
ID ABA23339 standard; DNA; 962 BP.
DE Probe #1805 for gene expression analysis in human heart cell sample.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 39.23% Conservative: 26
Best Local Similarity: 19.23% Mismatches: 50
Query Match: 6.85% Indels: 29
RESULT 999
ID AAK27309 standard; DNA; 962 BP.
DE Human bone marrow expressed single exon probe SEQ ID NO: 1866.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 39.23% Conservative: 26
Best Local Similarity: 19.23% Mismatches: 50
Query Match: 6.85% Indels: 29
RESULT 1000
ID AAK01850 standard; DNA; 962 BP.
DE Human brain expressed single exon probe SEQ ID NO: 1841.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 39.23% Conservative: 26
Best Local Similarity: 19.23% Mismatches: 50
Query Match: 6.85% Indels: 29
RESULT 1001
ID ABS26883 standard; DNA; 962 BP.
DE Human liver single exon probe, SEQ ID No 1873.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 39.23% Conservative: 26
Best Local Similarity: 19.23% Mismatches: 50
Query Match: 6.85% Indels: 29
RESULT 1002
ID AAI01821 standard; DNA; 962 BP.

DE Probe #1812 used to measure gene expression in human breast sample.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 39.23% Conservative: 26
Best Local Similarity: 19.23% Mismatches: 50
Query Match: 6.85% Indels: 29
RESULT 1003
ID ABS01829 standard; DNA; 962 BP.
DE Human genome-derived single exon probe from lung SEQ ID No 1820.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 39.23% Conservative: 26
Best Local Similarity: 19.23% Mismatches: 50
Query Match: 6.85% Indels: 29
RESULT 1004
ID ACA20212 standard; DNA; 972 BP.
DE Prokaryotic essential gene #1869.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 42.75% Conservative: 21
Best Local Similarity: 27.54% Mismatches: 44
Query Match: 6.85% Indels: 35
RESULT 1005
ID ACF73847 standard; DNA; 1011 BP.
DE Staphylococcus aureus DNA #1527.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Percent Similarity: 42.75% Conservative: 21
Best Local Similarity: 27.54% Mismatches: 44
Query Match: 6.85% Indels: 35
RESULT 1006
ID AAQ24679 standard; DNA; 1074 BP.
DE H23-ETA-T antigen C-terminal coding sequence.
PN WO9207000-A1.
PD 30-APR-1992.
PA (TRGE) TRANSGENE SA.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1007
ID ADJ34831 standard; DNA; 1137 BP.
DE DNA encoding xylanase from an environmental sample seq id 47.
PN WO2003106654-A2.
PD 24-DEC-2003.
PA (DIVE-) DIVERSA CORP.
Percent Similarity: 32.84% Conservative: 34
Best Local Similarity: 20.15% Mismatches: 87
Query Match: 6.85% Indels: 93
RESULT 1008
ID ADE43993 standard; DNA; 1164 BP.
DE Plasmid JNW389 gutted MUC-1 encoding DNA.
PN WO2003099193-A2.
PD 04-DEC-2003.
PA (GLAX) GLAXO GROUP LTD.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1009
ID ADI57704 standard; cDNA; 1216 BP.
DE Human breast specific nucleic acid (BSNA) #75.
PN WO2003106648-A2.
PD 24-DEC-2003.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 38.65% Conservative: 30
Best Local Similarity: 20.25% Mismatches: 77
Query Match: 6.85% Indels: 24
RESULT 1010
ID ADI57700 standard; cDNA; 1258 BP.
DE Human breast specific nucleic acid (BSNA) #71.
PN WO2003106648-A2.
PD 24-DEC-2003.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 38.31% Conservative: 27
Best Local Similarity: 20.78% Mismatches: 77
Query Match: 6.85% Indels: 19
RESULT 1011
ID ADI57702 standard; cDNA; 1266 BP.
DE Human breast specific nucleic acid (BSNA) #73.
PN WO2003106648-A2.
PD 24-DEC-2003.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1012
ID ADI57695 standard; cDNA; 1285 BP.
DE Human breast specific nucleic acid (BSNA) #66.
PN WO2003106648-A2.
PD 24-DEC-2003.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 38.81% Conservative: 35
Best Local Similarity: 21.39% Mismatches: 105
Query Match: 6.85% Indels: 21
RESULT 1013
ID ADR89849 standard; cDNA; 1290 BP.
DE Human mucin MUC-1 gene (7x VNTR removed), codon optimised.
PN WO2004076665-A2.
PD 10-SEP-2004.
PA (GLAX) GLAXO GROUP LTD.
Percent Similarity: 37.90% Conservative: 18
Best Local Similarity: 23.39% Mismatches: 63
Query Match: 6.85% Indels: 15
RESULT 1014
ID ADR89847 standard; cDNA; 1290 BP.
DE Human mucin MUC-1 gene (7x VNTR removed).
PN WO2004076665-A2.
PD 10-SEP-2004.
PA (GLAX) GLAXO GROUP LTD.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1015
ID ADR89848 standard; cDNA; 1290 BP.
DE Human mucin MUC-1 gene (7x VNTR removed), codon optimised.
PN WO2004076665-A2.
PD 10-SEP-2004.
PA (GLAX) GLAXO GROUP LTD.
Percent Similarity: 42.86% Conservative: 17
Best Local Similarity: 24.18% Mismatches: 51
Query Match: 6.85% Indels: 1
RESULT 1016
ID ADI57680 standard; cDNA; 1312 BP.
DE Human breast specific nucleic acid (BSNA) #51.
PN WO2003106648-A2.
PD 24-DEC-2003.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1017
ID AAT29190 standard; cDNA to mRNA; 1320 BP.
DE Glycoprotein 39 3' fragment.
PN JP07051065-A.
PD 28-FEB-1995.
PA (NIKO-) NIPPON KOTAI KENKYUSHO KK.
PA (UYKA-) UNIV KAGOSHIMA.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1018
ID ADR89850 standard; cDNA; 1330 BP.
DE Human mucin MUC-1 gene (7x VNTR removed), codon optimised.

PN WO2004076665-A2.
PD 10-SEP-2004.
PA (GLAX) GLAXO GROUP LTD.
Percent Similarity: 37.90% Conservative: 18
Best Local Similarity: 23.39% Mismatches: 63
Query Match: 6.85% Indels: 15
RESULT 1019
ID AAC77625 standard; cDNA; 1355 BP.
DE Human cancer associated gene sequence SEQ ID NO:19.
PN WO200055350-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1020
ID AAD00388 standard; DNA; 1371 BP.
DE Human Mucin 1 (MUC-1) protein fragment encoding DNA #5.
PN WO200025827-A2.
PD 11-MAY-2000.
PA (MENA) MENARINI RICERCHE SPA.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1021
ID ABL02275 standard; cDNA; 1391 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 1307.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 40.56% Conservative: 30
Best Local Similarity: 23.89% Mismatches: 67
Query Match: 6.85% Indels: 40
RESULT 1022
ID AAS16149 standard; cDNA; 1398 BP.
DE Human leukocyte immunoglobulin receptor-like (LIR-like) cDNA #5.
PN WO200155335-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 34.70% Conservative: 39
Best Local Similarity: 20.15% Mismatches: 74
Query Match: 6.85% Indels: 102
RESULT 1023
ID ADE43995 standard; DNA; 1404 BP.
DE Plasmid JNW399 MUC-1 encoding DNA.
PN WO2003099193-A2.
PD 04-DEC-2003.
PA (GLAX) GLAXO GROUP LTD.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1024
ID ABL60159 standard; cDNA; 1428 BP.
DE Human MUC1 encoding cDNA SEQ ID NO 2.
PN WO200226765-A2.
PD 04-APR-2002.
PA (GENA-) GENAISSANCE PHARM INC.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1025
ID ADO23125 standard; RNA; 1428 BP.
DE Human MUC1 mucin glycoprotein RNA (coding sequence) SeqID 20.
PN WO2004044160-A2.
PD 27-MAY-2004.
PA (DAND) DANA FARBER CANCER INST INC.
PA (ILEX-) ILEX PROD INC.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1026
ID AAQ29276 standard; cDNA; 1452 BP.
DE Encodes transmembrane form of H23-ETA antigen.
PN WO9207000-A1.
PD 30-APR-1992.
PA (TRGE) TRANSGENE SA.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1027
ID AAS16150 standard; cDNA; 1455 BP.
DE Human leukocyte immunoglobulin receptor-like (LIR-like) cDNA #6.
PN WO200155335-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 34.70% Conservative: 39
Best Local Similarity: 20.15% Mismatches: 74
Query Match: 6.85% Indels: 102
RESULT 1028
ID AAL49724 standard; cDNA; 1455 BP.
DE Human secreted LIR-like protein cDNA SEQ ID NO: 39.
PN WO200266600-A2.
PD 29-AUG-2002.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 34.70% Conservative: 39
Best Local Similarity: 20.15% Mismatches: 74
Query Match: 6.85% Indels: 102
RESULT 1029
ID ADS10215 standard; DNA; 1455 BP.
DE Human therapeutic DNA - SEQ ID 452.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Percent Similarity: 34.70% Conservative: 39
Best Local Similarity: 20.15% Mismatches: 74
Query Match: 6.85% Indels: 102
RESULT 1030
ID ADF32627 standard; DNA; 1457 BP.
DE Plasmid JNW358 MUC-1 nucleotide sequence.
PN WO2003100060-A2.
PD 04-DEC-2003.
PA (GLAX) GLAXO GROUP LTD.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1031
ID ADS09841 standard; DNA; 1505 BP.
DE Human therapeutic DNA - SEQ ID 78.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Percent Similarity: 34.70% Conservative: 39
Best Local Similarity: 20.15% Mismatches: 74
Query Match: 6.85% Indels: 102
RESULT 1032
ID ADI57696 standard; cDNA; 1517 BP.
DE Human breast specific nucleic acid (BSNA) #67.
PN WO2003106648-A2.
PD 24-DEC-2003.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 38.65% Conservative: 30
Best Local Similarity: 20.25% Mismatches: 77
Query Match: 6.85% Indels: 24
RESULT 1033
ID ADI57674 standard; cDNA; 1530 BP.
DE Human breast specific nucleic acid (BSNA) #45.
PN WO2003106648-A2.
PD 24-DEC-2003.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 38.31% Conservative: 27
Best Local Similarity: 20.78% Mismatches: 77
Query Match: 6.85% Indels: 19
RESULT 1034
ID AAS00585 standard; DNA; 1572 BP.
DE Human MUC1 DNA sequence.
PN WO200118035-A2.

PD 15-MAR-2001.
PA (TRGE) TRANSGENE SA.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1035
ID ADK70370 standard; cDNA; 1614 BP.
DE Respiratory disease differentially expressed cDNA #106.
PN WO2003101283-A2.
PD 11-DEC-2003.
PA (INCY-) INCYTE CORP.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1036
ID ADI57689 standard; cDNA; 1634 BP.
DE Human breast specific nucleic acid (BSNA) #60.
PN WO2003106648-A2.
PD 24-DEC-2003.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1037
ID ACA18749 standard; DNA; 1650 BP.
DE Prokaryotic essential gene #406.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 35.75% Conservative: 32
Best Local Similarity: 20.29% Mismatches: 84
Query Match: 6.85% Indels: 49
RESULT 1038
ID ABS76475 standard; cDNA; 1721 BP.
DE cDNA encoding human ovarian cancer marker OV45.
PN WO200271928-A2.
PD 19-SEP-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1039
ID ABL68032 standard; DNA; 1721 BP.
DE Ovary cancer related gene sequence SEQ ID NO:6369.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1040
ID ABK09743 standard; cDNA; 1721 BP.
DE Human ovarian tumour protein encoding cDNA #276.
PN WO200190154-A2.
PD 29-NOV-2001.
PA (CORI-) CORIXA CORP.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1041
ID ABV94067 standard; cDNA; 1721 BP.
DE Breast carcinoma related nucleotide sequence SEQ ID NO:58.
PN WO200246467-A2.
PD 13-JUN-2002.
PA (IPSO-) IPSOGEN.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1042
ID ADA50566 standard; DNA; 1721 BP.
DE Mucin 1 (MUC-1) encoding DNA, SEQ ID NO:21.
PN WO2003031569-A2.
PD 17-APR-2003.
PA (CENZ) CENTOCOR INC.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1043
ID ACF12906 standard; cDNA; 1721 BP.
DE Human cervical cancer cell marker encoding cDNA SEQ ID NO:155.
PN WO2002101075-A2.
PD 19-DEC-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1044
ID AAD56938 standard; cDNA; 1721 BP.
DE Human mucin 1 transmembrane cDNA.
PN WO2003054154-A2.
PD 03-JUL-2003.
PA (ISIS-) ISIS PHARM INC.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1045
ID ADK65926 standard; cDNA; 1721 BP.
DE Human immunostimulating mucin MUC1 coding sequence.
PN WO2004009632-A2.
PD 29-JAN-2004.
PA (NEMO-) NEMOD IMMUNTHERAPIE AG.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1046
ID ADR24914 standard; DNA; 1721 BP.
DE Breast cancer prognosis marker #775.
PN WO2004065545-A2.
PD 05-AUG-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
PA (NECA-) NETHERLANDS CANCER INST.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1047
ID AAD00394 standard; DNA; 1737 BP.
DE Ubiquitin-E. coli LacI-human Mucin 1 fusion protein encoding DNA #5.
PN WO200025827-A2.
PD 11-MAY-2000.
PA (MENA) MENARINI RICERCHE SPA.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1048
ID ADI57669 standard; cDNA; 1738 BP.
DE Human breast specific nucleic acid (BSNA) #40.
PN WO2003106648-A2.
PD 24-DEC-2003.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1049
ID ADI57673 standard; cDNA; 1755 BP.
DE Human breast specific nucleic acid (BSNA) #44.
PN WO2003106648-A2.
PD 24-DEC-2003.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1050
ID ADE43991 standard; DNA; 1774 BP.
DE Plasmid JNW283 MUC-1 encoding DNA.
PN WO2003099193-A2.

PD 04-DEC-2003.
PA (GLAX) GLAXO GROUP LTD.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1051
ID ADF32625 standard; DNA; 1774 BP.
DE Plasmid JNW283 MUC-1 nucleotide sequence.
PN WO2003100060-A2.
PD 04-DEC-2003.
PA (GLAX) GLAXO GROUP LTD.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1052
ID ADI57679 standard; cDNA; 1798 BP.
DE Human breast specific nucleic acid (BSNA) #50.
PN WO2003106648-A2.
PD 24-DEC-2003.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1053
ID ADO23124 standard; RNA; 1799 BP.
DE Human MUC1 mucin glycoprotein RNA SeqID 19.
PN WO2004044160-A2.
PD 27-MAY-2004.
PA (DAND) DANA FARBER CANCER INST INC.
PA (ILEX-) ILEX PROD INC.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1054
ID ADR89853 standard; cDNA; 1800 BP.
DE Human mucin MUC-1 gene coding sequence.
PN WO2004076665-A2.
PD 10-SEP-2004.
PA (GLAX) GLAXO GROUP LTD.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1055
ID ADI57699 standard; cDNA; 1803 BP.
DE Human breast specific nucleic acid (BSNA) #70.
PN WO2003106648-A2.
PD 24-DEC-2003.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1056
ID ABL67539 standard; DNA; 1804 BP.
DE Thyroid cancer related gene sequence SEQ ID NO:5876.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1057
ID AAD56950 standard; cDNA; 1804 BP.
DE Human mucin 1 transmembrane variant, MUC1-VI cDNA.
PN WO2003054154-A2.
PD 03-JUL-2003.
PA (ISIS-) ISIS PHARM INC.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1058
ID ADD14719 standard; cDNA; 1804 BP.
DE Human src biomarker polynucleotide SEQ ID NO:113.
PN WO2003062395-A2.
PD 31-JUL-2003.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1059
ID ADP13294 standard; DNA; 1804 BP.
DE Renal cell carcinoma differentially expressed gene #30.
PN WO2004048933-A2.
PD 10-JUN-2004.
PA (AMHP) WYETH.
PA (TWIN/) TWINE N C.
PA (BURC/) BURCZYNSKI M E.
PA (TREP/) TREPICCHIO W L.
PA (DORN/) DORNER A.
PA (STOV/) STOVER J A.
PA (SLON/) SLONI D K.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1060
ID ADO28642 standard; cDNA; 1805 BP.
DE Human MUC1 encoding cDNA SEQ ID NO:71.
PN WO2004044178-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1061
ID ADQ83917 standard; cDNA; 1805 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #731.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1062
ID ADQ86329 standard; cDNA; 1805 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #3201.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1063
ID ADQ85148 standard; cDNA; 1805 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #1962.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1064
ID ADQ83237 standard; cDNA; 1805 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #51.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2

RESULT 1065
ID ADF32633 standard; DNA; 1818 BP.
DE Plasmid JNW656 7x VNTR MUC-1 nucleotide sequence.
PN WO2003100060-A2.
PD 04-DEC-2003.
PA (GLAX) GLAXO GROUP LTD.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1066
ID ADR89851 standard; cDNA; 1818 BP.
DE Human mucin MUC-1 gene (7x VNTR) expression cassette, codon optimised.
PN WO2004076665-A2.
PD 10-SEP-2004.
PA (GLAX) GLAXO GROUP LTD.
Percent Similarity: 37.90% Conservative: 18
Best Local Similarity: 23.39% Mismatches: 63
Query Match: 6.85% Indels: 15
RESULT 1067
ID ADR89846 standard; cDNA; 1818 BP.
DE Human mucin MUC-1 gene coding sequence.
PN WO2004076665-A2.
PD 10-SEP-2004.
PA (GLAX) GLAXO GROUP LTD.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1068
ID ABZ35228 standard; cDNA; 1823 BP.
DE Human gene expression profile polynucleotide SEQ ID NO 339.
PN WO200274979-A2.
PD 26-SEP-2002.
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1069
ID ADF32631 standard; DNA; 1835 BP.
DE Plasmid JNW321 2x VNTR MUC-1 nucleotide sequence.
PN WO2003100060-A2.
PD 04-DEC-2003.
PA (GLAX) GLAXO GROUP LTD.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1070
ID ADI57688 standard; cDNA; 1874 BP.
DE Human breast specific nucleic acid (BSNA) #59.
PN WO2003106648-A2.
PD 24-DEC-2003.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1071
ID ADI57677 standard; cDNA; 1882 BP.
DE Human breast specific nucleic acid (BSNA) #48.
PN WO2003106648-A2.
PD 24-DEC-2003.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1072
ID ADI57672 standard; cDNA; 1918 BP.
DE Human breast specific nucleic acid (BSNA) #43.
PN WO2003106648-A2.
PD 24-DEC-2003.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1073
ID ADI57678 standard; cDNA; 1930 BP.
DE Human breast specific nucleic acid (BSNA) #49.
PN WO2003106648-A2.
PD 24-DEC-2003.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1074
ID ADI57676 standard; cDNA; 1945 BP.
DE Human breast specific nucleic acid (BSNA) #47.
PN WO2003106648-A2.
PD 24-DEC-2003.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1075
ID ADI57698 standard; cDNA; 1949 BP.
DE Human breast specific nucleic acid (BSNA) #69.
PN WO2003106648-A2.
PD 24-DEC-2003.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1076
ID ADI57668 standard; cDNA; 1953 BP.
DE Human breast specific nucleic acid (BSNA) #39.
PN WO2003106648-A2.
PD 24-DEC-2003.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1077
ID ADH10475 standard; DNA; 1971 BP.
DE Human MUC-1-CPC fusion protein encoding DNA.
PN WO2003104272-A1.
PD 18-DEC-2003.
PA (GLAX) GLAXOSMITHKLINE BIOLOGICALS SA.
PA (GLAX) GLAXO GROUP LTD.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1078
ID ACN91439 standard; DNA; 2026 BP.
DE Breast cancer related marker, seq id 12589.
PN US2003099974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1079
ID ADH10477 standard; DNA; 2037 BP.
DE CPC-MUC-1 fusion protein encoding DNA.
PN WO2003104272-A1.
PD 18-DEC-2003.
PA (GLAX) GLAXOSMITHKLINE BIOLOGICALS SA.
PA (GLAX) GLAXO GROUP LTD.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1080
ID ADI57701 standard; cDNA; 2045 BP.
DE Human breast specific nucleic acid (BSNA) #72.
PN WO2003106648-A2.
PD 24-DEC-2003.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2

RESULT 1081
ID ADI57682 standard; cDNA; 2049 BP.
DE Human breast specific nucleic acid (BSNA) #53.
PN WO2003106648-A2.
PD 24-DEC-2003.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1082
ID ADF32629 standard; DNA; 2135 BP.
DE Plasmid JNW319 7x VNTR MUC-1 nucleotide sequence.
PN WO2003100060-A2.
PD 04-DEC-2003.
PA (GLAX) GLAXO GROUP LTD.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1083
ID ADE53756 standard; cDNA; 2678 BP.
DE Human prostate cancer cDNA #103.
PN US2003190640-A1.
PD 09-OCT-2003.
PA (FARI/) FARIS M.
PA (PEAR/) PEARSON C I.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1084
ID ADE53756 standard; cDNA; 2678 BP.
DE Human prostate cancer cDNA #103.
PN US2003190640-A1.
PD 09-OCT-2003.
PA (FARI/) FARIS M.
PA (PEAR/) PEARSON C I.
Percent Similarity: 38.12% Conservative: 28
Best Local Similarity: 20.62% Mismatches: 79
Query Match: 6.85% Indels: 21
RESULT 1085
ID ADC91583 standard; DNA; 2835 BP.
DE E. faecium DNA sequence SEQ ID 1210.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 41.95% Conservative: 36
Best Local Similarity: 21.26% Mismatches: 76
Query Match: 6.85% Indels: 25
RESULT 1086
ID ABL05460 standard; cDNA; 3187 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 10862.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 38.10% Conservative: 23
Best Local Similarity: 25.93% Mismatches: 65
Query Match: 6.85% Indels: 52
RESULT 1087
ID ABL18139 standard; DNA; 3840 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 5890.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 39.20% Conservative: 19
Best Local Similarity: 24.00% Mismatches: 49
Query Match: 6.85% Indels: 27
RESULT 1088
ID ABL67071 standard; DNA; 4139 BP.
DE Thyroid cancer related gene sequence SEQ ID NO:5408.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1089
ID ABL67544 standard; DNA; 4139 BP.
DE Thyroid cancer related gene sequence SEQ ID NO:5881.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1090
ID ABL68884 standard; DNA; 4139 BP.
DE Kidney cancer related gene sequence SEQ ID NO:7221.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1091
ID ABK09797 standard; cDNA; 4139 BP.
DE Human ovarian tumour protein encoding cDNA #330.
PN WO200190154-A2.
PD 29-NOV-2001.
PA (CORI-) CORIXA CORP.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1092
ID ABN95623 standard; DNA; 4139 BP.
DE Gene #2121 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1093
ID ACC50234 standard; cDNA; 4139 BP.
DE Breast cancer associated cDNA sequence SEQ ID NO:310.
PN WO2003004989-A2.
PD 16-JAN-2003.
PA (MILL-) MILLENIUM PHARM INC.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1094
ID ACF12907 standard; cDNA; 4139 BP.
DE Human cervical cancer cell marker encoding cDNA SEQ ID NO:157.
PN WO2002101075-A2.
PD 19-DEC-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1095
ID ADH17156 standard; cDNA; 4139 BP.
DE Human mucin 1 cDNA.
PN WO2003097854-A2.
PD 27-NOV-2003.
PA (SUGE-) SUGEN INC.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1096
ID ADQ29627 standard; DNA; 4139 BP.
DE Human colorectal cancer-associated protein coding sequence #49.
PN EP1439393-A2.
PD 21-JUL-2004.
PA (FARB) BAYER HEALTHCARE LLC.
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57

Query Match: 6.85% Indels: 2
RESULT 1097
ID ADR44006 standard; DNA; 4139 BP.
DE Human breast tumour associated gene clone-19 SEQ ID NO:16.
PN WO2004074506-A2.
PD 02-SEP-2004.
PA (MERG-) MERGEN LTD.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1098
ID ADI57666 standard; cDNA; 4144 BP.
DE Human breast specific nucleic acid (BSNA) #37.
PN WO2003106648-A2.
PD 24-DEC-2003.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 43.69% Conservative: 20
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1099
ID ADA69635 standard; DNA; 4425 BP.
DE Rice gene, SEQ ID 2958.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Percent Similarity: 48.28% Conservative: 24
Best Local Similarity: 27.59% Mismatches: 39
Query Match: 6.85% Indels: 21
RESULT 1100
ID ADQ22765 standard; DNA; 5037 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5585.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Percent Similarity: 40.86% Conservative: 16
Best Local Similarity: 23.66% Mismatches: 20
Query Match: 6.85% Indels: 35
RESULT 1101
ID ABL27091 standard; DNA; 5167 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 32746.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 39.15% Conservative: 32
Best Local Similarity: 24.06% Mismatches: 84
Query Match: 6.85% Indels: 45
RESULT 1102
ID AAS57189 standard; cDNA; 5167 BP.
DE cDNA encoding Drosophila G-protein coupled receptor, GCPR #59.
PN WO200170980-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 39.15% Conservative: 32
Best Local Similarity: 24.06% Mismatches: 84
Query Match: 6.85% Indels: 45
RESULT 1103
ID ADC35924 standard; cDNA; 5167 BP.
DE Drosophila G protein coupled receptor cDNA seq id 60.
PN US2003092124-A1.
PD 15-MAY-2003.
PA (APPL-) APPLERA CORP.
Percent Similarity: 39.15% Conservative: 32
Best Local Similarity: 24.06% Mismatches: 84
Query Match: 6.85% Indels: 45
RESULT 1104
ID ABL28080 standard; DNA; 5350 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 35713.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 38.10% Conservative: 23
Best Local Similarity: 25.93% Mismatches: 65
Query Match: 6.85% Indels: 52
RESULT 1105
ID AAQ90511 standard; DNA; 14556 BP.
DE CEA genomic clone.
PN WO9514100-A2.
PD 26-MAY-1995.
PA (WELL) WELLCOME FOUND LTD.
Percent Similarity: 61.22% Conservative: 7
Best Local Similarity: 46.94% Mismatches: 14
Query Match: 6.85% Indels: 6
RESULT 1106
ID ADA02756 standard; DNA; 96594 BP.
DE Human MORF carcinoma associated gene, SEQ ID NO:1274.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Percent Similarity: 33.49% Conservative: 25
Best Local Similarity: 21.86% Mismatches: 75
Query Match: 6.85% Indels: 69
RESULT 1107
ID ADB72494 standard; DNA; 96594 BP.
DE Human MORF gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Percent Similarity: 33.49% Conservative: 25
Best Local Similarity: 21.86% Mismatches: 75
Query Match: 6.85% Indels: 69
RESULT 1108
ID ADC85236 standard; DNA; 96594 BP.
DE Human Morf genomic sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Percent Similarity: 33.49% Conservative: 25
Best Local Similarity: 21.86% Mismatches: 75
Query Match: 6.85% Indels: 69
RESULT 1109
ID ADM74351 standard; DNA; 96594 BP.
DE Human carcinoma associated (CA) nucleic acid #10.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.
PA (ENGE/) ENGELHARD E K.
Percent Similarity: 33.49% Conservative: 25
Best Local Similarity: 21.86% Mismatches: 75
Query Match: 6.85% Indels: 69
RESULT 1110
ID ACN44734 standard; DNA; 102980 BP.
DE Human genomic sequence hCG27644.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Percent Similarity: 42.47% Conservative: 26
Best Local Similarity: 24.66% Mismatches: 68
Query Match: 6.85% Indels: 17
RESULT 1111
ID AAC04386 standard; cDNA; 414 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 8461.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Percent Similarity: 41.53% Conservative: 20
Best Local Similarity: 24.58% Mismatches: 31
Query Match: 6.81% Indels: 38
RESULT 1112
ID AAS52951 standard; DNA; 867 BP.
DE Enterococcus faecalis DNA for cellular proliferation protein #379.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 45.71% Conservative: 17
Best Local Similarity: 29.52% Mismatches: 43
Query Match: 6.81% Indels: 15

RESULT 1113
ID ADC86988 standard; DNA; 1324 BP.
DE Human GPCR gene SEQ ID NO:1441.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Percent Similarity: 35.98% Conservative: 27
Best Local Similarity: 23.36% Mismatches: 69
Query Match: 6.81% Indels: 68
RESULT 1114
ID ADS04421 standard; DNA; 1647 BP.
DE Staphylococcus epidermis polynucleotide seqid 3716.
PN US2004147734-A1.
PD 29-JUL-2004.
PA (DOUC/) DOUCETTE-STAMM L.
PA (BUSH/) BUSH D.
Percent Similarity: 46.15% Conservative: 14
Best Local Similarity: 32.69% Mismatches: 30
Query Match: 6.81% Indels: 26
RESULT 1115
ID AAS80665 standard; cDNA; 1863 BP.
DE DNA encoding novel human diagnostic protein #16469.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 42.45% Conservative: 32
Best Local Similarity: 19.42% Mismatches: 46
Query Match: 6.81% Indels: 34
RESULT 1116
ID AAD09561 standard; cDNA; 1986 BP.
DE Human transporter and ion channel-10 (TRICH-10) cDNA.
PN WO200146258-A2.
PD 28-JUN-2001.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 37.67% Conservative: 31
Best Local Similarity: 23.26% Mismatches: 82
Query Match: 6.81% Indels: 52
RESULT 1117
ID ADO30284 standard; cDNA; 2048 BP.
DE Mouse GPCR MRGF polynucleotide, SEQ ID NO:1387.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Percent Similarity: 34.55% Conservative: 30
Best Local Similarity: 20.91% Mismatches: 76
Query Match: 6.81% Indels: 68
RESULT 1118
ID ADL27141 standard; cDNA; 3029 BP.
DE Human cDNA sequence for KCNJ9.
PN US2003216558-A1.
PD 20-NOV-2003.
PA (MORR/) MORRIS D W.
PA (ENGE/) ENGELHARD E K.
Percent Similarity: 39.68% Conservative: 33
Best Local Similarity: 22.22% Mismatches: 82
Query Match: 6.81% Indels: 32
RESULT 1119
ID ABL13145 standard; cDNA; 3443 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 33917.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 35.26% Conservative: 25
Best Local Similarity: 22.11% Mismatches: 58
Query Match: 6.81% Indels: 65
RESULT 1120
ID ADD49068 standard; DNA; 3462 BP.
DE Human NOV11a coding sequence, SEQ ID 41.
PN WO2003060149-A2.
PD 24-JUL-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 47.46% Conservative: 27
Best Local Similarity: 24.58% Mismatches: 47
Query Match: 6.81% Indels: 15
RESULT 1121
ID ADH71107 standard; DNA; 3462 BP.
DE Human gene of the invention NOV2a SEQ ID NO:3.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 47.46% Conservative: 27
Best Local Similarity: 24.58% Mismatches: 47
Query Match: 6.81% Indels: 15
RESULT 1122
ID AAT40235 standard; cDNA to mRNA; 3546 BP.
DE GPIa precursor cDNA for Br-a allele.
PN US5516634-A.
PD 14-MAY-1996.
PA (SANT/) SANTOSO S S.
PA (NEWM/) NEWMAN P J.
Percent Similarity: 47.46% Conservative: 27
Best Local Similarity: 24.58% Mismatches: 47
Query Match: 6.81% Indels: 15
RESULT 1123
ID ADN96153 standard; cDNA; 3972 BP.
DE Human NOVX polynucleotide #104.
PN US2004067490-A1.
PD 08-APR-2004.
PA (ZHON/) ZHONG M.
PA (LILL/) LI L.
PA (GORM/) GORMAN L.
PA (SPYT/) SPYTEK K A.
PA (KEKU/) KEKUDA R.
PA (TAUP/) TAUPIER R J.
PA (ANDE/) ANDERSON D W.
PA (VERN/) VERNET C A M.
PA (CATT/) CATTERTON E.
PA (MILL/) MILLER C E.
PA (SHEN/) SHENOY S G.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (TCHE/) TCHERNEV V T.
PA (PADI/) PADIGARU M.
PA (GUSE/) GUSEV V Y.
PA (MALY/) MALYANKAR U M.
PA (BURG/) BURGESS C E.
PA (GERL/) GERLACH V.
PA (CASM/) CASMAN S J.
PA (RIEG/) RIEGER D K.
PA (GROS/) GROSSE W M.
PA (SMIT/) SMITHSON G.
PA (PEYM/) PEYMAN J A.
PA (STAR/) STARLING G.
PA (ROTH/) ROTHENBERG M E.
PA (LARO/) LAROCHELLE W J.
PA (SHIM/) SHIMKETS R A.
PA (CRAB/) CRABTREE J.
PA (RAST/) RASTELLI L.
PA (VOSS/) VOSS E Z.
PA (BOLD/) BOLDOG F L.
PA (EDIN/) EDINGER S R.
PA (MILL/) MILLET I.
PA (MACD/) MACDOUGALL J R.
PA (ELLE/) ELLERMAN K.
PA (CHAP/) CHAPOVAL A.
Percent Similarity: 40.44% Conservative: 25
Best Local Similarity: 22.06% Mismatches: 33
Query Match: 6.81% Indels: 48
RESULT 1124
ID ADS63543 standard; cDNA; 4140 BP.
DE Bacterial polynucleotide #15530.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.

PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Percent Similarity: 34.90% Conservative: 27
Best Local Similarity: 20.83% Mismatches: 70
Query Match: 6.81% Indels: 55
RESULT 1125
ID ADS63914 standard; cDNA; 4140 BP.
DE Bacterial polynucleotide #15901.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Percent Similarity: 34.90% Conservative: 27
Best Local Similarity: 20.83% Mismatches: 70
Query Match: 6.81% Indels: 55
RESULT 1126
ID ADS64286 standard; cDNA; 4140 BP.
DE Bacterial polynucleotide #16273.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Percent Similarity: 34.90% Conservative: 27
Best Local Similarity: 20.83% Mismatches: 70
Query Match: 6.81% Indels: 55
RESULT 1127
ID ABD32898 standard; cDNA; 4780 BP.
DE Human cancer-associated cDNA HR18-037.1.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Percent Similarity: 47.46% Conservative: 27
Best Local Similarity: 24.58% Mismatches: 47
Query Match: 6.81% Indels: 15
RESULT 1128
ID ACC81097 standard; mRNA; 5361 BP.
DE Human VLA-2 receptor alpha 2 subunit mRNA.
PN WO2003029277-A2.
PD 10-APR-2003.
PA (RIGE-) RIGEL PHARM INC.
Percent Similarity: 47.46% Conservative: 27
Best Local Similarity: 24.58% Mismatches: 47
Query Match: 6.81% Indels: 15
RESULT 1129
ID ABA00829 standard; cDNA; 5361 BP.
DE Alpha2 integrin coding sequence.
PN WO2002101070-A2.
PD 19-DEC-2002.
PA (RIGE-) RIGEL PHARM INC.
Percent Similarity: 47.46% Conservative: 27
Best Local Similarity: 24.58% Mismatches: 47
Query Match: 6.81% Indels: 15
RESULT 1130
ID ABX08832 standard; cDNA; 5361 BP.
DE Angiogenesis-associated human polynucleotide sequence #94.
PN WO200279492-A2.
PD 10-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Percent Similarity: 47.46% Conservative: 27
Best Local Similarity: 24.58% Mismatches: 47
Query Match: 6.81% Indels: 15
RESULT 1131
ID ADN39751 standard; cDNA; 5361 BP.
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:C123.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Percent Similarity: 47.46% Conservative: 27
Best Local Similarity: 24.58% Mismatches: 47
Query Match: 6.81% Indels: 15
RESULT 1132
ID ADR46606 standard; DNA; 5361 BP.
DE Cancer-associated protein coding sequence, SEQ ID 19.
PN WO2004073657-A2.
PD 02-SEP-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Percent Similarity: 47.46% Conservative: 27
Best Local Similarity: 24.58% Mismatches: 47
Query Match: 6.81% Indels: 15
RESULT 1133
ID ADI31992 standard; cDNA; 5373 BP.
DE Human cDNA #1318.
PN US6607879-B1.
PD 19-AUG-2003.
PA (INCY-) INCYTE CORP.
Percent Similarity: 47.46% Conservative: 27
Best Local Similarity: 24.58% Mismatches: 47
Query Match: 6.81% Indels: 15
RESULT 1134
ID ADJ74578 standard; mRNA; 5373 BP.
DE Human integrin alpha-2 subunit mRNA SEQ ID NO:2.
PN WO2004015104-A1.
PD 19-FEB-2004.
PA (NAGO-) NAGOYA IND SCI RES INST.
PA (GIFU-) GIFU INT INST BIOTECHNOLOGY.
Percent Similarity: 47.46% Conservative: 27
Best Local Similarity: 24.58% Mismatches: 47
Query Match: 6.81% Indels: 15
RESULT 1135
ID ADO44024 standard; DNA; 5373 BP.
DE Nucleotide sequence of human polynucleotide #1.
PN WO2004029243-A1.
PD 08-APR-2004.
PA (NAGO-) NAGOYA IND SCI RES INST.
PA (GIFU-) GIFU INT INST BIOTECHNOLOGY.
Percent Similarity: 47.46% Conservative: 27
Best Local Similarity: 24.58% Mismatches: 47
Query Match: 6.81% Indels: 15
RESULT 1136
ID AAS93426 standard; cDNA; 5375 BP.
DE DNA encoding novel human diagnostic protein #29230.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 47.46% Conservative: 27
Best Local Similarity: 24.58% Mismatches: 47
Query Match: 6.81% Indels: 15
RESULT 1137
ID ACN42598 standard; cDNA; 5622 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:1473.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Percent Similarity: 47.46% Conservative: 27
Best Local Similarity: 24.58% Mismatches: 47
Query Match: 6.81% Indels: 15
RESULT 1138
ID AAS94779 standard; DNA; 5701 BP.
DE Human DNA sequence #34 expressed during foam cell differentiation.
PN WO200177389-A2.
PD 18-OCT-2001.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 47.46% Conservative: 27
Best Local Similarity: 24.58% Mismatches: 47
Query Match: 6.81% Indels: 15
RESULT 1139
ID ABD32899 standard; cDNA; 7886 BP.
DE Human cancer-associated cDNA HR18-037.2.
PN WO2004074320-A2.

PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Percent Similarity: 47.46% Conservative: 27
Best Local Similarity: 24.58% Mismatches: 47
Query Match: 6.81% Indels: 15
RESULT 1140
ID AAK84027 standard; DNA; 11872 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38839.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 52.81% Conservative: 15
Best Local Similarity: 35.96% Mismatches: 31
Query Match: 6.81% Indels: 13
RESULT 1141
ID AAK66893 standard; DNA; 11872 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21705.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 52.81% Conservative: 15
Best Local Similarity: 35.96% Mismatches: 31
Query Match: 6.81% Indels: 13
RESULT 1142
ID AAZ35272 standard; DNA; 12571 BP.
DE Soybean retroelement Calypso 1-2.
PN WO9960842-A2.
PD 02-DEC-1999.
PA (WRIG/) WRIGHT D A.
PA (VOYT/) VOYTAS D F.
Percent Similarity: 57.35% Conservative: 20
Best Local Similarity: 27.94% Mismatches: 29
Query Match: 6.81% Indels: 0
RESULT 1143
ID ADQ59449 standard; DNA; 153740 BP.
DE Human cancer-associated (CA) gene sequence SEQ ID NO:85.
PN WO2004058288-A1.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Percent Similarity: 45.74% Conservative: 18
Best Local Similarity: 26.60% Mismatches: 37
Query Match: 6.81% Indels: 14
RESULT 1144
ID AAC48728 standard; DNA; 666 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 58545.
PN EP1033405-A2.
PD 06-SEP-2000.
Percent Similarity: 42.40% Conservative: 20
Best Local Similarity: 26.40% Mismatches: 33
Query Match: 6.76% Indels: 39
RESULT 1145
ID AAZ09494 standard; DNA; 794 BP.
DE Rat olfactory Ih ion channel DNA fragment #4.
PN WO9942574-A1.
PD 26-AUG-1999.
PA (KERJ) FORSCHUNGSZENTRUM JUELICH GMBH.
Percent Similarity: 37.89% Conservative: 33
Best Local Similarity: 23.35% Mismatches: 73
Query Match: 6.76% Indels: 69
RESULT 1146
ID ADM33294 standard; cDNA; 921 BP.
DE Human bitter taste receptor TAS2R41 encoding cDNA SEQ ID NO:8.
PN WO2004029087-A2.
PD 08-APR-2004.
PA (DEER-) DEUT INST ERNAEHRUNGSFORSCHUNG POTSDAM.
Percent Similarity: 36.87% Conservative: 26
Best Local Similarity: 23.74% Mismatches: 68
Query Match: 6.76% Indels: 57
RESULT 1147
ID AAS18172 standard; cDNA; 924 BP.
DE Human T2R71 (hT2R71) cDNA.
PN WO200177676-A1.
PD 18-OCT-2001.
PA (SENO-) SENOMYX INC.
Percent Similarity: 36.87% Conservative: 26
Best Local Similarity: 23.74% Mismatches: 68
Query Match: 6.76% Indels: 57
RESULT 1148
ID ABZ43209 standard; DNA; 924 BP.
DE Human GPCR polynucleotide SEQ ID NO 679.
PN WO200216548-A2.
PD 28-FEB-2002.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Percent Similarity: 36.87% Conservative: 26
Best Local Similarity: 23.74% Mismatches: 68
Query Match: 6.76% Indels: 57
RESULT 1149
ID ADR29249 standard; DNA; 924 BP.
DE Taste receptor modulation-related human T2R71 gene sequence SeqID188.
PN WO2004069191-A2.
PD 19-AUG-2004.
PA (SENO-) SENOMYX INC.
Percent Similarity: 36.87% Conservative: 26
Best Local Similarity: 23.74% Mismatches: 68
Query Match: 6.76% Indels: 57
RESULT 1150
ID ABK34698 standard; cDNA; 1239 BP.
DE Human cDNA for novel secreted protein, SEQ ID 467.
PN WO200177290-A2.
PD 18-OCT-2001.
PA (GEMY) GENETICS INST INC.
Percent Similarity: 39.38% Conservative: 35
Best Local Similarity: 21.24% Mismatches: 72
Query Match: 6.76% Indels: 45
RESULT 1151
ID ADI40346 standard; DNA; 1534 BP.
DE Human purified secretory polynucleotide (sptm), seq id 39.
PN WO2003062385-A2.
PD 31-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
PA (JONE/) JONES A L.
PA (DAHL/) DAHL C R.
PA (GIET/) GIETZEN D.
PA (CHIN/) CHINN J.
PA (DUFO/) DUFOUR G E.
PA (JACK/) JACKSON J L.
PA (YUJY/) YU J Y.
PA (TUAS/) TUASON O.
PA (YAPP/) YAP P E.
PA (AMSH/) AMSHEY S R.
PA (DAMT/) DAM T C.
PA (LIUT/) LIU T F.
PA (GERS/) GERSTIN E H.
PA (PERA/) PERALTA C H.
PA (LEWI/) LEWIS S A.
PA (CHEN/) CHEN A J.
PA (MARW/) MARWAHA R.
PA (LANR/) LAN R Y.
PA (URAS/) URASHKA M E.
PA (KRIS/) KRISTNAM S R.
PA (KOLL/) KOLLURU V.
PA (PANE/) PANESAR I S.
Percent Similarity: 39.69% Conservative: 18
Best Local Similarity: 25.95% Mismatches: 67
Query Match: 6.76% Indels: 12
RESULT 1152
ID AAH75169 standard; cDNA; 1561 BP.
DE Nucleotide sequence of a human enzyme.
PN WO200164896-A2.
PD 07-SEP-2001.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 39.77% Conservative: 27
Best Local Similarity: 24.43% Mismatches: 63
Query Match: 6.76% Indels: 43
RESULT 1153
ID ADB52998 standard; DNA; 1711 BP.

DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3540.
PN WO2003065993-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Percent Similarity: 43.48% Conservative: 22
Best Local Similarity: 24.35% Mismatches: 36
Query Match: 6.76% Indels: 30

RESULT 1154
ID ABT42063 standard; DNA; 1711 BP.
DE Toxicity modelling related rat gene SEQ ID No 1765.
PN WO200295000-A2.
PD 28-NOV-2002.
PA (GENE-) GENE LOGIC INC.
Percent Similarity: 43.48% Conservative: 22
Best Local Similarity: 24.35% Mismatches: 36
Query Match: 6.76% Indels: 30

RESULT 1155
ID ABQ72565 standard; cDNA; 1725 BP.
DE Human MDDT encoding cDNA SEQ ID NO 117.
PN WO200240715-A2.
PD 23-MAY-2002.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 39.13% Conservative: 24
Best Local Similarity: 21.74% Mismatches: 37
Query Match: 6.76% Indels: 47

RESULT 1156
ID AAS62254 standard; cDNA; 1727 BP.
DE cDNA sequence #41 encoding novel human secreted protein.
PN WO200177291-A2.
PD 18-OCT-2001.
PA (GEMY) GENETICS INST INC.
Percent Similarity: 39.13% Conservative: 24
Best Local Similarity: 21.74% Mismatches: 37
Query Match: 6.76% Indels: 47

RESULT 1157
ID ADQ87535 standard; cDNA; 2047 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #4413.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Percent Similarity: 39.77% Conservative: 27
Best Local Similarity: 24.43% Mismatches: 63
Query Match: 6.76% Indels: 43

RESULT 1158
ID ADI31439 standard; cDNA; 2149 BP.
DE Human cDNA #765.
PN US6607879-B1.
PD 19-AUG-2003.
PA (INCY-) INCYTE CORP.
Percent Similarity: 41.10% Conservative: 31
Best Local Similarity: 22.09% Mismatches: 48
Query Match: 6.76% Indels: 48

RESULT 1159
ID ADM91273 standard; DNA; 2545 BP.
DE DNA homologue of a human DNA sequence encoding a protein SeqID 628.
PN WO2004020595-A2.
PD 11-MAR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
PA (RIKE-) RIKEN INST PHYSICAL & CHEM RES.
PA (DNAF-) DNAFORM KK.
Percent Similarity: 45.78% Conservative: 15
Best Local Similarity: 27.71% Mismatches: 24
Query Match: 6.76% Indels: 21

RESULT 1160
ID ADF90852 standard; DNA; 2829 BP.
DE Human hepatic-fibrosis disease marker SEQ ID 314.
PN JP2003259877-A.
PD 16-SEP-2003.
PA (SUMU) SUMITOMO SEIYAKU KK.
Percent Similarity: 39.77% Conservative: 27
Best Local Similarity: 24.43% Mismatches: 63
Query Match: 6.76% Indels: 43

RESULT 1161
ID ADF90849 standard; DNA; 2829 BP.
DE Human hepatic-fibrosis disease marker SEQ ID 311.
PN JP2003259877-A.
PD 16-SEP-2003.
PA (SUMU) SUMITOMO SEIYAKU KK.
Percent Similarity: 39.77% Conservative: 27
Best Local Similarity: 24.43% Mismatches: 63
Query Match: 6.76% Indels: 43

RESULT 1162
ID ADA69512 standard; DNA; 3624 BP.
DE Rice gene, SEQ ID 2835.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Percent Similarity: 48.86% Conservative: 19
Best Local Similarity: 27.27% Mismatches: 30
Query Match: 6.76% Indels: 15

RESULT 1163
ID AAK84138 standard; DNA; 17758 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38950.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 39.69% Conservative: 18
Best Local Similarity: 25.95% Mismatches: 67
Query Match: 6.76% Indels: 12

RESULT 1164
ID ABD33201 standard; DNA; 36312 BP.
DE Murine cancer-associated (CA) gene MD07-031.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Percent Similarity: 36.65% Conservative: 33
Best Local Similarity: 19.37% Mismatches: 56
Query Match: 6.76% Indels: 65

RESULT 1165
ID ABZ22473 standard; DNA; 36521 BP.
DE Chimpanzee C68 adenovirus nucleotide sequence SEQ ID NO:33.
PN WO2003000851-A2.
PD 03-JAN-2003.
PA (UYPE-) UNIV PENNSYLVANIA.
Percent Similarity: 36.68% Conservative: 37
Best Local Similarity: 18.09% Mismatches: 77
Query Match: 6.76% Indels: 49

RESULT 1166
ID ADQ97563 standard; DNA; 79084 BP.
DE Human cancer associated sequence HD09-014, SEQ ID 540.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Percent Similarity: 50.67% Conservative: 14
Best Local Similarity: 32.00% Mismatches: 29
Query Match: 6.76% Indels: 9

RESULT 1167
Percent Similarity: 41.26% Conservative: 23
Best Local Similarity: 25.17% Mismatches: 59
Query Match: 6.76% Indels: 26

RESULT 1168
ID ABK83461 standard; cDNA; 128600 BP.
DE Human cDNA differentially expressed in granulocytic cells #32.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Percent Similarity: 40.43% Conservative: 14
Best Local Similarity: 25.53% Mismatches: 27
Query Match: 6.76% Indels: 29

RESULT 1169
ID ADM39522 standard; cDNA; 797 BP.
DE Chicken cDNA encoding survival of motor neuron, SMN.
PN US6646113-B1.
PD 11-NOV-2003.

PA (UYPE-) UNIV PENNSYLVANIA.
Percent Similarity: 38.38% Conservative: 14
Best Local Similarity: 24.24% Mismatches: 29
Query Match: 6.72% Indels: 32
RESULT 1170
ID ABN67635 standard; DNA; 870 BP.
DE Streptococcus polynucleotide SEQ ID NO 3183.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Percent Similarity: 40.94% Conservative: 25
Best Local Similarity: 24.16% Mismatches: 68
Query Match: 6.72% Indels: 20
RESULT 1171
ID ABK13033 standard; cDNA; 895 BP.
DE DNA encoding mouse B7-like protein, B7-L_m2.
PN WO200200710-A2.
PD 03-JAN-2002.
PA (AMGE-) AMGEN INC.
Percent Similarity: 40.09% Conservative: 35
Best Local Similarity: 23.96% Mismatches: 71
Query Match: 6.72% Indels: 59
RESULT 1172
ID ADO05741 standard; cDNA; 1122 BP.
DE Human endothelial differentiation gene 2 (EDG2) coding sequence.
PN EP1418185-A1.
PD 12-MAY-2004.
PA (AVET) AVENTIS PHARMA DEUT GMBH.
Percent Similarity: 47.12% Conservative: 25
Best Local Similarity: 23.08% Mismatches: 42
Query Match: 6.72% Indels: 14
RESULT 1173
ID ADS47615 standard; cDNA; 1287 BP.
DE Bacterial polynucleotide #2358.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Percent Similarity: 35.61% Conservative: 27
Best Local Similarity: 22.44% Mismatches: 71
Query Match: 6.72% Indels: 61
RESULT 1174
ID ADO80507 standard; DNA; 1290 BP.
DE Schizosaccharomyces pombe metY DNA.
PN DE10239082-A1.
PD 04-MAR-2004.
PA (BADI) BASF AG.
Percent Similarity: 35.61% Conservative: 27
Best Local Similarity: 22.44% Mismatches: 71
Query Match: 6.72% Indels: 61
RESULT 1175
ID ABN67682 standard; DNA; 1482 BP.
DE Streptococcus polynucleotide SEQ ID NO 3277.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Percent Similarity: 34.92% Conservative: 22
Best Local Similarity: 23.28% Mismatches: 57
Query Match: 6.72% Indels: 66
RESULT 1176
ID AAS87336 standard; cDNA; 1515 BP.
DE DNA encoding novel human diagnostic protein #23140.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 38.89% Conservative: 21
Best Local Similarity: 24.31% Mismatches: 58
Query Match: 6.72% Indels: 30

RESULT 1177
ID ADT48563 standard; cDNA; 1770 BP.
DE Bacterial polynucleotide #23314.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Percent Similarity: 33.00% Conservative: 19
Best Local Similarity: 23.65% Mismatches: 49
Query Match: 6.72% Indels: 88
RESULT 1178
ID ABA95063 standard; cDNA; 1919 BP.
DE Human speckled 110 splice variant (Sp110b) encoding cDNA.
PN WO200208383-A2.
PD 31-JAN-2002.
PA (GEHO) GEN HOSPITAL CORP.
Percent Similarity: 39.72% Conservative: 23
Best Local Similarity: 23.40% Mismatches: 46
Query Match: 6.72% Indels: 41
RESULT 1179
ID ADR14348 standard; DNA; 1919 BP.
DE Human NF-kappaB pathway-associated gene SeqID349.
PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Percent Similarity: 39.72% Conservative: 23
Best Local Similarity: 23.40% Mismatches: 46
Query Match: 6.72% Indels: 41
RESULT 1180
ID ACA20999 standard; DNA; 2304 BP.
DE Prokaryotic essential gene #2656.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 43.09% Conservative: 24
Best Local Similarity: 23.58% Mismatches: 41
Query Match: 6.72% Indels: 29
RESULT 1181
ID AAZ58295 standard; DNA; 2862 BP.
DE Sorghum resistance gene homologue S6-1 coding region.
PN WO200004155-A2.
PD 27-JAN-2000.
PA (PURD) PURDUE RES FOUND.
Percent Similarity: 44.93% Conservative: 10
Best Local Similarity: 30.43% Mismatches: 28
Query Match: 6.72% Indels: 10
RESULT 1182
ID AAZ58294 standard; DNA; 2954 BP.
DE Sorghum resistance gene homologue S6-1 coding region.
PN WO200004155-A2.
PD 27-JAN-2000.
PA (PURD) PURDUE RES FOUND.
Percent Similarity: 44.93% Conservative: 10
Best Local Similarity: 30.43% Mismatches: 28
Query Match: 6.72% Indels: 10
RESULT 1183
ID ADH18920 standard; cDNA; 3231 BP.
DE Human cell adhesion and extracellular matrix CADECM-16 cDNA - SEQ 47.
PN WO2003094843-A2.
PD 20-NOV-2003.
PA (INCY-) INCYTE CORP.
Percent Similarity: 52.86% Conservative: 17
Best Local Similarity: 28.57% Mismatches: 21
Query Match: 6.72% Indels: 12
RESULT 1184
ID AAZ58293 standard; DNA; 6760 BP.
DE Sorghum resistance gene homologue S6-1.
PN WO200004155-A2.
PD 27-JAN-2000.
PA (PURD) PURDUE RES FOUND.

Percent Similarity: 44.93% Conservative: 10
Best Local Similarity: 30.43% Mismatches: 28
Query Match: 6.72% Indels: 10
RESULT 1185
ID ADR84309 standard; DNA; 8415 BP.
DE Aspergillus fumigatus essential gene genomic sequence #120.
PN WO2004067709-A2.
PD 12-AUG-2004.
PA (ELIT-) ELITRA PHARM INC.
PA (ELIT-) ELITRA CANADA LTD.
Percent Similarity: 32.89% Conservative: 29
Best Local Similarity: 20.00% Mismatches: 62
Query Match: 6.72% Indels: 89
RESULT 1186
ID AAK69113 standard; DNA; 10553 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23925.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 42.97% Conservative: 22
Best Local Similarity: 25.78% Mismatches: 40
Query Match: 6.72% Indels: 33
RESULT 1187
ID ABA16395 standard; DNA; 10553 BP.
DE Human nervous system related polynucleotide SEQ ID NO 8726.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 42.97% Conservative: 22
Best Local Similarity: 25.78% Mismatches: 40
Query Match: 6.72% Indels: 33
RESULT 1188
ID AAF28534 standard; DNA; 39003 BP.
DE Genomic fragment #21.
PN WO200078968-A2.
PD 28-DEC-2000.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 38.30% Conservative: 44
Best Local Similarity: 19.57% Mismatches: 81
Query Match: 6.72% Indels: 64
RESULT 1189
ID ACN44772 standard; DNA; 45152 BP.
DE Mouse genomic sequence mCG3775.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Percent Similarity: 33.94% Conservative: 23
Best Local Similarity: 20.00% Mismatches: 33
Query Match: 6.72% Indels: 76
RESULT 1190
ID ADQ97934 standard; DNA; 69648 BP.
DE Human cancer associated sequence HD11-025, SEQ ID 911.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Percent Similarity: 37.79% Conservative: 25
Best Local Similarity: 23.26% Mismatches: 64
Query Match: 6.72% Indels: 43
RESULT 1191
Percent Similarity: 45.71% Conservative: 23
Best Local Similarity: 23.81% Mismatches: 45
Query Match: 6.72% Indels: 12
RESULT 1192
Percent Similarity: 40.94% Conservative: 25
Best Local Similarity: 24.16% Mismatches: 68
Query Match: 6.72% Indels: 20
RESULT 1193
Percent Similarity: 40.82% Conservative: 23
Best Local Similarity: 25.17% Mismatches: 42
Query Match: 6.72% Indels: 46
RESULT 1194
Percent Similarity: 40.82% Conservative: 23
Best Local Similarity: 25.17% Mismatches: 42
Query Match: 6.72% Indels: 46
RESULT 1195
ID ACN44850 standard; DNA; 142318 BP.
DE Human genomic sequence hCG33122.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Percent Similarity: 45.00% Conservative: 19
Best Local Similarity: 26.00% Mismatches: 33
Query Match: 6.72% Indels: 22
RESULT 1196
ID ADS01853 standard; DNA; 375 BP.
DE Staphylococcus epidermis polynucleotide seqid 1148.
PN US2004147734-A1.
PD 29-JUL-2004.
PA (DOUC/) DOUCETTE-STAMM L.
PA (BUSH/) BUSH D.
Percent Similarity: 43.41% Conservative: 17
Best Local Similarity: 30.23% Mismatches: 25
Query Match: 6.67% Indels: 48
RESULT 1197
ID ACH42016 standard; cDNA; 453 BP.
DE Human foetal brain cDNA #3383.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Percent Similarity: 48.96% Conservative: 20
Best Local Similarity: 28.12% Mismatches: 20
Query Match: 6.67% Indels: 29
RESULT 1198
ID ABL03163 standard; cDNA; 465 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 3971.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 53.03% Conservative: 12
Best Local Similarity: 34.85% Mismatches: 24
Query Match: 6.67% Indels: 7
RESULT 1199
ID ABN92099 standard; DNA; 753 BP.
DE Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:1562.
PN US6380370-B1.
PD 30-APR-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 43.41% Conservative: 17
Best Local Similarity: 30.23% Mismatches: 25
Query Match: 6.67% Indels: 48
RESULT 1200
ID AAH66699 standard; DNA; 804 BP.
DE C glutamicum coding sequence fragment SEQ ID NO: 1734.
PN EP1108790-A2.
PD 20-JUN-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Percent Similarity: 41.12% Conservative: 15
Best Local Similarity: 27.10% Mismatches: 53
Query Match: 6.67% Indels: 10
RESULT 1201
ID ACA00849 standard; DNA; 804 BP.
DE C. glutamicum derived ORF SEQ ID 840.
PN DE10128510-A1.
PD 19-DEC-2002.
PA (DEGS) DEGUSSA AG.
Percent Similarity: 41.12% Conservative: 15
Best Local Similarity: 27.10% Mismatches: 53
Query Match: 6.67% Indels: 10
RESULT 1202
ID ADS46926 standard; cDNA; 825 BP.
DE Bacterial polynucleotide #1669.
PN US2003233675-A1.

PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Percent Similarity: 36.36% Conservative: 17
Best Local Similarity: 22.31% Mismatches: 39
Query Match: 6.67% Indels: 39
RESULT 1203
ID ABV94489 standard; cDNA; 900 BP.
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:3.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.51% Conservative: 29
Best Local Similarity: 21.60% Mismatches: 57
Query Match: 6.67% Indels: 41
RESULT 1204
ID ADM18638 standard; cDNA; 900 BP.
DE Human co-stimulatory molecule encoding cDNA SEQ ID NO:3.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.51% Conservative: 29
Best Local Similarity: 21.60% Mismatches: 57
Query Match: 6.67% Indels: 41
RESULT 1205
ID ABV94548 standard; cDNA; 912 BP.
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:109.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.51% Conservative: 29
Best Local Similarity: 21.60% Mismatches: 57
Query Match: 6.67% Indels: 41
RESULT 1206
ID ABV94561 standard; cDNA; 912 BP.
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:122.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.51% Conservative: 29
Best Local Similarity: 21.60% Mismatches: 57
Query Match: 6.67% Indels: 41
RESULT 1207
ID ADM18744 standard; cDNA; 912 BP.
DE Human co-stimulatory molecule encoding cDNA SEQ ID NO:109.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.51% Conservative: 29
Best Local Similarity: 21.60% Mismatches: 57
Query Match: 6.67% Indels: 41
RESULT 1208
ID ADM18757 standard; cDNA; 912 BP.
DE Human co-stimulatory molecule encoding cDNA SEQ ID NO:122.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.51% Conservative: 29
Best Local Similarity: 21.60% Mismatches: 57
Query Match: 6.67% Indels: 41
RESULT 1209
ID ABV94560 standard; cDNA; 913 BP.
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:121.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.51% Conservative: 29
Best Local Similarity: 21.60% Mismatches: 57
Query Match: 6.67% Indels: 41
RESULT 1210
ID ADM18756 standard; cDNA; 913 BP.
DE Human co-stimulatory molecule encoding cDNA SEQ ID NO:121.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.51% Conservative: 29
Best Local Similarity: 21.60% Mismatches: 57
Query Match: 6.67% Indels: 41
RESULT 1211
ID ADS01537 standard; DNA; 915 BP.
DE Staphylococcus epidermis polynucleotide seqid 832.
PN US2004147734-A1.
PD 29-JUL-2004.
PA (DOUC/) DOUCETTE-STAMM L.
PA (BUSH/) BUSH D.
Percent Similarity: 43.41% Conservative: 17
Best Local Similarity: 30.23% Mismatches: 25
Query Match: 6.67% Indels: 48
RESULT 1212
ID ADL65970 standard; DNA; 934 BP.
DE C. glutamicum RXA-associated DNA #164.
PN DE10154177-A1.
PD 08-MAY-2003.
PA (BADI) BASF AG.
Percent Similarity: 41.12% Conservative: 15
Best Local Similarity: 27.10% Mismatches: 53
Query Match: 6.67% Indels: 10
RESULT 1213
ID ADM42775 standard; DNA; 942 BP.
DE DNA encoding the murine carvone receptor car-c5 SeqID 19.
PN WO2003100057-A1.
PD 04-DEC-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
Percent Similarity: 40.61% Conservative: 32
Best Local Similarity: 24.37% Mismatches: 79
Query Match: 6.67% Indels: 38
RESULT 1214
ID AAS69112 standard; cDNA; 1002 BP.
DE DNA encoding novel human diagnostic protein #4916.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 39.60% Conservative: 26
Best Local Similarity: 22.15% Mismatches: 60
Query Match: 6.67% Indels: 30
RESULT 1215
ID ABX65804 standard; DNA; 1024 BP.
DE Helicobacter pylori selected interacting domain (SID) DNA #403.
PN WO200266501-A2.
PD 29-AUG-2002.
PA (HYBR-) HYBRIGENICS.
PA (INSP) INST PASTEUR.
Percent Similarity: 43.14% Conservative: 15
Best Local Similarity: 28.43% Mismatches: 42
Query Match: 6.67% Indels: 16
RESULT 1216
ID ACD06271 standard; cDNA; 1034 BP.
DE Human cDNA encoding protein NOV36j.
PN WO2003023008-A2.
PD 20-MAR-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 38.80% Conservative: 31
Best Local Similarity: 21.86% Mismatches: 53
Query Match: 6.67% Indels: 59
RESULT 1217
ID AAA56702 standard; DNA; 1046 BP.
DE EcoRI/XbaI fragment from pscFv24-PDGFR DNA sequence SEQ ID NO:163.
PN WO200023593-A2.
PD 27-APR-2000.
PA (FRAU) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.
Percent Similarity: 37.37% Conservative: 36
Best Local Similarity: 18.42% Mismatches: 64
Query Match: 6.67% Indels: 55

RESULT 1218
ID ABQ76938 standard; DNA; 1188 BP.
DE Muvbeta-hucbeta-huCD3epsilon fusion construct DNA.
PN DE10109854-A1.
PD 12-SEP-2002.
PA (STAN/) STANISLAWSKI T.
Percent Similarity: 42.76% Conservative: 27
Best Local Similarity: 24.14% Mismatches: 61
Query Match: 6.67% Indels: 22
RESULT 1219
ID ADF00600 standard; DNA; 1209 BP.
DE Bacterial polynucleotide #885.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 44.53% Conservative: 32
Best Local Similarity: 21.17% Mismatches: 37
Query Match: 6.67% Indels: 39
RESULT 1220
ID AAS41209 standard; cDNA; 1270 BP.
DE cDNA encoding novel human enzyme polypeptide #425.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 39.20% Conservative: 26
Best Local Similarity: 24.43% Mismatches: 64
Query Match: 6.67% Indels: 43
RESULT 1221
ID ABA06628 standard; cDNA; 1270 BP.
DE Human cDNA SEQ ID NO: 294.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 39.20% Conservative: 26
Best Local Similarity: 24.43% Mismatches: 64
Query Match: 6.67% Indels: 43
RESULT 1222
ID ABV83965 standard; cDNA; 1270 BP.
DE Human polynucleotide SEQ ID NO 294.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Percent Similarity: 39.20% Conservative: 26
Best Local Similarity: 24.43% Mismatches: 64
Query Match: 6.67% Indels: 43
RESULT 1223
ID ACA29487 standard; DNA; 1272 BP.
DE Prokaryotic essential gene #11144.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 45.00% Conservative: 11
Best Local Similarity: 31.25% Mismatches: 31
Query Match: 6.67% Indels: 13
RESULT 1224
ID ADP98747 standard; DNA; 1353 BP.
DE C. albicans specific gene, orf19.3956, DNA sequence.
PN WO2004056965-A2.
PD 08-JUL-2004.
PA (ELIT-) ELITRA PHARM INC.
PA (ELIT-) ELITRA CANADA LTD.
Percent Similarity: 41.67% Conservative: 18
Best Local Similarity: 28.03% Mismatches: 60
Query Match: 6.67% Indels: 17
RESULT 1225
ID ACC61861 standard; DNA; 1398 BP.
DE Gene sequence #SEQ ID 2504.
PN EP1258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZOME AG.
Percent Similarity: 33.50% Conservative: 27
Best Local Similarity: 20.00% Mismatches: 60
Query Match: 6.67% Indels: 73
RESULT 1226
ID ADK65005 standard; DNA; 1398 BP.
DE Disease treating protein complex-derived gene #1514.
PN EP1338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Percent Similarity: 33.50% Conservative: 27
Best Local Similarity: 20.00% Mismatches: 60
Query Match: 6.67% Indels: 73
RESULT 1227
ID ACA53884 standard; DNA; 1488 BP.
DE Prokaryotic essential gene #35541.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 35.93% Conservative: 20
Best Local Similarity: 23.95% Mismatches: 45
Query Match: 6.67% Indels: 62
RESULT 1228
ID ADS57032 standard; cDNA; 1494 BP.
DE Bacterial polynucleotide #9019.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Percent Similarity: 37.69% Conservative: 24
Best Local Similarity: 19.23% Mismatches: 64
Query Match: 6.67% Indels: 17
RESULT 1229
ID AAH52763 standard; DNA; 1605 BP.
DE S. epidermidis open reading frame nucleotide sequence SEQ ID NO:919.
PN WO200134809-A2.
PD 17-MAY-2001.
PA (GLAX) GLAXO GROUP LTD.
Percent Similarity: 43.41% Conservative: 17
Best Local Similarity: 30.23% Mismatches: 25
Query Match: 6.67% Indels: 48
RESULT 1230
ID AAX14344 standard; DNA; 1631 BP.
DE H. pylori GHPO 265 gene.
PN WO9843478-A1.
PD 08-OCT-1998.
PA (INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 43.14% Conservative: 15
Best Local Similarity: 28.43% Mismatches: 42
Query Match: 6.67% Indels: 16
RESULT 1231
ID ABV99336 standard; DNA; 1681 BP.
DE Human NOV3a coding sequence.
PN WO200272771-A2.
PD 19-SEP-2002.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 37.00% Conservative: 34
Best Local Similarity: 20.00% Mismatches: 48
Query Match: 6.67% Indels: 78
RESULT 1232
ID ACH95608 standard; DNA; 1689 BP.
DE Klebsiella pneumoniae polynucleotide seqid 1403.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 35.75% Conservative: 33
Best Local Similarity: 19.81% Mismatches: 84
Query Match: 6.67% Indels: 49
RESULT 1233
ID ABK90489 standard; cDNA; 1822 BP.
DE Human transporter protein cDNA.

PN US2002082191-A1.
PD 27-JUN-2002.
PA (GUEG/) GUEGLER K.
PA (BRAN/) BRANDON R C.
PA (MERK/) MERKULOV G V.
PA (KETC/) KETCHUM K A.
PA (DFRA/) DI FRANCESCO V.
PA (BEAS/) BEASLEY E M.
Percent Similarity: 37.00% Conservative: 34
Best Local Similarity: 20.00% Mismatches: 48
Query Match: 6.67% Indels: 78
RESULT 1234
ID AAV33673 standard; DNA; 1949 BP.
DE Candida parapsilosis IPC synthase encoding DNA.
PN EP872485-A2.
PD 21-OCT-1998.
PA (ELIL) LILLY & CO ELI.
Percent Similarity: 48.08% Conservative: 27
Best Local Similarity: 22.12% Mismatches: 32
Query Match: 6.67% Indels: 22
RESULT 1235
ID AAH73591 standard; DNA; 1949 BP.
DE Candida parapsilosis IPC synthase gene.
PN US2001012615-A1.
PD 09-AUG-2001.
PA (HEID/) HEIDLER S A.
PA (RADD/) RADDING J A.
Percent Similarity: 48.08% Conservative: 27
Best Local Similarity: 22.12% Mismatches: 32
Query Match: 6.67% Indels: 22
RESULT 1236
ID ACA62411 standard; DNA; 1949 BP.
DE C. parapsilosis inositolphosphoryl ceramide synthase gene.
PN US2003022343-A1.
PD 30-JAN-2003.
PA (HEID/) HEIDLER S A.
PA (RADD/) RADDING J A.
Percent Similarity: 48.08% Conservative: 27
Best Local Similarity: 22.12% Mismatches: 32
Query Match: 6.67% Indels: 22
RESULT 1237
ID ACA62358 standard; DNA; 1949 BP.
DE Gene encoding C. parapsilosis inositolphosphoryl ceramide (IPC) synthase.
PN US2003022342-A1.
PD 30-JAN-2003.
PA (HEID/) HEIDLER S A.
PA (RADD/) RADDING J A.
Percent Similarity: 48.08% Conservative: 27
Best Local Similarity: 22.12% Mismatches: 32
Query Match: 6.67% Indels: 22
RESULT 1238
ID AAS82555 standard; cDNA; 2182 BP.
DE DNA encoding novel human diagnostic protein #18359.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 38.81% Conservative: 26
Best Local Similarity: 25.87% Mismatches: 66
Query Match: 6.67% Indels: 57
RESULT 1239
ID AAT85403 standard; cDNA; 2625 BP.
DE Human cadherin-11 coding sequence.
PN US5646250-A.
PD 08-JUL-1997.
PA (DOHE-) DOHENY EYE INST.
Percent Similarity: 40.00% Conservative: 26
Best Local Similarity: 20.74% Mismatches: 45
Query Match: 6.67% Indels: 36
RESULT 1240
ID AAT61925 standard; cDNA; 2625 BP.
DE Full length human cadherin-11 cDNA.
PN US5597725-A.
PD 28-JAN-1997.
PA (DOHE-) DOHENY EYE INST.
Percent Similarity: 40.00% Conservative: 26
Best Local Similarity: 20.74% Mismatches: 45
Query Match: 6.67% Indels: 36
RESULT 1241
ID AAV83124 standard; cDNA; 2625 BP.
DE Cadherin-11 cDNA.
PN WO9849560-A1.
PD 05-NOV-1998.
PA (UYBR-) UNIV BRITISH COLUMBIA.
Percent Similarity: 40.00% Conservative: 26
Best Local Similarity: 20.74% Mismatches: 45
Query Match: 6.67% Indels: 36
RESULT 1242
ID AAF55586 standard; DNA; 2625 BP.
DE Nucleotide sequence of a human cadherin-11 polypeptide.
PN WO200117557-A1.
PD 15-MAR-2001.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
Percent Similarity: 40.00% Conservative: 26
Best Local Similarity: 20.74% Mismatches: 45
Query Match: 6.67% Indels: 36
RESULT 1243
ID ADP18641 standard; cDNA; 2625 BP.
DE Human TAT400 cDNA used to treat cancer SeqID 1.
PN WO2004045516-A2.
PD 03-JUN-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 40.00% Conservative: 26
Best Local Similarity: 20.74% Mismatches: 45
Query Match: 6.67% Indels: 36
RESULT 1244
ID ADP26918 standard; cDNA; 2625 BP.
DE Human OB-cadherin encoding cDNA SEQ ID NO:19.
PN EP1428893-A2.
PD 16-JUN-2004.
PA (SPRE/) SPRECHER E.
PA (BERG/) BERGMAN R.
Percent Similarity: 40.00% Conservative: 26
Best Local Similarity: 20.74% Mismatches: 45
Query Match: 6.67% Indels: 36
RESULT 1245
ID ADR24809 standard; DNA; 2625 BP.
DE Breast cancer prognosis marker #670.
PN WO2004065545-A2.
PD 05-AUG-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
PA (NECA-) NETHERLANDS CANCER INST.
Percent Similarity: 40.00% Conservative: 26
Best Local Similarity: 20.74% Mismatches: 45
Query Match: 6.67% Indels: 36
RESULT 1246
ID ABV23234 standard; cDNA; 2828 BP.
DE Human prostate expression marker cDNA 23225.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Percent Similarity: 40.48% Conservative: 31
Best Local Similarity: 22.02% Mismatches: 40
Query Match: 6.67% Indels: 61
RESULT 1247
ID ABV29077 standard; cDNA; 2828 BP.
DE Human prostate expression marker cDNA 29068.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Percent Similarity: 40.48% Conservative: 31
Best Local Similarity: 22.02% Mismatches: 40
Query Match: 6.67% Indels: 61
RESULT 1248
ID ABN59956 standard; cDNA; 2828 BP.
DE Novel human coding sequence SEQ ID NO: 367.
PN WO200222660-A2.

PD 21-MAR-2002.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 40.48% Conservative: 31
Best Local Similarity: 22.02% Mismatches: 40
Query Match: 6.67% Indels: 61
RESULT 1249
ID ACN91315 standard; DNA; 2828 BP.
DE Breast cancer related marker, seq id 12465.
PN US2003099974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Percent Similarity: 40.48% Conservative: 31
Best Local Similarity: 22.02% Mismatches: 40
Query Match: 6.67% Indels: 61
RESULT 1250
ID AAH54530 standard; DNA; 2998 BP.
DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:3894.
PN WO200134809-A2.
PD 17-MAY-2001.
PA (GLAX) GLAXO GROUP LTD.
Percent Similarity: 43.41% Conservative: 17
Best Local Similarity: 30.23% Mismatches: 25
Query Match: 6.67% Indels: 48
RESULT 1251
ID AAH54434 standard; DNA; 3118 BP.
DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:3798.
PN WO200134809-A2.
PD 17-MAY-2001.
PA (GLAX) GLAXO GROUP LTD.
Percent Similarity: 43.41% Conservative: 17
Best Local Similarity: 30.23% Mismatches: 25
Query Match: 6.67% Indels: 48
RESULT 1252
ID ABX63597 standard; cDNA; 3403 BP.
DE Human cDNA #597 differentially expressed in activated vascular tissue.
PN US2002137081-A1.
PD 26-SEP-2002.
PA (BAND/) BANDMAN O.
Percent Similarity: 40.00% Conservative: 26
Best Local Similarity: 20.74% Mismatches: 45
Query Match: 6.67% Indels: 36
RESULT 1253
ID ADJ56330 standard; cDNA; 3403 BP.
DE Human cDNA differentially expressed in MYCN activated cells SeqID 136.
PN US2003119009-A1.
PD 26-JUN-2003.
PA (STUA/) STUART S G.
PA (NUCH/) NUCHTERN J G.
PA (PLON/) PLON S E.
PA (SHOH/) SHOHET J M.
Percent Similarity: 40.00% Conservative: 26
Best Local Similarity: 20.74% Mismatches: 45
Query Match: 6.67% Indels: 36
RESULT 1254
ID AAA70202 standard; DNA; 3501 BP.
DE Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:335.
PN WO200025728-A2.
PD 11-MAY-2000.
PA (HOFF/) HOFFMAN S.
PA (CARU/) CARUCCI D.
PA (GARD/) GARDNER M.
PA (VENT/) VENTER J C.
Percent Similarity: 40.00% Conservative: 26
Best Local Similarity: 22.07% Mismatches: 56
Query Match: 6.67% Indels: 31
RESULT 1255
ID ADR48217 standard; cDNA; 3654 BP.
DE Human cadherin 11 type 2 OB-cadherin encoding cDNA SEQ:5.
PN WO2004074510-A1.
PD 02-SEP-2004.
PA (GARV-) GARVAN INST MEDICAL RES.
Percent Similarity: 40.00% Conservative: 26
Best Local Similarity: 20.74% Mismatches: 45
Query Match: 6.67% Indels: 36
RESULT 1256
ID ADH17152 standard; cDNA; 3661 BP.
DE Human OB-cadherin-1 cDNA.
PN WO2003097854-A2.
PD 27-NOV-2003.
PA (SUGE-) SUGEN INC.
Percent Similarity: 40.00% Conservative: 26
Best Local Similarity: 20.74% Mismatches: 45
Query Match: 6.67% Indels: 36
RESULT 1257
ID AAQ44392 standard; cDNA to mRNA; 3712 BP.
DE Sequence of human OSF-4-1 cDNA.
PN EP585801-A2.
PD 09-MAR-1994.
PA (FARH) HOECHST JAPAN LTD.
Percent Similarity: 40.00% Conservative: 26
Best Local Similarity: 20.74% Mismatches: 45
Query Match: 6.67% Indels: 36
RESULT 1258
ID ABA96103 standard; cDNA; 3767 BP.
DE Human membrane transporter protein 58289 cDNA.
PN WO200190146-A2.
PD 29-NOV-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Percent Similarity: 37.00% Conservative: 34
Best Local Similarity: 20.00% Mismatches: 48
Query Match: 6.67% Indels: 78
RESULT 1259
ID ACN91063 standard; DNA; 3925 BP.
DE Breast cancer related marker, seq id 12213.
PN US2003099974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Percent Similarity: 37.00% Conservative: 34
Best Local Similarity: 20.00% Mismatches: 48
Query Match: 6.67% Indels: 78
RESULT 1260
ID ABL03162 standard; cDNA; 5189 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 3968.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 53.03% Conservative: 12
Best Local Similarity: 34.85% Mismatches: 24
Query Match: 6.67% Indels: 7
RESULT 1261
ID AAK69142 standard; DNA; 12997 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23954.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 41.18% Conservative: 22
Best Local Similarity: 25.00% Mismatches: 53
Query Match: 6.67% Indels: 27
RESULT 1262
ID AAZ93705 standard; DNA; 18402 BP.
DE CYB5RP fatty acid desaturase gene.
PN WO200021557-A1.
PD 20-APR-2000.
PA (MERI) MERCK & CO INC.
Percent Similarity: 38.27% Conservative: 25
Best Local Similarity: 22.84% Mismatches: 55
Query Match: 6.67% Indels: 45
RESULT 1263
ID ABX13172 standard; DNA; 65464 BP.
DE Human gene encoding a Noelin-1-like secreted protein.
PN US2002173459-A1.
PD 21-NOV-2002.
PA (PEKE) PE CORP NY.
Percent Similarity: 43.69% Conservative: 14
Best Local Similarity: 30.10% Mismatches: 37
Query Match: 6.67% Indels: 21

RESULT 1264
ID ABD32542 standard; DNA; 108845 BP.
DE Mouse cancer-associated genomic DNA MD7-024.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Percent Similarity: 39.71% Conservative: 15
Best Local Similarity: 28.68% Mismatches: 33
Query Match: 6.67% Indels: 50
RESULT 1265
Percent Similarity: 36.44% Conservative: 33
Best Local Similarity: 21.78% Mismatches: 76
Query Match: 6.67% Indels: 67
RESULT 1266
ID AAH68529 standard; DNA; 349980 BP.
DE C glutamicum coding sequence fragment SEQ ID NO: 7064.
PN EP1108790-A2.
PD 20-JUN-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Percent Similarity: 41.12% Conservative: 15
Best Local Similarity: 27.10% Mismatches: 53
Query Match: 6.67% Indels: 10
RESULT 1267
ID ACH32505 standard; cDNA; 452 BP.
DE Human endothelial cell cDNA #638.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Percent Similarity: 36.03% Conservative: 23
Best Local Similarity: 19.12% Mismatches: 45
Query Match: 6.62% Indels: 42
RESULT 1268
ID ADF03528 standard; DNA; 588 BP.
DE Bacterial polynucleotide #3813.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 40.61% Conservative: 32
Best Local Similarity: 21.21% Mismatches: 66
Query Match: 6.62% Indels: 32
RESULT 1269
ID AAT03017 standard; cDNA to mRNA; 618 BP.
DE Endothelial cell polypeptide coding sequence.
PN EP682113-A2.
PD 15-NOV-1995.
PA (ONOY) ONO PHARM CO LTD.
Percent Similarity: 36.03% Conservative: 23
Best Local Similarity: 19.12% Mismatches: 45
Query Match: 6.62% Indels: 42
RESULT 1270
ID ADR59253 standard; cDNA; 794 BP.
DE Cotton cDNA sequence, SEQ ID 34.
PN US2004181830-A1.
PD 16-SEP-2004.
PA (KOVA/) KOVALIC D K.
PA (ZHOU/) ZHOU Y.
PA (CAOY/) CAO Y.
Percent Similarity: 45.00% Conservative: 19
Best Local Similarity: 26.00% Mismatches: 29
Query Match: 6.62% Indels: 26
RESULT 1271
ID AAH33705 standard; cDNA; 813 BP.
DE Human colon cancer antigen encoding cDNA SEQ ID NO:761.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 34.12% Conservative: 21
Best Local Similarity: 21.76% Mismatches: 64
Query Match: 6.62% Indels: 48

RESULT 1272
ID ACA33175 standard; DNA; 864 BP.
DE Prokaryotic essential gene #14832.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 46.67% Conservative: 18
Best Local Similarity: 29.52% Mismatches: 42
Query Match: 6.62% Indels: 15
RESULT 1273
ID ADJ33272 standard; DNA; 867 BP.
DE Enterococcus faecalis ORF1 encoding DNA SEQ ID NO:32.
PN WO2003056295-A2.
PD 10-JUL-2003.
PA (GEHO) GEN HOSPITAL CORP.
Percent Similarity: 46.67% Conservative: 18
Best Local Similarity: 29.52% Mismatches: 42
Query Match: 6.62% Indels: 15
RESULT 1274
ID ADF61795 standard; cDNA; 914 BP.
DE Human D1-1 cDNA.
PN WO2003091447-A2.
PD 06-NOV-2003.
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
Percent Similarity: 36.03% Conservative: 23
Best Local Similarity: 19.12% Mismatches: 45
Query Match: 6.62% Indels: 42
RESULT 1275
ID ADJ67700 standard; DNA; 935 BP.
DE Kif1C DNA #16.
PN US2004038222-A1.
PD 26-FEB-2004.
PA (DIET/) DIETRICH W F.
PA (WATT/) WATTERS J W.
Percent Similarity: 45.95% Conservative: 22
Best Local Similarity: 26.13% Mismatches: 32
Query Match: 6.62% Indels: 28
RESULT 1276
ID AAT03018 standard; cDNA to mRNA; 983 BP.
DE Endothelial cell polypeptide full length sequence.
PN EP682113-A2.
PD 15-NOV-1995.
PA (ONOY) ONO PHARM CO LTD.
Percent Similarity: 36.03% Conservative: 23
Best Local Similarity: 19.12% Mismatches: 45
Query Match: 6.62% Indels: 42
RESULT 1277
ID ABK35835 standard; cDNA; 983 BP.
DE cDNA sequence #226 encoding novel human secreted protein.
PN WO200177289-A2.
PD 18-OCT-2001.
PA (GEMY) GENETICS INST INC.
Percent Similarity: 36.03% Conservative: 23
Best Local Similarity: 19.12% Mismatches: 45
Query Match: 6.62% Indels: 42
RESULT 1278
ID ADE77092 standard; cDNA; 1002 BP.
DE Human cDNA differentially expressed in a liver disorder #190.
PN US2003108871-A1.
PD 12-JUN-2003.
PA (KASE/) KASER M R.
Percent Similarity: 36.03% Conservative: 23
Best Local Similarity: 19.12% Mismatches: 45
Query Match: 6.62% Indels: 42
RESULT 1279
ID ACC69471 standard; cDNA; 1030 BP.
DE Human malignant neoplasm related protein encoding cDNA SEQ ID NO:13.
PN WO2003025135-A2.
PD 27-MAR-2003.
PA (GENE-) GENE LOGIC INC.
Percent Similarity: 36.03% Conservative: 23
Best Local Similarity: 19.12% Mismatches: 45
Query Match: 6.62% Indels: 42

RESULT 1280
ID AAF21798 standard; DNA; 1040 BP.
DE Human breast and ovarian cancer associated antigen gene SEQ ID 185.
PN WO200055173-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 36.03% Conservative: 23
Best Local Similarity: 19.12% Mismatches: 45
Query Match: 6.62% Indels: 42
RESULT 1281
ID AAC69513 standard; DNA; 1047 BP.
DE Human secreted protein gene 2 clone HEMFQ46.
PN WO200061623-A1.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 36.03% Conservative: 23
Best Local Similarity: 19.12% Mismatches: 45
Query Match: 6.62% Indels: 42
RESULT 1282
ID AAK51736 standard; cDNA; 1070 BP.
DE Human polynucleotide SEQ ID NO 281.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 36.03% Conservative: 23
Best Local Similarity: 19.12% Mismatches: 45
Query Match: 6.62% Indels: 42
RESULT 1283
ID AAK52720 standard; cDNA; 1079 BP.
DE Human polynucleotide SEQ ID NO 2249.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 36.03% Conservative: 23
Best Local Similarity: 19.12% Mismatches: 45
Query Match: 6.62% Indels: 42
RESULT 1284
ID AAK52719 standard; cDNA; 1080 BP.
DE Human polynucleotide SEQ ID NO 2248.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 36.03% Conservative: 23
Best Local Similarity: 19.12% Mismatches: 45
Query Match: 6.62% Indels: 42
RESULT 1285
ID ADE53693 standard; cDNA; 1094 BP.
DE Human prostate cancer cDNA #40.
PN US2003190640-A1.
PD 09-OCT-2003.
PA (FARI/) FARIS M.
PA (PEAR/) PEARSON C I.
Percent Similarity: 36.03% Conservative: 23
Best Local Similarity: 19.12% Mismatches: 45
Query Match: 6.62% Indels: 42
RESULT 1286
ID ADA98577 standard; DNA; 1119 BP.
DE Human secreted protein-related DNA sequence #170.
PN WO2003004623-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 33.95% Conservative: 36
Best Local Similarity: 20.66% Mismatches: 76
Query Match: 6.62% Indels: 103
RESULT 1287
ID ADA44309 standard; DNA; 1119 BP.
DE Human secreted protein DNA SEQ ID 502.
PN WO2003000865-A2.
PD 03-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 33.95% Conservative: 36
Best Local Similarity: 20.66% Mismatches: 76
Query Match: 6.62% Indels: 103
RESULT 1288
ID ADC20693 standard; DNA; 1119 BP.
DE Human secreted protein-related DNA sequence #111.
PN WO200292787-A2.
PD 21-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 33.95% Conservative: 36
Best Local Similarity: 20.66% Mismatches: 76
Query Match: 6.62% Indels: 103
RESULT 1289
ID ADF10874 standard; DNA; 1119 BP.
DE Human secreted protein encoding sequence #196.
PN WO200299085-A2.
PD 12-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 33.95% Conservative: 36
Best Local Similarity: 20.66% Mismatches: 76
Query Match: 6.62% Indels: 103
RESULT 1290
ID ADA98576 standard; DNA; 1121 BP.
DE Human secreted protein-related DNA sequence #169.
PN WO2003004623-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 33.95% Conservative: 36
Best Local Similarity: 20.66% Mismatches: 76
Query Match: 6.62% Indels: 103
RESULT 1291
ID ADA44308 standard; DNA; 1121 BP.
DE Human secreted protein DNA SEQ ID 501.
PN WO2003000865-A2.
PD 03-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 33.95% Conservative: 36
Best Local Similarity: 20.66% Mismatches: 76
Query Match: 6.62% Indels: 103
RESULT 1292
ID ADC20692 standard; DNA; 1121 BP.
DE Human secreted protein-related DNA sequence #110.
PN WO200292787-A2.
PD 21-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 33.95% Conservative: 36
Best Local Similarity: 20.66% Mismatches: 76
Query Match: 6.62% Indels: 103
RESULT 1293
ID ADF10873 standard; DNA; 1121 BP.
DE Human secreted protein encoding sequence #195.
PN WO200299085-A2.
PD 12-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 33.95% Conservative: 36
Best Local Similarity: 20.66% Mismatches: 76
Query Match: 6.62% Indels: 103
RESULT 1294
ID AAC59477 standard; cDNA; 1125 BP.
DE Human secreted protein gene 29 SEQ ID NO:39.
PN WO200056755-A1.
PD 28-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 33.95% Conservative: 36
Best Local Similarity: 20.66% Mismatches: 76
Query Match: 6.62% Indels: 103
RESULT 1295
ID ADA97977 standard; cDNA; 1125 BP.
DE Human secreted protein cDNA sequence #71.
PN WO2003004623-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 33.95% Conservative: 36
Best Local Similarity: 20.66% Mismatches: 76
Query Match: 6.62% Indels: 103
RESULT 1296

ID ADA43883 standard; cDNA; 1125 BP.
DE Human secreted protein cDNA SEQ ID 71.
PN WO2003000865-A2.
PD 03-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 33.95% Conservative: 36
Best Local Similarity: 20.66% Mismatches: 76
Query Match: 6.62% Indels: 103
RESULT 1297
ID ADC20138 standard; DNA; 1125 BP.
DE Human secreted protein coding sequence #77.
PN WO200292787-A2.
PD 21-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 33.95% Conservative: 36
Best Local Similarity: 20.66% Mismatches: 76
Query Match: 6.62% Indels: 103
RESULT 1298
ID ADF10588 standard; DNA; 1125 BP.
DE Human secreted protein encoding sequence #41.
PN WO200299085-A2.
PD 12-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 33.95% Conservative: 36
Best Local Similarity: 20.66% Mismatches: 76
Query Match: 6.62% Indels: 103
RESULT 1299
ID ABK13032 standard; cDNA; 1195 BP.
DE DNA encoding mouse B7-like protein, B7-L_m1.
PN WO200200710-A2.
PD 03-JAN-2002.
PA (AMGE-) AMGEN INC.
Percent Similarity: 33.91% Conservative: 20
Best Local Similarity: 22.41% Mismatches: 55
Query Match: 6.62% Indels: 60
RESULT 1300
ID AAD45161 standard; DNA; 1478 BP.
DE Flea chitinase DNA, nCfCHT1478.
PN US6416977-B1.
PD 09-JUL-2002.
PA (HESK-) HESKA CORP.
Percent Similarity: 42.57% Conservative: 25
Best Local Similarity: 25.68% Mismatches: 63
Query Match: 6.62% Indels: 22
RESULT 1301
ID ADR99937 standard; DNA; 1539 BP.
DE Immune Response Associated Protein, IRAP-13, coding sequence, SEQ ID 45.
PN WO2004081197-A2.
PD 23-SEP-2004.
PA (INCY-) INCYTE CORP.
Percent Similarity: 34.83% Conservative: 28
Best Local Similarity: 20.90% Mismatches: 65
Query Match: 6.62% Indels: 66
RESULT 1302
ID ABL27300 standard; DNA; 1592 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 33373.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 35.51% Conservative: 19
Best Local Similarity: 21.74% Mismatches: 33
Query Match: 6.62% Indels: 56
RESULT 1303
ID ADI42377 standard; DNA; 1637 BP.
DE Plant transcription factor polynucleotide #512.
PN US2004019927-A1.
PD 29-JAN-2004.
PA (SHER/) SHERMAN B K.
PA (RIEC/) RIECHMANN J L.
PA (JIAN/) JIANG C.
PA (HEAR/) HEARD J E.
PA (HAAK/) HAAKE V.
PA (CREE/) CREELMAN R A.
PA (RATC/) RATCLIFFE O.
PA (ADAM/) ADAM L J.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J.
PA (BROU/) BROUN P E.
PA (PILG/) PILGRIM M L.
PA (DUBE/) DUBELL A N.
PA (PINE/) PINEDA O.
PA (YUGG/) YU G.
Percent Similarity: 38.07% Conservative: 29
Best Local Similarity: 21.59% Mismatches: 85
Query Match: 6.62% Indels: 24
RESULT 1304
ID AAQ96124 standard; DNA; 1727 BP.
DE T-cell receptor eta DNA.
PN WO9521528-A1.
PD 17-AUG-1995.
PA (GEHO) GEN HOSPITAL CORP.
Percent Similarity: 41.45% Conservative: 24
Best Local Similarity: 25.66% Mismatches: 53
Query Match: 6.62% Indels: 36
RESULT 1305
ID ADR65967 standard; DNA; 1957 BP.
DE Human prostatic carcinoma derived DNA SEQ ID 163 #1.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Percent Similarity: 38.71% Conservative: 24
Best Local Similarity: 23.23% Mismatches: 51
Query Match: 6.62% Indels: 44
RESULT 1306
ID AAD27272 standard; cDNA; 2074 BP.
DE Human transporter and ion channel-19 (TRICH-19) cDNA.
PN WO200192304-A2.
PD 06-DEC-2001.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 34.74% Conservative: 24
Best Local Similarity: 22.11% Mismatches: 52
Query Match: 6.62% Indels: 72
RESULT 1307
ID AAV29911 standard; cDNA; 2103 BP.
DE Mouse hedgehog interacting protein (HIP) cDNA.
PN WO9812326-A1.
PD 26-MAR-1998.
PA (HARD) HARVARD COLLEGE.
Percent Similarity: 44.55% Conservative: 20
Best Local Similarity: 26.36% Mismatches: 45
Query Match: 6.62% Indels: 16
RESULT 1308
ID ADE86235 standard; cDNA; 2103 BP.
DE Mouse hedgehog interacting protein (HIP) cDNA sequence.
PN US2003143595-A1.
PD 31-JUL-2003.
PA (MCMA/) MCMAHON A P.
PA (CHUA/) CHUANG P.
Percent Similarity: 44.55% Conservative: 20
Best Local Similarity: 26.36% Mismatches: 45
Query Match: 6.62% Indels: 16
RESULT 1309
ID AAH18175 standard; cDNA; 2122 BP.
DE Human cDNA sequence SEQ ID NO:18074.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Percent Similarity: 38.00% Conservative: 18
Best Local Similarity: 26.00% Mismatches: 54
Query Match: 6.62% Indels: 39
RESULT 1310
ID ABK63725 standard; cDNA; 2171 BP.

DE Rat sequence differentially expressed in response to a hepatotoxin #1632.
PN WO200210453-A2.
PD 07-FEB-2002.
PA (GENE-) GENE LOGIC INC.
Percent Similarity: 43.70% Conservative: 24
Best Local Similarity: 23.53% Mismatches: 48
Query Match: 6.62% Indels: 19
RESULT 1311
ID ABT17417 standard; DNA; 2171 BP.
DE Human IG gene related nucleic acid SEQ ID No 43.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Percent Similarity: 43.70% Conservative: 24
Best Local Similarity: 23.53% Mismatches: 48
Query Match: 6.62% Indels: 19
RESULT 1312
ID ADB52771 standard; DNA; 2171 BP.
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3313.
PN WO2003065993-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Percent Similarity: 43.70% Conservative: 24
Best Local Similarity: 23.53% Mismatches: 48
Query Match: 6.62% Indels: 19
RESULT 1313
ID ABT41948 standard; DNA; 2171 BP.
DE Toxicity modelling related rat gene SEQ ID No 1650.
PN WO200295000-A2.
PD 28-NOV-2002.
PA (GENE-) GENE LOGIC INC.
Percent Similarity: 43.70% Conservative: 24
Best Local Similarity: 23.53% Mismatches: 48
Query Match: 6.62% Indels: 19
RESULT 1314
ID AAX90848 standard; DNA; 2360 BP.
DE cDNA clone cc359_4.
PN WO9950405-A1.
PD 07-OCT-1999.
PA (GEMY) GENETICS INST INC.
Percent Similarity: 39.13% Conservative: 38
Best Local Similarity: 20.77% Mismatches: 61
Query Match: 6.62% Indels: 65
RESULT 1315
ID AAA37899 standard; DNA; 2669 BP.
DE Mouse Hedgehog interacting protein coding sequence.
PN WO200074706-A1.
PD 14-DEC-2000.
PA (LORA-) LORANTIS LTD.
Percent Similarity: 44.55% Conservative: 20
Best Local Similarity: 26.36% Mismatches: 45
Query Match: 6.62% Indels: 16
RESULT 1316
ID ABS55985 standard; DNA; 2669 BP.
DE Mouse hedgehog-interacting protein (HIP) DNA.
PN WO200280952-A2.
PD 17-OCT-2002.
PA (LORA-) LORANTIS LTD.
Percent Similarity: 44.55% Conservative: 20
Best Local Similarity: 26.36% Mismatches: 45
Query Match: 6.62% Indels: 16
RESULT 1317
ID ACN38684 standard; cDNA; 3617 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA324988, SEQ ID NO:2351.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 34.12% Conservative: 21
Best Local Similarity: 21.76% Mismatches: 64
Query Match: 6.62% Indels: 48
RESULT 1318
ID ADB84160 standard; DNA; 7800 BP.
DE Gene expression estimation method-related DNA sequence #20.
PN WO2003044227-A1.
PD 30-MAY-2003.
PA (NAAG-) NAT INST AGROBIOLOGICAL SCI.
Percent Similarity: 44.44% Conservative: 18
Best Local Similarity: 26.26% Mismatches: 29
Query Match: 6.62% Indels: 27
RESULT 1319
ID ADJ33271 standard; DNA; 8347 BP.
DE Enterococcus faecalis biosynthetic gene cluster SEQ ID NO:31.
PN WO2003056295-A2.
PD 10-JUL-2003.
PA (GEHO) GEN HOSPITAL CORP.
Percent Similarity: 46.67% Conservative: 18
Best Local Similarity: 29.52% Mismatches: 42
Query Match: 6.62% Indels: 15
RESULT 1320
ID AAX13067 standard; DNA; 9767 BP.
DE Enterococcus faecalis genome contig SEQ ID NO:130.
PN WO9850555-A2.
PD 12-NOV-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 46.10% Conservative: 34
Best Local Similarity: 21.99% Mismatches: 38
Query Match: 6.62% Indels: 38
RESULT 1321
ID ABS98862 standard; DNA; 9767 BP.
DE Enterococcus faecalis contig sequence #130.
PN US2002120116-A1.
PD 29-AUG-2002.
PA (KUNS/) KUNSCH C A.
PA (DILL/) DILLON P J.
PA (BARA/) BARASH S.
Percent Similarity: 46.10% Conservative: 34
Best Local Similarity: 21.99% Mismatches: 38
Query Match: 6.62% Indels: 38
RESULT 1322
ID AAS59571 standard; DNA; 11808 BP.
DE Propionibacterium acnes immunogenic protein encoding DNA #66.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Percent Similarity: 34.10% Conservative: 30
Best Local Similarity: 20.28% Mismatches: 90
Query Match: 6.62% Indels: 53
RESULT 1323
ID ACF64500 standard; DNA; 11808 BP.
DE Propionibacterium acnes DNA contig sequence #66.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Percent Similarity: 34.10% Conservative: 30
Best Local Similarity: 20.28% Mismatches: 90
Query Match: 6.62% Indels: 53
RESULT 1324
ID AAX13118 standard; DNA; 11879 BP.
DE Enterococcus faecalis genome contig SEQ ID NO:181.
PN WO9850555-A2.
PD 12-NOV-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 46.67% Conservative: 18
Best Local Similarity: 29.52% Mismatches: 42
Query Match: 6.62% Indels: 15
RESULT 1325
ID ABS98913 standard; DNA; 11879 BP.
DE Enterococcus faecalis contig sequence #181.
PN US2002120116-A1.
PD 29-AUG-2002.
PA (KUNS/) KUNSCH C A.
PA (DILL/) DILLON P J.
PA (BARA/) BARASH S.
Percent Similarity: 46.67% Conservative: 18
Best Local Similarity: 29.52% Mismatches: 42
Query Match: 6.62% Indels: 15

RESULT 1326
ID AAS46477 standard; DNA; 14112 BP.
DE Tumour suppressor gene derived chemically modified sequence #199.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Percent Similarity: 39.35% Conservative: 23
Best Local Similarity: 24.52% Mismatches: 62
Query Match: 6.62% Indels: 32
RESULT 1327
ID ABL33442 standard; DNA; 14112 BP.
DE Human immune system associated gene SEQ ID NO: 1415.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Percent Similarity: 39.35% Conservative: 23
Best Local Similarity: 24.52% Mismatches: 62
Query Match: 6.62% Indels: 32
RESULT 1328
ID ABK31332 standard; DNA; 14112 BP.
DE Signal transduction associated gene modified DNA #88.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Percent Similarity: 39.35% Conservative: 23
Best Local Similarity: 24.52% Mismatches: 62
Query Match: 6.62% Indels: 32
RESULT 1329
ID ABQ66979 standard; DNA; 14112 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 9.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Percent Similarity: 39.35% Conservative: 23
Best Local Similarity: 24.52% Mismatches: 62
Query Match: 6.62% Indels: 32
RESULT 1330
ID ADQ97543 standard; DNA; 65590 BP.
DE Human cancer associated sequence HD09-011, SEQ ID 520.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Percent Similarity: 50.91% Conservative: 22
Best Local Similarity: 30.91% Mismatches: 38
Query Match: 6.62% Indels: 16
RESULT 1331
ID ABX14591 standard; DNA; 106323 BP.
DE Human chloride intracellular channel isoform protein genomic DNA.
PN US2002132292-A1.
PD 19-SEP-2002.
PA (WEIM/) WEI M.
PA (YANC/) YAN C.
PA (DFRA/) DI FRANCESCO V.
PA (BEAS/) BEASLEY E M.
Percent Similarity: 39.23% Conservative: 20
Best Local Similarity: 23.85% Mismatches: 48
Query Match: 6.62% Indels: 31
RESULT 1332
ID AAD58821 standard; DNA; 106323 BP.
DE Human transporter gene.
Percent Similarity: 39.23% Conservative: 20
Best Local Similarity: 23.85% Mismatches: 48
Query Match: 6.62% Indels: 31
RESULT 1333
Percent Similarity: 47.45% Conservative: 25
Best Local Similarity: 29.20% Mismatches: 59
Query Match: 6.62% Indels: 13
RESULT 1334
Percent Similarity: 43.24% Conservative: 28
Best Local Similarity: 24.32% Mismatches: 60
Query Match: 6.62% Indels: 24
RESULT 1335
Percent Similarity: 43.24% Conservative: 28
Best Local Similarity: 24.32% Mismatches: 60
Query Match: 6.62% Indels: 24
RESULT 1336
Percent Similarity: 43.24% Conservative: 28
Best Local Similarity: 24.32% Mismatches: 60
Query Match: 6.62% Indels: 24
RESULT 1337
Percent Similarity: 34.72% Conservative: 27
Best Local Similarity: 22.22% Mismatches: 79
Query Match: 6.62% Indels: 62
RESULT 1338
Percent Similarity: 49.30% Conservative: 12
Best Local Similarity: 32.39% Mismatches: 22
Query Match: 6.62% Indels: 14
RESULT 1339
Percent Similarity: 49.30% Conservative: 12
Best Local Similarity: 32.39% Mismatches: 22
Query Match: 6.62% Indels: 14
RESULT 1340
Percent Similarity: 49.30% Conservative: 12
Best Local Similarity: 32.39% Mismatches: 22
Query Match: 6.62% Indels: 14
RESULT 1341
Percent Similarity: 49.30% Conservative: 12
Best Local Similarity: 32.39% Mismatches: 22
Query Match: 6.62% Indels: 14
RESULT 1342
Percent Similarity: 49.30% Conservative: 12
Best Local Similarity: 32.39% Mismatches: 22
Query Match: 6.62% Indels: 14
RESULT 1343
Percent Similarity: 49.30% Conservative: 12
Best Local Similarity: 32.39% Mismatches: 22
Query Match: 6.62% Indels: 14
RESULT 1344
ID ABT10146 standard; cDNA; 140167 BP.
DE Human breast cancer associated coding sequence SEQ ID NO: 280.
PN WO200259271-A2.
PD 01-AUG-2002.
PA (GENE-) GENE LOGIC INC.
Percent Similarity: 53.03% Conservative: 17
Best Local Similarity: 27.27% Mismatches: 15
Query Match: 6.62% Indels: 16
RESULT 1345
ID AAC81914 standard; DNA; 273254 BP.
DE Chlamydia pneumoniae genome DNA.
PN WO200027994-A2.
PD 18-MAY-2000.
PA (REGC) UNIV CALIFORNIA.
Percent Similarity: 47.45% Conservative: 25
Best Local Similarity: 29.20% Mismatches: 59
Query Match: 6.62% Indels: 13
RESULT 1346
ID ABD32602 standard; DNA; 277616 BP.
DE Human cancer-associated genomic DNA HD7-221.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Percent Similarity: 34.83% Conservative: 16
Best Local Similarity: 25.84% Mismatches: 33
Query Match: 6.62% Indels: 84
RESULT 1347
ID ABK89296 standard; DNA; 326014 BP.
DE Human gene for novel serine/threonine serine kinase.
Percent Similarity: 44.72% Conservative: 23
Best Local Similarity: 26.02% Mismatches: 48
Query Match: 6.62% Indels: 20
RESULT 1348
ID ADQ94981 standard; DNA; 326014 BP.
DE Human kinase genomic DNA.
Percent Similarity: 44.72% Conservative: 23
Best Local Similarity: 26.02% Mismatches: 48
Query Match: 6.62% Indels: 20

RESULT 1349
ID AAX36693 standard; DNA; 486 BP.
DE Mouse OHP106 protein coding sequence.
PN WO9918205-A1.
PD 15-APR-1999.
PA (ONOY) ONO PHARM CO LTD.
Percent Similarity: 44.25% Conservative: 24
Best Local Similarity: 23.01% Mismatches: 32
Query Match: 6.58% Indels: 31
RESULT 1350
ID ADL67238 standard; DNA; 492 BP.
DE Chimeric TCR related human DNA.
PN US2004043401-A1.
PD 04-MAR-2004.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
Percent Similarity: 42.74% Conservative: 21
Best Local Similarity: 24.79% Mismatches: 43
Query Match: 6.58% Indels: 24
RESULT 1351
ID ADI32056 standard; cDNA; 585 BP.
DE Human cDNA #1382.
PN US6607879-B1.
PD 19-AUG-2003.
PA (INCY-) INCYTE CORP.
Percent Similarity: 42.74% Conservative: 21
Best Local Similarity: 24.79% Mismatches: 43
Query Match: 6.58% Indels: 24
RESULT 1352
ID ADA50578 standard; DNA; 759 BP.
DE Mucin 1 (MUC-1) splice variant #4 (MUC1Y variant) DNA, SEQ ID NO:33.
PN WO2003031569-A2.
PD 17-APR-2003.
PA (CENZ) CENTOCOR INC.
Percent Similarity: 38.31% Conservative: 28
Best Local Similarity: 20.13% Mismatches: 77
Query Match: 6.58% Indels: 19
RESULT 1353
ID AAD56945 standard; cDNA; 759 BP.
DE Human mucin 1 transmembrane variant, MUC1/Y cDNA.
PN WO2003054154-A2.
PD 03-JUL-2003.
PA (ISIS-) ISIS PHARM INC.
Percent Similarity: 38.31% Conservative: 28
Best Local Similarity: 20.13% Mismatches: 77
Query Match: 6.58% Indels: 19
RESULT 1354
ID AAZ16180 standard; cDNA; 776 BP.
DE Human gene expression product cDNA sequence SEQ ID NO:3650.
PN WO9938972-A2.
PD 05-AUG-1999.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 44.34% Conservative: 14
Best Local Similarity: 31.13% Mismatches: 29
Query Match: 6.58% Indels: 31
RESULT 1355
ID AAZ09234 standard; DNA; 900 BP.
DE Rabbit B7-1 DNA.
PN WO9941368-A2.
PD 19-AUG-1999.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.38% Conservative: 29
Best Local Similarity: 21.25% Mismatches: 56
Query Match: 6.58% Indels: 41
RESULT 1356
ID ABV94626 standard; cDNA; 900 BP.
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:276.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.38% Conservative: 29
Best Local Similarity: 21.25% Mismatches: 56
Query Match: 6.58% Indels: 41
RESULT 1357
ID ADM18911 standard; cDNA; 900 BP.
DE Rabbit B7-1 encoding cDNA SEQ ID NO:276.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.38% Conservative: 29
Best Local Similarity: 21.25% Mismatches: 56
Query Match: 6.58% Indels: 41
RESULT 1358
ID ABV94622 standard; cDNA; 910 BP.
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:262.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 38.89% Conservative: 28
Best Local Similarity: 21.60% Mismatches: 58
Query Match: 6.58% Indels: 41
RESULT 1359
ID ADM18897 standard; cDNA; 910 BP.
DE Human co-stimulatory molecule encoding cDNA SEQ ID NO:262.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 38.89% Conservative: 28
Best Local Similarity: 21.60% Mismatches: 58
Query Match: 6.58% Indels: 41
RESULT 1360
ID ABV94546 standard; cDNA; 912 BP.
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:107.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.13% Conservative: 20
Best Local Similarity: 24.64% Mismatches: 49
Query Match: 6.58% Indels: 35
RESULT 1361
ID ABV94553 standard; cDNA; 912 BP.
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:114.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.13% Conservative: 20
Best Local Similarity: 24.64% Mismatches: 49
Query Match: 6.58% Indels: 35
RESULT 1362
ID ABV94557 standard; cDNA; 912 BP.
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:118.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.13% Conservative: 20
Best Local Similarity: 24.64% Mismatches: 49
Query Match: 6.58% Indels: 35
RESULT 1363
ID ABV94500 standard; cDNA; 912 BP.
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:14.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.13% Conservative: 20
Best Local Similarity: 24.64% Mismatches: 49
Query Match: 6.58% Indels: 35
RESULT 1364
ID ABV94545 standard; cDNA; 912 BP.
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:106.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.13% Conservative: 20
Best Local Similarity: 24.64% Mismatches: 49
Query Match: 6.58% Indels: 35
RESULT 1365

ID ADM18649 standard; cDNA; 912 BP.
DE Human co-stimulatory molecule encoding cDNA SEQ ID NO:14.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.13% Conservative: 20
Best Local Similarity: 24.64% Mismatches: 49
Query Match: 6.58% Indels: 35
RESULT 1366
ID ADM18749 standard; cDNA; 912 BP.
DE Human co-stimulatory molecule encoding cDNA SEQ ID NO:114.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.13% Conservative: 20
Best Local Similarity: 24.64% Mismatches: 49
Query Match: 6.58% Indels: 35
RESULT 1367
ID ADM18742 standard; cDNA; 912 BP.
DE Human co-stimulatory molecule encoding cDNA SEQ ID NO:107.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.13% Conservative: 20
Best Local Similarity: 24.64% Mismatches: 49
Query Match: 6.58% Indels: 35
RESULT 1368
ID ADM18753 standard; cDNA; 912 BP.
DE Human co-stimulatory molecule encoding cDNA SEQ ID NO:118.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.13% Conservative: 20
Best Local Similarity: 24.64% Mismatches: 49
Query Match: 6.58% Indels: 35
RESULT 1369
ID ADM18741 standard; cDNA; 912 BP.
DE Human co-stimulatory molecule encoding cDNA SEQ ID NO:106.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.13% Conservative: 20
Best Local Similarity: 24.64% Mismatches: 49
Query Match: 6.58% Indels: 35
RESULT 1370
ID AAX36694 standard; DNA; 996 BP.
DE Mouse OHP106 protein coding sequence.
PN WO9918205-A1.
PD 15-APR-1999.
PA (ONOY) ONO PHARM CO LTD.
Percent Similarity: 44.25% Conservative: 24
Best Local Similarity: 23.01% Mismatches: 32
Query Match: 6.58% Indels: 31
RESULT 1371
ID AAC40859 standard; DNA; 1072 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 29802.
PN EP1033405-A2.
PD 06-SEP-2000.
Percent Similarity: 41.94% Conservative: 24
Best Local Similarity: 22.58% Mismatches: 45
Query Match: 6.58% Indels: 27
RESULT 1372
ID ABQ76937 standard; DNA; 1074 BP.
DE Muvalpha-hucalpha-huCD3epsilon fusion construct DNA.
PN DE10109854-A1.
PD 12-SEP-2002.
PA (STAN/) STANISLAWSKI T.
Percent Similarity: 42.74% Conservative: 21
Best Local Similarity: 24.79% Mismatches: 43
Query Match: 6.58% Indels: 24
RESULT 1373
ID AAC49689 standard; DNA; 1174 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 62075.
PN EP1033405-A2.
PD 06-SEP-2000.
Percent Similarity: 41.94% Conservative: 24
Best Local Similarity: 22.58% Mismatches: 45
Query Match: 6.58% Indels: 27
RESULT 1374
ID AAC39377 standard; DNA; 1175 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 24411.
PN EP1033405-A2.
PD 06-SEP-2000.
Percent Similarity: 41.94% Conservative: 24
Best Local Similarity: 22.58% Mismatches: 45
Query Match: 6.58% Indels: 27
RESULT 1375
ID AAC49684 standard; DNA; 1233 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 62055.
PN EP1033405-A2.
PD 06-SEP-2000.
Percent Similarity: 41.94% Conservative: 24
Best Local Similarity: 22.58% Mismatches: 45
Query Match: 6.58% Indels: 27
RESULT 1376
ID ADA71366 standard; DNA; 1266 BP.
DE Rice gene, SEQ ID 4689.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Percent Similarity: 46.96% Conservative: 22
Best Local Similarity: 27.83% Mismatches: 43
Query Match: 6.58% Indels: 19
RESULT 1377
ID AAT97844 standard; DNA; 1350 BP.
DE DNA of a single chain T-cell receptor specific for hemaglutinin antigen.
PN WO9732603-A1.
PD 12-SEP-1997.
PA (SCRI) SCRIPPS RES INST.
Percent Similarity: 42.74% Conservative: 21
Best Local Similarity: 24.79% Mismatches: 43
Query Match: 6.58% Indels: 24
RESULT 1378
ID AAL49722 standard; cDNA; 1398 BP.
DE Human secreted LIR-like protein cDNA SEQ ID NO: 36.
PN WO200266600-A2.
PD 29-AUG-2002.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 35.07% Conservative: 40
Best Local Similarity: 20.15% Mismatches: 72
Query Match: 6.58% Indels: 104
RESULT 1379
ID AAT90509 standard; DNA; 1422 BP.
DE DNA encoding chimeric receptor hCTMO1/CD8/zeta.
PN WO9723613-A2.
PD 03-JUL-1997.
PA (CLLT) CELLTECH THERAPEUTICS LTD.
Percent Similarity: 42.74% Conservative: 21
Best Local Similarity: 24.79% Mismatches: 43
Query Match: 6.58% Indels: 24
RESULT 1380
ID AAT90510 standard; DNA; 1545 BP.
DE DNA encoding chimeric receptor hCTMO1/CD8/zeta-CD28.
PN WO9723613-A2.
PD 03-JUL-1997.
PA (CLLT) CELLTECH THERAPEUTICS LTD.
Percent Similarity: 42.74% Conservative: 21
Best Local Similarity: 24.79% Mismatches: 43
Query Match: 6.58% Indels: 24
RESULT 1381
ID ACA24284 standard; DNA; 1587 BP.
DE Prokaryotic essential gene #5941.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 50.00% Conservative: 11

Best Local Similarity: 32.81% Mismatches: 29
Query Match: 6.58% Indels: 3
RESULT 1382
ID ADG32711 standard; DNA; 1723 BP.
DE Human DNA differentially expressed in patients with SLE SeqID35.
PN WO2003090694-A2.
PD 06-NOV-2003.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Percent Similarity: 42.74% Conservative: 21
Best Local Similarity: 24.79% Mismatches: 43
Query Match: 6.58% Indels: 24
RESULT 1383
ID ADR24663 standard; DNA; 1723 BP.
DE Breast cancer prognosis marker #524.
PN WO2004065545-A2.
PD 05-AUG-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
PA (NECA-) NETHERLANDS CANCER INST.
Percent Similarity: 42.74% Conservative: 21
Best Local Similarity: 24.79% Mismatches: 43
Query Match: 6.58% Indels: 24
RESULT 1384
ID ABD33068 standard; cDNA; 1724 BP.
DE Human cancer-associated cDNA HR23-013.2.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Percent Similarity: 42.74% Conservative: 21
Best Local Similarity: 24.79% Mismatches: 43
Query Match: 6.58% Indels: 24
RESULT 1385
ID ADR20362 standard; DNA; 1944 BP.
DE Recombinant pDAB2097 cosmid open reading frame 3 DNA SeqID 11.
PN WO2004067750-A2.
PD 12-AUG-2004.
PA (DOWC) DOW AGROSCIENCES LLC.
Percent Similarity: 45.45% Conservative: 7
Best Local Similarity: 32.73% Mismatches: 21
Query Match: 6.58% Indels: 9
RESULT 1386
ID ADR21491 standard; DNA; 1944 BP.
DE Xenorhabdus strain Xwi cosmid pDAB2097 ORF3 SEQ ID NO:11.
PN WO2004067727-A2.
PD 12-AUG-2004.
PA (DOWC) DOW AGROSCIENCES LLC.
Percent Similarity: 45.45% Conservative: 7
Best Local Similarity: 32.73% Mismatches: 21
Query Match: 6.58% Indels: 9
RESULT 1387
ID ADR20372 standard; DNA; 1947 BP.
DE Recombinant pDAB2097 cosmid DNA encoding an exochitinase SeqID 21.
PN WO2004067750-A2.
PD 12-AUG-2004.
PA (DOWC) DOW AGROSCIENCES LLC.
Percent Similarity: 45.45% Conservative: 7
Best Local Similarity: 32.73% Mismatches: 21
Query Match: 6.58% Indels: 9
RESULT 1388
ID AAT90512 standard; DNA; 1956 BP.
DE DNA encoding chimeric receptor hCTMO1/G1/zeta.
PN WO9723613-A2.
PD 03-JUL-1997.
PA (CLLT) CELLTECH THERAPEUTICS LTD.
Percent Similarity: 42.74% Conservative: 21
Best Local Similarity: 24.79% Mismatches: 43
Query Match: 6.58% Indels: 24
RESULT 1389
ID AAT90513 standard; DNA; 2079 BP.
DE DNA encoding chimeric receptor hCTMO1/G1/zeta-CD28.
PN WO9723613-A2.
PD 03-JUL-1997.
PA (CLLT) CELLTECH THERAPEUTICS LTD.
Percent Similarity: 42.74% Conservative: 21
Best Local Similarity: 24.79% Mismatches: 43
Query Match: 6.58% Indels: 24
RESULT 1390
ID AAH16102 standard; cDNA; 2582 BP.
DE Human cDNA sequence SEQ ID NO:14822.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Percent Similarity: 42.15% Conservative: 15
Best Local Similarity: 29.75% Mismatches: 42
Query Match: 6.58% Indels: 28
RESULT 1391
ID ACF68678 standard; DNA; 2718 BP.
DE Photorhabdus luminescens nucleotide sequence #7145.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Percent Similarity: 38.46% Conservative: 32
Best Local Similarity: 22.05% Mismatches: 69
Query Match: 6.58% Indels: 51
RESULT 1392
ID AAV62748 standard; cDNA; 2911 BP.
DE Human secreted protein clone er80_1 cDNA.
PN WO9846757-A2.
PD 22-OCT-1998.
PA (GEMY) GENETICS INST INC.
Percent Similarity: 48.74% Conservative: 28
Best Local Similarity: 25.21% Mismatches: 46
Query Match: 6.58% Indels: 15
RESULT 1393
ID ABQ92051 standard; cDNA; 2911 BP.
DE Human polynucleotide SEQ ID NO 48.
PN US2002065394-A1.
PD 30-MAY-2002.
PA (JACO/) JACOBS K.
PA (MCCO/) MCCOY J M.
PA (LAVA/) LAVALLIE E R.
PA (COLL/) COLLINS-RACIE L A.
PA (EVAN/) EVANS C.
PA (MERB/) MERBERG D.
PA (TREA/) TREACY M.
PA (SPAU/) SPAULDING V.
Percent Similarity: 48.74% Conservative: 28
Best Local Similarity: 25.21% Mismatches: 46
Query Match: 6.58% Indels: 15
RESULT 1394
ID AAD07726 standard; cDNA; 2913 BP.
DE Human secreted protein-encoding gene 2 cDNA clone HWLEZ82, SEQ ID NO:32.
PN WO200134800-A1.
PD 17-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 48.74% Conservative: 28
Best Local Similarity: 25.21% Mismatches: 46
Query Match: 6.58% Indels: 15
RESULT 1395
ID AAI99481 standard; DNA; 3178 BP.
DE Human excretory related polynucleotide SEQ ID NO 1245.
PN WO200155313-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 43.01% Conservative: 31
Best Local Similarity: 26.34% Mismatches: 62
Query Match: 6.58% Indels: 44
RESULT 1396
ID AAI64126 standard; cDNA; 3178 BP.
DE Human bladder related polynucleotide, SEQ ID NO: 159.
PN WO200159064-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 43.01% Conservative: 31
Best Local Similarity: 26.34% Mismatches: 62
Query Match: 6.58% Indels: 44

RESULT 1397
ID ADF71724 standard; DNA; 3178 BP.
DE Human bladder associated antigen #37 genomic DNA #1.
PN US2003199008-A1.
PD 23-OCT-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 43.01% Conservative: 31
Best Local Similarity: 26.34% Mismatches: 62
Query Match: 6.58% Indels: 44
RESULT 1398
ID ADS08282 standard; DNA; 7489 BP.
DE Plasmid pBRT7Q containing the Qbeta genome.
PN AU2004200867-A1.
PD 25-MAR-2004.
PA (DIAT-) DIATECH PTY LTD.
Percent Similarity: 38.81% Conservative: 31
Best Local Similarity: 24.66% Mismatches: 50
Query Match: 6.58% Indels: 84
RESULT 1399
ID AAL06039 standard; DNA; 20987 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8727.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 43.09% Conservative: 24
Best Local Similarity: 23.58% Mismatches: 36
Query Match: 6.58% Indels: 34
RESULT 1400
ID ABL98604 standard; DNA; 20987 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 3256.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 43.09% Conservative: 24
Best Local Similarity: 23.58% Mismatches: 36
Query Match: 6.58% Indels: 34
RESULT 1401
ID ADR20357 standard; DNA; 39005 BP.
DE Recombinant pDAB2097 cosmid containing 7 open reading frames Seq 6.
PN WO2004067750-A2.
PD 12-AUG-2004.
PA (DOWC) DOW AGROSCIENCES LLC.
Percent Similarity: 45.45% Conservative: 7
Best Local Similarity: 32.73% Mismatches: 21
Query Match: 6.58% Indels: 9
RESULT 1402
ID ADR21486 standard; DNA; 39005 BP.
DE Xenorhabdus strain Xwi cosmid pDAB2097 SEQ ID NO:6.
PN WO2004067727-A2.
PD 12-AUG-2004.
PA (DOWC) DOW AGROSCIENCES LLC.
Percent Similarity: 45.45% Conservative: 7
Best Local Similarity: 32.73% Mismatches: 21
Query Match: 6.58% Indels: 9
RESULT 1403
ID AAK85590 standard; DNA; 75384 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40402.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 47.69% Conservative: 13
Best Local Similarity: 27.69% Mismatches: 29
Query Match: 6.58% Indels: 5
RESULT 1404
ID ADC85340 standard; DNA; 96597 BP.
DE Human Lmo2 coding sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Percent Similarity: 38.82% Conservative: 16
Best Local Similarity: 29.41% Mismatches: 51
Query Match: 6.58% Indels: 54
RESULT 1405
ID ADA02861 standard; DNA; 96598 BP.
DE Mouse Itpr1 carcinoma associated gene, SEQ ID NO:1379.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Percent Similarity: 38.82% Conservative: 16
Best Local Similarity: 29.41% Mismatches: 51
Query Match: 6.58% Indels: 54
RESULT 1406
ID ADB72599 standard; DNA; 96598 BP.
DE Mouse Itpr1 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Percent Similarity: 38.82% Conservative: 16
Best Local Similarity: 29.41% Mismatches: 51
Query Match: 6.58% Indels: 54
RESULT 1407
ID ADM74456 standard; DNA; 96598 BP.
DE Murine carcinoma associated (CA) nucleic acid #64.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.
PA (ENGE/) ENGELHARD E K.
Percent Similarity: 38.82% Conservative: 16
Best Local Similarity: 29.41% Mismatches: 51
Query Match: 6.58% Indels: 54
RESULT 1408
Percent Similarity: 38.46% Conservative: 32
Best Local Similarity: 22.05% Mismatches: 69
Query Match: 6.58% Indels: 51
RESULT 1409
ID ACF65381 standard; DNA; 249878 BP.
DE Photorhabdus luminescens nucleotide sequence #34.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Percent Similarity: 38.46% Conservative: 32
Best Local Similarity: 22.05% Mismatches: 69
Query Match: 6.58% Indels: 51
RESULT 1410
ID AAH41226 standard; DNA; 349980 BP.
DE Pyrococcus abyssi genomic fragment #5.
PN FR2792651-A1.
PD 27-OCT-2000.
PA (CNRS) CNRS CENT NAT RECH SCI.
PA (IFRE-) IFREMER INST FR RECH EXPL MER.
Percent Similarity: 38.12% Conservative: 30
Best Local Similarity: 23.27% Mismatches: 74
Query Match: 6.58% Indels: 51
RESULT 1411
ID AAK30260 standard; DNA; 424 BP.
DE Human bone marrow expressed single exon probe SEQ ID NO: 4817.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 38.35% Conservative: 13
Best Local Similarity: 28.57% Mismatches: 45
Query Match: 6.53% Indels: 37
RESULT 1412
ID ABV42919 standard; cDNA; 470 BP.
DE Human prostate expression marker cDNA 42910.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Percent Similarity: 40.71% Conservative: 23
Best Local Similarity: 24.29% Mismatches: 49
Query Match: 6.53% Indels: 34
RESULT 1413
ID ABV34052 standard; cDNA; 470 BP.
DE Human prostate expression marker cDNA 34043.
PN WO200160860-A2.

PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Percent Similarity: 40.71% Conservative: 23
Best Local Similarity: 24.29% Mismatches: 49
Query Match: 6.53% Indels: 34
RESULT 1414
ID AAD56948 standard; cDNA; 577 BP.
DE Human mucin 1 transmembrane variant, MUC1-IV cDNA.
PN WO2003054154-A2.
PD 03-JUL-2003.
PA (ISIS-) ISIS PHARM INC.
Percent Similarity: 45.00% Conservative: 18
Best Local Similarity: 27.00% Mismatches: 49
Query Match: 6.53% Indels: 6
RESULT 1415
ID AAV07189 standard; cDNA; 591 BP.
DE cDNA encoding a human phospholemman-like protein.
PN WO9814572-A1.
PD 09-APR-1998.
PA (INCY-) INCYTE PHARM INC.
Percent Similarity: 38.19% Conservative: 23
Best Local Similarity: 22.22% Mismatches: 33
Query Match: 6.53% Indels: 56
RESULT 1416
ID ACD92381 standard; cDNA; 630 BP.
DE Human colon cancer cell expressed cDNA #793.
PN US2002155438-A1.
PD 24-OCT-2002.
PA (SIMP/) SIMPSON A J G.
PA (NETO/) NETO E D.
PA (BREN/) BRENTANI R R.
Percent Similarity: 42.35% Conservative: 14
Best Local Similarity: 25.88% Mismatches: 43
Query Match: 6.53% Indels: 6
RESULT 1417
ID ABS67307 standard; cDNA; 667 BP.
DE Breast specifc polynucleotide #43.
PN WO200264741-A2.
PD 22-AUG-2002.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 48.10% Conservative: 13
Best Local Similarity: 31.65% Mismatches: 37
Query Match: 6.53% Indels: 4
RESULT 1418
ID ADC75106 standard; cDNA; 730 BP.
DE Poppy phytopathogen resistance-related contig cDNA - SEQ ID 30.
PN WO2003020905-A2.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
Percent Similarity: 47.24% Conservative: 30
Best Local Similarity: 23.62% Mismatches: 42
Query Match: 6.53% Indels: 25
RESULT 1419
ID AAK86322 standard; DNA; 783 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41134.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 32.80% Conservative: 24
Best Local Similarity: 19.89% Mismatches: 59
Query Match: 6.53% Indels: 66
RESULT 1420
ID ADC76034 standard; DNA; 796 BP.
DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 958.
PN WO2003020905-A2.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
Percent Similarity: 33.12% Conservative: 20
Best Local Similarity: 20.13% Mismatches: 55
Query Match: 6.53% Indels: 48
RESULT 1421
ID ADK59012 standard; DNA; 796 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #6395.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
PA (DOWC) DOW AGROSCIENCES LLC.
Percent Similarity: 33.12% Conservative: 20
Best Local Similarity: 20.13% Mismatches: 55
Query Match: 6.53% Indels: 48
RESULT 1422
ID ADL46032 standard; DNA; 870 BP.
DE Human ovarian cancer DNA marker #19922.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Percent Similarity: 38.35% Conservative: 13
Best Local Similarity: 28.57% Mismatches: 45
Query Match: 6.53% Indels: 37
RESULT 1423
ID ABV75311 standard; cDNA; 981 BP.
DE Murine OX2R full-length protein encoding cDNA.
PN WO200288164-A1.
PD 07-NOV-2002.
PA (IMMV) IMMUNEX CORP.
Percent Similarity: 42.25% Conservative: 36
Best Local Similarity: 22.99% Mismatches: 81
Query Match: 6.53% Indels: 27
RESULT 1424
ID AAK86971 standard; DNA; 999 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41783.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 38.64% Conservative: 18
Best Local Similarity: 25.00% Mismatches: 46
Query Match: 6.53% Indels: 35
RESULT 1425
ID AAK86970 standard; DNA; 999 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41782.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 38.64% Conservative: 18
Best Local Similarity: 25.00% Mismatches: 46
Query Match: 6.53% Indels: 35
RESULT 1426
ID ADJ94242 standard; DNA; 1165 BP.
DE Mouse IPC marker Ly-49Q coding sequence, SEQ ID 1.
PN WO2004013325-A1.
PD 12-FEB-2004.
PA (GINK-) GINKGO BIOMEDICAL RES INST CO LTD.
Percent Similarity: 45.74% Conservative: 28
Best Local Similarity: 24.03% Mismatches: 50
Query Match: 6.53% Indels: 20
RESULT 1427
ID AAS10874 standard; cDNA; 1245 BP.
DE Human cDNA encoding NOV7 polypeptide.
PN WO200149729-A2.
PD 12-JUL-2001.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 38.35% Conservative: 13
Best Local Similarity: 28.57% Mismatches: 45
Query Match: 6.53% Indels: 37
RESULT 1428
ID ADS85090 standard; DNA; 1413 BP.
DE Mouse atopic dermatitis-related gene sequence SeqID92.
PN WO2004031386-A1.
PD 15-APR-2004.
PA (GENO-) GENOX RES INC.
PA (UYJU-) UNIV JUNTENDO.
Percent Similarity: 40.00% Conservative: 41
Best Local Similarity: 20.00% Mismatches: 67
Query Match: 6.53% Indels: 56
RESULT 1429
ID AAZ97021 standard; cDNA; 1445 BP.

DE Human secreted protein gene 3 cDNA clone HWHGU54, SEQ ID NO:13.
PN WO9966041-A1.
PD 23-DEC-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 38.35% Conservative: 13
Best Local Similarity: 28.57% Mismatches: 45
Query Match: 6.53% Indels: 37
RESULT 1430
ID ADA40242 standard; cDNA; 1445 BP.
DE Human secreted protein encoding cDNA.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 38.35% Conservative: 13
Best Local Similarity: 28.57% Mismatches: 45
Query Match: 6.53% Indels: 37
RESULT 1431
ID ACH66650 standard; cDNA; 1445 BP.
DE Novel human secreted protein #3 cDNA.
PN US2003065151-A1.
PD 03-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 38.35% Conservative: 13
Best Local Similarity: 28.57% Mismatches: 45
Query Match: 6.53% Indels: 37
RESULT 1432
ID ADA56404 standard; DNA; 1445 BP.
DE Gene encoding human secreted protein #583.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 38.35% Conservative: 13
Best Local Similarity: 28.57% Mismatches: 45
Query Match: 6.53% Indels: 37
RESULT 1433
ID ADN05951 standard; cDNA; 1445 BP.
DE Antipsoriatic cDNA sequence #1210.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 38.35% Conservative: 13
Best Local Similarity: 28.57% Mismatches: 45
Query Match: 6.53% Indels: 37
RESULT 1434
ID AAC84169 standard; DNA; 1490 BP.
DE Mouse OX2R homologue 1 (OX2RH1) nucleotide sequence.
PN WO200070045-A1.
PD 23-NOV-2000.
PA (MEDI-) MEDICAL RES COUNCIL.
PA (SCHE) SCHERING CORP.
Percent Similarity: 42.25% Conservative: 36
Best Local Similarity: 22.99% Mismatches: 81
Query Match: 6.53% Indels: 27
RESULT 1435
ID AAD09549 standard; cDNA; 1497 BP.
DE Human protease protein-12 (PRTS-12) cDNA.
PN WO200146443-A2.
PD 28-JUN-2001.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 38.35% Conservative: 13
Best Local Similarity: 28.57% Mismatches: 45
Query Match: 6.53% Indels: 37
RESULT 1436
ID ABK73077 standard; DNA; 1512 BP.
DE Bacillus licheniformis genomic sequence tag (GST) #368.
PN WO200229113-A2.
PD 11-APR-2002.
PA (NOVO) NOVOZYMES BIOTECH INC.
PA (NOVO) NOVOZYMES AS.
Percent Similarity: 34.93% Conservative: 28
Best Local Similarity: 21.53% Mismatches: 53
Query Match: 6.53% Indels: 83
RESULT 1437
ID ADL02542 standard; DNA; 1533 BP.
DE DNA encoding a M. catarrhalis protein #228.
PN US6673910-B1.
PD 06-JAN-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 38.30% Conservative: 44
Best Local Similarity: 19.57% Mismatches: 81
Query Match: 6.53% Indels: 64
RESULT 1438
ID AAQ28706 standard; DNA; 1599 BP.
DE DNA encoding CD4:gamma peptide chimeric protein.
PN WO9215322-A1.
PD 17-SEP-1992.
PA (GEHO) GEN HOSPITAL CORP.
Percent Similarity: 41.45% Conservative: 24
Best Local Similarity: 25.66% Mismatches: 53
Query Match: 6.53% Indels: 36
RESULT 1439
ID AAT10803 standard; DNA; 1599 BP.
DE CD4:eta fusion protein coding sequence.
PN WO9603883-A1.
PD 15-FEB-1996.
PA (GEHO) GEN HOSPITAL CORP.
Percent Similarity: 41.45% Conservative: 24
Best Local Similarity: 25.66% Mismatches: 53
Query Match: 6.53% Indels: 36
RESULT 1440
ID AAV70157 standard; DNA; 1599 BP.
DE Chimeric receptor containing human eta polypeptide encoding DNA.
PN US5843728-A.
PD 01-DEC-1998.
PA (GEHO) GEN HOSPITAL CORP.
Percent Similarity: 41.45% Conservative: 24
Best Local Similarity: 25.66% Mismatches: 53
Query Match: 6.53% Indels: 36
RESULT 1441
ID AAL56192 standard; DNA; 1624 BP.
DE Murine inhibitory receptor CD200Ra coding sequence.
PN WO2003077947-A1.
PD 25-SEP-2003.
PA (SCHE) SCHERING CORP.
Percent Similarity: 42.25% Conservative: 36
Best Local Similarity: 22.99% Mismatches: 81
Query Match: 6.53% Indels: 27
RESULT 1442
ID AAK52031 standard; cDNA; 1646 BP.
DE Human polynucleotide SEQ ID NO 576.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 38.35% Conservative: 13
Best Local Similarity: 28.57% Mismatches: 45
Query Match: 6.53% Indels: 37
RESULT 1443
ID ABL28927 standard; DNA; 1767 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 38254.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 40.83% Conservative: 18
Best Local Similarity: 25.83% Mismatches: 41
Query Match: 6.53% Indels: 30
RESULT 1444
ID ABA09076 standard; cDNA; 1778 BP.
DE Human secreted protein homologue-encoding cDNA, SEQ ID NO:852.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 38.35% Conservative: 13
Best Local Similarity: 28.57% Mismatches: 45
Query Match: 6.53% Indels: 37
RESULT 1445
ID AAK53015 standard; cDNA; 1778 BP.

DE Human polynucleotide SEQ ID NO 2544.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 38.35% Conservative: 13
Best Local Similarity: 28.57% Mismatches: 45
Query Match: 6.53% Indels: 37
RESULT 1446
ID AAF81799 standard; cDNA; 1799 BP.
DE Human secreted protein gene 13 SEQ ID NO:23.
PN WO200112775-A2.
PD 22-FEB-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 44.66% Conservative: 23
Best Local Similarity: 22.33% Mismatches: 33
Query Match: 6.53% Indels: 24
RESULT 1447
ID ADM03363 standard; cDNA; 1953 BP.
DE Human cDNA of the invention SEQ ID NO:2048.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity: 36.67% Conservative: 17
Best Local Similarity: 25.33% Mismatches: 34
Query Match: 6.53% Indels: 61
RESULT 1448
ID AAC85823 standard; DNA; 1977 BP.
DE hOAT4 DNA.
PN WO200104283-A2.
PD 18-JAN-2001.
PA (META-) METABASIS THERAPEUTICS INC.
Percent Similarity: 39.35% Conservative: 29
Best Local Similarity: 25.93% Mismatches: 78
Query Match: 6.53% Indels: 54
RESULT 1449
ID AAC61892 standard; cDNA; 2027 BP.
DE cDNA encoding a human secreted protein.
PN WO200061755-A2.
PD 19-OCT-2000.
PA (CHIR) CHIRON CORP.
Percent Similarity: 39.35% Conservative: 29
Best Local Similarity: 25.93% Mismatches: 78
Query Match: 6.53% Indels: 54
RESULT 1450
ID ADS92515 standard; DNA; 2072 BP.
DE B. licheniformis mutant protease gene SEQ ID NO:61.
PN WO2003087149-A2.
PD 23-OCT-2003.
PA (NOVO) NOVOZYMES AS.
Percent Similarity: 34.93% Conservative: 28
Best Local Similarity: 21.53% Mismatches: 53
Query Match: 6.53% Indels: 83
RESULT 1451
ID ADA69794 standard; DNA; 2115 BP.
DE Rice gene, SEQ ID 3117.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Percent Similarity: 34.24% Conservative: 30
Best Local Similarity: 17.93% Mismatches: 60
Query Match: 6.53% Indels: 62
RESULT 1452
ID ADE82901 standard; DNA; 2342 BP.
DE Human sulfate conjugate organic anion transporter hOAT7 gene.
PN WO2003076617-A1.
PD 18-SEP-2003.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Percent Similarity: 39.35% Conservative: 29
Best Local Similarity: 25.93% Mismatches: 78
Query Match: 6.53% Indels: 54
RESULT 1453
ID ABL28926 standard; DNA; 3767 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 38251.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 40.83% Conservative: 18
Best Local Similarity: 25.83% Mismatches: 41
Query Match: 6.53% Indels: 30
RESULT 1454
ID ADB53912 standard; DNA; 3774 BP.
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:4454.
PN WO2003065993-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Percent Similarity: 40.41% Conservative: 26
Best Local Similarity: 22.60% Mismatches: 37
Query Match: 6.53% Indels: 50
RESULT 1455
ID ABL20016 standard; DNA; 4417 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 11521.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 39.29% Conservative: 22
Best Local Similarity: 26.19% Mismatches: 66
Query Match: 6.53% Indels: 37
RESULT 1456
ID ADP10572 standard; DNA; 4633 BP.
DE Reference mRNA sequences for marker probe #249.
PN WO2004042346-A2.
PD 21-MAY-2004.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Percent Similarity: 40.37% Conservative: 22
Best Local Similarity: 20.18% Mismatches: 31
Query Match: 6.53% Indels: 34
RESULT 1457
ID ABL24614 standard; DNA; 6888 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 25315.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 39.29% Conservative: 22
Best Local Similarity: 26.19% Mismatches: 66
Query Match: 6.53% Indels: 37
RESULT 1458
ID ABL10730 standard; cDNA; 8436 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 26672.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 42.68% Conservative: 28
Best Local Similarity: 25.61% Mismatches: 69
Query Match: 6.53% Indels: 26
RESULT 1459
ID ABL03974 standard; cDNA; 9576 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 6404.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 38.67% Conservative: 22
Best Local Similarity: 24.00% Mismatches: 63
Query Match: 6.53% Indels: 29
RESULT 1460
ID ABL18540 standard; DNA; 12727 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 7093.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 38.67% Conservative: 22
Best Local Similarity: 24.00% Mismatches: 63
Query Match: 6.53% Indels: 29
RESULT 1461
ID AAX99560 standard; DNA; 15016 BP.
DE Nucleic acid sequence from U. urealyticum.
PN WO9939007-A1.

PD 05-AUG-1999.
PA (UABR-) UAB RES FOUND.
Percent Similarity: 47.92% Conservative: 23
Best Local Similarity: 23.96% Mismatches: 42
Query Match: 6.53% Indels: 8
RESULT 1462
ID ACA52817 standard; DNA; 15018 BP.
DE Prokaryotic essential gene #34474.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 47.92% Conservative: 23
Best Local Similarity: 23.96% Mismatches: 42
Query Match: 6.53% Indels: 8
RESULT 1463
ID AAK65305 standard; DNA; 22916 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20117.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 32.66% Conservative: 29
Best Local Similarity: 18.09% Mismatches: 68
Query Match: 6.53% Indels: 66
RESULT 1464
ID ACN44860 standard; DNA; 48133 BP.
DE Mouse genomic sequence mCG49939.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Percent Similarity: 43.75% Conservative: 4
Best Local Similarity: 35.42% Mismatches: 15
Query Match: 6.53% Indels: 12
RESULT 1465
ID ACN44300 standard; DNA; 57137 BP.
DE Mouse genomic sequence mCG17164.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Percent Similarity: 32.24% Conservative: 31
Best Local Similarity: 19.59% Mismatches: 88
Query Match: 6.53% Indels: 78
RESULT 1466
ID ACN44706 standard; DNA; 59341 BP.
DE Human genomic sequence hCG17286.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Percent Similarity: 43.68% Conservative: 41
Best Local Similarity: 20.11% Mismatches: 61
Query Match: 6.53% Indels: 37
RESULT 1467
ID ADQ97703 standard; DNA; 103665 BP.
DE Human cancer associated sequence HD10-031, SEQ ID 680.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Percent Similarity: 37.30% Conservative: 16
Best Local Similarity: 24.60% Mismatches: 35
Query Match: 6.53% Indels: 44
RESULT 1468
ID ABD32804 standard; DNA; 608916 BP.
DE Mouse cancer-associated genomic DNA MD16-059.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Percent Similarity: 33.95% Conservative: 17
Best Local Similarity: 23.46% Mismatches: 59
Query Match: 6.53% Indels: 49
RESULT 1469
Percent Similarity: 33.95% Conservative: 17
Best Local Similarity: 23.46% Mismatches: 59
Query Match: 6.53% Indels: 49
RESULT 1470
ID ABQ81850 standard; DNA; 156638 BP.
DE Bifidobacterium longum NCC2705 related nucleotide sequence SEQ ID:1106.
PN EP1227152-A1.
PD 31-JUL-2002.
PA (NEST) SOC PROD NESTLE SA.
Percent Similarity: 36.45% Conservative: 27
Best Local Similarity: 23.15% Mismatches: 60
Query Match: 6.53% Indels: 69
RESULT 1471
ID ABD33389 standard; DNA; 197526 BP.
DE Human cancer-associated (CA) gene HD07-072.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Percent Similarity: 51.79% Conservative: 11
Best Local Similarity: 32.14% Mismatches: 19
Query Match: 6.53% Indels: 8
RESULT 1472
ID ADL13693 standard; DNA; 231222 BP.
DE Osteoarthritis-associated polymorphic nucleotide #225.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 40.68% Conservative: 29
Best Local Similarity: 24.29% Mismatches: 60
Query Match: 6.53% Indels: 46
RESULT 1473
ID ABQ67392 standard; DNA; 321 BP.
DE Listeria innocua DNA sequence #194.
PN WO200228891-A2.
PD 11-APR-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Percent Similarity: 47.73% Conservative: 17
Best Local Similarity: 28.41% Mismatches: 33
Query Match: 6.49% Indels: 13
RESULT 1474
ID AAC51744 standard; DNA; 424 BP.
DE Zea mays DNA fragment SEQ ID NO: 69628.
PN EP1033405-A2.
PD 06-SEP-2000.
Percent Similarity: 42.86% Conservative: 27
Best Local Similarity: 22.56% Mismatches: 54
Query Match: 6.49% Indels: 22
RESULT 1475
ID ADQ20718 standard; DNA; 468 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 3538.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Percent Similarity: 54.00% Conservative: 12
Best Local Similarity: 30.00% Mismatches: 16
Query Match: 6.49% Indels: 7
RESULT 1476
ID ABV94493 standard; cDNA; 546 BP.
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:7.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.13% Conservative: 20
Best Local Similarity: 24.64% Mismatches: 49
Query Match: 6.49% Indels: 35
RESULT 1477
ID ADJ66748 standard; DNA; 710 BP.
DE Muc 16 Stump plasmid construct DNA sequence.
PN WO2004005470-A2.
PD 15-JAN-2004.
PA (IMMU-) IMMUNOGEN INC.
Percent Similarity: 34.13% Conservative: 31
Best Local Similarity: 19.23% Mismatches: 60
Query Match: 6.49% Indels: 77
RESULT 1478
ID AAH04390 standard; cDNA; 856 BP.

DE Human cDNA clone (5'-primer) SEQ ID NO:1225.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Percent Similarity: 46.72% Conservative: 28
Best Local Similarity: 23.77% Mismatches: 48
Query Match: 6.49% Indels: 17
RESULT 1479
ID ABV94567 standard; cDNA; 903 BP.
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:128.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.13% Conservative: 20
Best Local Similarity: 24.64% Mismatches: 49
Query Match: 6.49% Indels: 35
RESULT 1480
ID ABV94504 standard; cDNA; 903 BP.
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:18.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.13% Conservative: 20
Best Local Similarity: 24.64% Mismatches: 49
Query Match: 6.49% Indels: 35
RESULT 1481
ID ADM18763 standard; cDNA; 903 BP.
DE Human co-stimulatory molecule encoding cDNA SEQ ID NO:128.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.13% Conservative: 20
Best Local Similarity: 24.64% Mismatches: 49
Query Match: 6.49% Indels: 35
RESULT 1482
ID ADM18653 standard; cDNA; 903 BP.
DE Human co-stimulatory molecule encoding cDNA SEQ ID NO:18.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.13% Conservative: 20
Best Local Similarity: 24.64% Mismatches: 49
Query Match: 6.49% Indels: 35
RESULT 1483
ID ABV94569 standard; cDNA; 912 BP.
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:130.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.13% Conservative: 20
Best Local Similarity: 24.64% Mismatches: 49
Query Match: 6.49% Indels: 35
RESULT 1484
ID ABV94495 standard; cDNA; 912 BP.
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:9.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.13% Conservative: 20
Best Local Similarity: 24.64% Mismatches: 49
Query Match: 6.49% Indels: 35
RESULT 1485
ID ABV94568 standard; cDNA; 912 BP.
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:129.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.13% Conservative: 20
Best Local Similarity: 24.64% Mismatches: 49
Query Match: 6.49% Indels: 35
RESULT 1486
ID ABV94541 standard; cDNA; 912 BP.
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:102.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.13% Conservative: 20
Best Local Similarity: 24.64% Mismatches: 49
Query Match: 6.49% Indels: 35
RESULT 1487
ID ABV94565 standard; cDNA; 912 BP.
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:126.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.13% Conservative: 20
Best Local Similarity: 24.64% Mismatches: 49
Query Match: 6.49% Indels: 35
RESULT 1488
ID ABV94494 standard; cDNA; 912 BP.
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:8.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.13% Conservative: 20
Best Local Similarity: 24.64% Mismatches: 49
Query Match: 6.49% Indels: 35
RESULT 1489
ID ABV94499 standard; cDNA; 912 BP.
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:13.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.13% Conservative: 20
Best Local Similarity: 24.64% Mismatches: 49
Query Match: 6.49% Indels: 35
RESULT 1490
ID ABV94502 standard; cDNA; 912 BP.
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:16.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.13% Conservative: 20
Best Local Similarity: 24.64% Mismatches: 49
Query Match: 6.49% Indels: 35
RESULT 1491
ID ABV94506 standard; cDNA; 912 BP.
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:20.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.13% Conservative: 20
Best Local Similarity: 24.64% Mismatches: 49
Query Match: 6.49% Indels: 35
RESULT 1492
ID ABV94554 standard; cDNA; 912 BP.
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:115.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.13% Conservative: 20
Best Local Similarity: 24.64% Mismatches: 49
Query Match: 6.49% Indels: 35
RESULT 1493
ID ABV94496 standard; cDNA; 912 BP.
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:10.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.13% Conservative: 20
Best Local Similarity: 24.64% Mismatches: 49
Query Match: 6.49% Indels: 35
RESULT 1494
ID ABV94577 standard; cDNA; 912 BP.
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:138.
PN WO200200717-A2.

PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.13% Conservative: 20
Best Local Similarity: 24.64% Mismatches: 49
Query Match: 6.49% Indels: 35
RESULT 1495
ID ABV94491 standard; cDNA; 912 BP.
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:5.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.13% Conservative: 20
Best Local Similarity: 24.64% Mismatches: 49
Query Match: 6.49% Indels: 35
RESULT 1496
ID ABV94497 standard; cDNA; 912 BP.
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:11.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.13% Conservative: 20
Best Local Similarity: 24.64% Mismatches: 49
Query Match: 6.49% Indels: 35
RESULT 1497
ID ABV94539 standard; cDNA; 912 BP.
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:100.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.13% Conservative: 20
Best Local Similarity: 24.64% Mismatches: 49
Query Match: 6.49% Indels: 35
RESULT 1498
ID ABV94562 standard; cDNA; 912 BP.
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:123.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.13% Conservative: 20
Best Local Similarity: 24.64% Mismatches: 49
Query Match: 6.49% Indels: 35
RESULT 1499
ID ABV94505 standard; cDNA; 912 BP.
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:19.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.13% Conservative: 20
Best Local Similarity: 24.64% Mismatches: 49
Query Match: 6.49% Indels: 35
RESULT 1500
ID ABV94547 standard; cDNA; 912 BP.
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:108.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Percent Similarity: 39.13% Conservative: 20
Best Local Similarity: 24.64% Mismatches: 49
Query Match: 6.49% Indels: 35

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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 25, 2005, 00:57:24 ; Search time 160 Seconds
(without alignments)
2168.067 Million cell updates/sec

Title: US-09-989-724-387
Perfect score: 1102
Sequence: 1 MLWLLFFLVTAIHAELCQPG.....ENGIPSDPLDMKGGILMMPS 212

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Command line parameters:
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1064	96.6	848	3	US-08-905-223-27	Sequence 27, Appl
2	1064	96.6	848	3	US-09-247-155-27	Sequence 27, Appl
3	1064	96.6	848	4	US-09-663-600A-27	Sequence 27, Appl
4	1064	96.6	848	4	US-09-621-976-5	Sequence 5, Appli
5	1064	96.6	848	4	US-09-513-999C-5	Sequence 5, Appli
6	1064	96.6	848	4	US-09-471-276-5	Sequence 5, Appli
7	376	34.1	2415	3	US-08-989-299-3	Sequence 3, Appli
8	376	34.1	2415	4	US-09-407-427-3	Sequence 3, Appli
9	376	34.1	3388	4	US-09-949-016-5413	Sequence 5413, Ap
10	376	34.1	3396	3	US-08-989-299-1	Sequence 1, Appli
11	376	34.1	3396	4	US-10-158-847-141	Sequence 141, App
12	376	34.1	3396	4	US-09-407-427-1	Sequence 1, Appli
13	359	32.6	2920	4	US-10-158-847-137	Sequence 137, App
14	281	25.5	862	3	US-09-289-349-6	Sequence 6, Appli
c 15	233.5	21.2	2350	3	US-09-280-116-40	Sequence 40, Appl
16	207.5	18.8	43986	4	US-09-949-016-17155	Sequence 17155, A
c 17	91	8.3	580073	4	US-08-545-528D-1	Sequence 1, Appli
18	90	8.2	3136	1	US-08-188-228-41	Sequence 41, Appl
19	90	8.2	3136	1	US-08-332-638-41	Sequence 41, Appl
20	89.5	8.1	2550	1	US-08-188-228-53	Sequence 53, Appl
21	89.5	8.1	2550	1	US-08-332-643-47	Sequence 47, Appl
22	89.5	8.1	2550	1	US-08-332-638-53	Sequence 53, Appl
23	89.5	8.1	3146	4	US-09-620-312D-277	Sequence 277, App
24	89	8.1	2311	4	US-09-949-016-1552	Sequence 1552, Ap
25	86	7.8	3207	1	US-07-946-497-1	Sequence 1, Appli
26	86	7.8	3207	1	US-08-483-322-1	Sequence 1, Appli
27	86	7.8	3207	2	US-08-478-882-1	Sequence 1, Appli
28	85.5	7.8	5323	4	US-09-799-451-726	Sequence 726, App
29	85	7.7	4756	4	US-09-023-655-1461	Sequence 1461, Ap
30	84.5	7.7	3983	4	US-09-949-016-2021	Sequence 2021, Ap
31	83.5	7.6	5117	3	US-08-854-585-1	Sequence 1, Appli
32	83.5	7.6	5117	4	US-09-447-533-1	Sequence 1, Appli
33	83.5	7.6	5117	5	PCT-US95-05512-1	Sequence 1, Appli
34	83	7.5	1830121	4	US-09-557-884-1	Sequence 1, Appli
35	83	7.5	1830121	4	US-09-643-990A-1	Sequence 1, Appli
36	82.5	7.5	1590	4	US-09-134-000C-2543	Sequence 2543, Ap
c 37	82.5	7.5	421491	4	US-09-949-016-12805	Sequence 12805, A
c 38	82.5	7.5	421494	4	US-09-949-016-14060	Sequence 14060, A
c 39	82	7.4	1748	4	US-09-270-767-13324	Sequence 13324, A
40	82	7.4	1854	4	US-09-949-016-1931	Sequence 1931, Ap
41	82	7.4	9013	4	US-09-949-016-13673	Sequence 13673, A
42	82	7.4	139552	4	US-09-949-016-15300	Sequence 15300, A
43	81.5	7.4	5717	4	US-09-023-655-1333	Sequence 1333, Ap
44	81.5	7.4	5717	4	US-09-949-016-321	Sequence 321, App
45	81.5	7.4	7244	4	US-09-949-016-1530	Sequence 1530, Ap
c 46	81.5	7.4	109159	4	US-09-949-016-14169	Sequence 14169, A
c 47	81.5	7.4	109159	4	US-09-949-016-14170	Sequence 14170, A
48	81	7.4	1539	4	US-09-248-796A-116	Sequence 116, App
49	80	7.3	87563	3	US-09-453-702B-57	Sequence 57, Appl
50	79.5	7.2	1011	4	US-09-902-540-3912	Sequence 3912, Ap
51	79.5	7.2	21375	4	US-09-902-540-1193	Sequence 1193, Ap
c 52	79	7.2	96922	4	US-09-949-016-17061	Sequence 17061, A
53	78.5	7.1	1761	3	US-09-404-879A-387	Sequence 387, App
54	78.5	7.1	1761	4	US-09-667-857-387	Sequence 387, App
55	78.5	7.1	2608	3	US-09-404-879A-386	Sequence 386, App
56	78.5	7.1	2608	4	US-09-667-857-386	Sequence 386, App
57	78.5	7.1	2996	3	US-09-404-879A-311	Sequence 311, App
58	78.5	7.1	2996	4	US-09-338-933-311	Sequence 311, App
59	78.5	7.1	2996	4	US-09-667-857-311	Sequence 311, App
60	78.5	7.1	3581	2	US-08-738-349-1	Sequence 1, Appli
c 61	78.5	7.1	11288	3	US-08-646-301A-1	Sequence 1, Appli
c 62	78.5	7.1	11288	3	US-08-481-968A-4	Sequence 4, Appli
c 63	78.5	7.1	11288	3	US-08-154-712B-4	Sequence 4, Appli
c 64	78.5	7.1	11288	4	US-09-947-925A-4	Sequence 4, Appli
c 65	78.5	7.1	15056	4	US-09-474-699-10	Sequence 10, Appl
c 66	78.5	7.1	15056	4	US-09-814-351-14	Sequence 14, Appl
c 67	78.5	7.1	19703	4	US-09-949-016-14926	Sequence 14926, A
c 68	78	7.1	91665	4	US-09-949-016-12234	Sequence 12234, A
69	77.5	7.0	15894	1	US-08-348-891A-1	Sequence 1, Appli
70	77.5	7.0	15894	1	US-08-905-817-1	Sequence 1, Appli
c 71	77.5	7.0	81585	4	US-09-949-016-15427	Sequence 15427, A
c 72	77	7.0	1664976	4	US-08-916-421B-1	Sequence 1, Appli
c 73	77	7.0	1664976	4	US-09-692-570-1	Sequence 1, Appli
c 74	76.5	6.9	601	4	US-09-949-016-80947	Sequence 80947, A
c 75	76.5	6.9	960	4	US-09-134-000C-1545	Sequence 1545, Ap
76	76.5	6.9	981	4	US-09-248-796A-54	Sequence 54, Appl
77	76.5	6.9	6376	4	US-09-799-451-48	Sequence 48, Appl
c 78	76.5	6.9	19389	4	US-09-949-016-15113	Sequence 15113, A
79	76.5	6.9	199471	4	US-09-949-016-14083	Sequence 14083, A
c 80	76.5	6.9	481115	4	US-09-949-016-11940	Sequence 11940, A
c 81	76	6.9	601	4	US-09-949-016-160172	Sequence 160172,
82	76	6.9	730	4	US-10-029-517-20	Sequence 20, Appl
83	76	6.9	981	4	US-10-029-517-16	Sequence 16, Appl
c 84	76	6.9	1728	4	US-09-096-731A-1	Sequence 1, Appli
85	75.5	6.9	601	4	US-09-949-016-162822	Sequence 162822,

	86	75.5	6.9	601	4	US-09-949-016-162823	Sequence 162823,
	87	75.5	6.9	859	4	US-10-029-517-103	Sequence 103, App
	88	75.5	6.9	1721	4	US-10-029-517-3	Sequence 3, Appli
	89	75.5	6.9	1804	4	US-10-029-517-17	Sequence 17, Appl
	90	75.5	6.9	2835	4	US-09-107-532A-1210	Sequence 1210, Ap
c	91	75.5	6.9	2976	4	US-09-949-016-5710	Sequence 5710, Ap
	92	75.5	6.9	6192	2	US-08-479-537A-1	Sequence 1, Appli
	93	75.5	6.9	6192	3	US-09-083-116-1	Sequence 1, Appli
	94	75.5	6.9	6192	3	US-09-134-916A-1	Sequence 1, Appli
c	95	75.5	6.9	7646	4	US-08-956-171E-121	Sequence 121, App
c	96	75.5	6.9	7646	4	US-08-781-986A-121	Sequence 121, App
c	97	75.5	6.9	9461	3	US-09-221-017B-513	Sequence 513, App
c	98	75.5	6.9	29977	4	US-09-949-016-17452	Sequence 17452, A
	99	75.5	6.9	31166	4	US-09-949-016-13464	Sequence 13464, A
	100	75.5	6.9	41612	4	US-09-949-016-12769	Sequence 12769, A
	101	75.5	6.9	41639	4	US-09-949-016-12773	Sequence 12773, A
	102	75.5	6.9	49301	4	US-09-949-016-16296	Sequence 16296, A
c	103	75.5	6.9	86980	4	US-09-949-016-15344	Sequence 15344, A
	104	75.5	6.9	194933	4	US-09-949-016-14172	Sequence 14172, A
	105	75	6.8	414	4	US-09-513-999C-8461	Sequence 8461, Ap
c	106	75	6.8	601	4	US-09-949-016-59911	Sequence 59911, A
	107	75	6.8	3546	1	US-08-086-634-1	Sequence 1, Appli
	108	75	6.8	5349	4	US-09-949-016-4876	Sequence 4876, Ap
	109	75	6.8	5361	4	US-09-949-016-318	Sequence 318, App
	110	75	6.8	5373	4	US-09-023-655-1318	Sequence 1318, Ap
	111	75	6.8	5373	4	US-09-000-004A-3	Sequence 3, Appli
	112	75	6.8	8827	3	US-09-245-041-1	Sequence 1, Appli
	113	75	6.8	8827	4	US-09-358-055B-1	Sequence 1, Appli
	114	75	6.8	8827	4	US-09-893-238-1	Sequence 1, Appli
	115	75	6.8	12571	3	US-09-322-478-20	Sequence 20, Appl
	116	75	6.8	12571	4	US-09-586-106D-20	Sequence 20, Appl
	117	75	6.8	52655	4	US-09-949-016-13495	Sequence 13495, A
	118	75	6.8	205044	4	US-09-949-016-15851	Sequence 15851, A
	119	75	6.8	205044	4	US-09-949-016-15852	Sequence 15852, A
	120	75	6.8	205044	4	US-09-949-016-15853	Sequence 15853, A
	121	75	6.8	223471	4	US-09-949-016-12387	Sequence 12387, A
	122	75	6.8	223471	4	US-09-949-016-12724	Sequence 12724, A
	123	75	6.8	223471	4	US-09-949-016-12725	Sequence 12725, A
	124	74.5	6.8	601	4	US-09-949-016-59268	Sequence 59268, A
	125	74.5	6.8	2149	4	US-09-023-655-765	Sequence 765, App
	126	74.5	6.8	36519	3	US-08-923-137-2	Sequence 2, Appli
c	127	74.5	6.8	119032	4	US-09-949-016-12160	Sequence 12160, A
c	128	74.5	6.8	119032	4	US-09-949-016-17268	Sequence 17268, A
c	129	74.5	6.8	192506	4	US-09-949-016-15830	Sequence 15830, A
	130	74	6.7	467	4	US-09-621-976-1390	Sequence 1390, Ap
c	131	74	6.7	797	4	US-09-399-081A-9	Sequence 9, Appli
c	132	74	6.7	39003	4	US-09-596-002-21	Sequence 21, Appl
c	133	74	6.7	60141	4	US-09-949-016-15874	Sequence 15874, A
c	134	74	6.7	343352	4	US-09-949-016-13498	Sequence 13498, A
c	135	73.5	6.7	601	4	US-09-949-016-172825	Sequence 172825,
	136	73.5	6.7	753	3	US-09-134-001C-1562	Sequence 1562, Ap
	137	73.5	6.7	882	4	US-09-248-796A-11728	Sequence 11728, A
	138	73.5	6.7	1046	4	US-09-419-788-163	Sequence 163, App
	139	73.5	6.7	1209	4	US-09-543-681A-885	Sequence 885, App
	140	73.5	6.7	1368	4	US-09-248-796A-3432	Sequence 3432, Ap
	141	73.5	6.7	1605	4	US-09-710-279-919	Sequence 919, App
	142	73.5	6.7	1689	4	US-09-489-039A-1403	Sequence 1403, Ap
	143	73.5	6.7	1949	1	US-09-041-075A-7	Sequence 7, Appli
	144	73.5	6.7	2625	1	US-08-188-228-57	Sequence 57, Appl
	145	73.5	6.7	2625	1	US-08-332-643-51	Sequence 51, Appl
	146	73.5	6.7	2625	1	US-08-332-638-57	Sequence 57, Appl
	147	73.5	6.7	2625	4	US-09-654-328-1	Sequence 1, Appli
	148	73.5	6.7	2730	4	US-09-949-016-4103	Sequence 4103, Ap
c	149	73.5	6.7	2998	4	US-09-710-279-3894	Sequence 3894, Ap
	150	73.5	6.7	3118	4	US-09-710-279-3798	Sequence 3798, Ap
	151	73.5	6.7	3712	2	US-08-738-349-3	Sequence 3, Appli
	152	73.5	6.7	7015	3	US-09-177-249-6	Sequence 6, Appli
	153	73.5	6.7	7015	4	US-09-812-283-6	Sequence 6, Appli
	154	73.5	6.7	21978	4	US-09-949-016-16646	Sequence 16646, A
	155	73.5	6.7	41062	4	US-09-949-016-12761	Sequence 12761, A
	156	73.5	6.7	41062	4	US-09-949-016-16796	Sequence 16796, A
	157	73.5	6.7	98828	4	US-09-949-016-16630	Sequence 16630, A
c	158	73.5	6.7	141560	4	US-09-949-016-16476	Sequence 16476, A
	159	73	6.6	588	4	US-09-543-681A-3813	Sequence 3813, Ap
c	160	73	6.6	601	4	US-09-949-016-96451	Sequence 96451, A
c	161	73	6.6	601	4	US-09-949-016-96717	Sequence 96717, A
c	162	73	6.6	601	4	US-09-949-016-96983	Sequence 96983, A
c	163	73	6.6	601	4	US-09-949-016-97249	Sequence 97249, A
c	164	73	6.6	601	4	US-09-949-016-97515	Sequence 97515, A
c	165	73	6.6	601	4	US-09-949-016-97781	Sequence 97781, A
c	166	73	6.6	601	4	US-09-949-016-98047	Sequence 98047, A
c	167	73	6.6	601	4	US-09-949-016-98313	Sequence 98313, A
c	168	73	6.6	601	4	US-09-949-016-98579	Sequence 98579, A
c	169	73	6.6	601	4	US-09-949-016-98845	Sequence 98845, A
c	170	73	6.6	601	4	US-09-949-016-99111	Sequence 99111, A
c	171	73	6.6	601	4	US-09-949-016-99377	Sequence 99377, A
c	172	73	6.6	601	4	US-09-949-016-99643	Sequence 99643, A
c	173	73	6.6	601	4	US-09-949-016-99909	Sequence 99909, A
c	174	73	6.6	601	4	US-09-949-016-100175	Sequence 100175,
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c	177	73	6.6	601	4	US-09-949-016-101011	Sequence 101011,
c	178	73	6.6	601	4	US-09-949-016-101277	Sequence 101277,
c	179	73	6.6	601	4	US-09-949-016-101543	Sequence 101543,
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c	181	73	6.6	601	4	US-09-949-016-145820	Sequence 145820,
c	182	73	6.6	601	4	US-09-949-016-146088	Sequence 146088,
c	183	73	6.6	601	4	US-09-949-016-146356	Sequence 146356,
	184	73	6.6	1002	4	US-09-919-039-257	Sequence 257, App
c	185	73	6.6	1354	4	US-09-477-135A-121	Sequence 121, App
c	186	73	6.6	1478	3	US-09-545-814-28	Sequence 28, Appl
	187	73	6.6	1478	3	US-09-545-814-30	Sequence 30, Appl
c	188	73	6.6	1623	4	US-09-270-767-3557	Sequence 3557, Ap
c	189	73	6.6	1623	4	US-09-270-767-18839	Sequence 18839, A
	190	73	6.6	1930	4	US-09-270-767-9205	Sequence 9205, Ap
	191	73	6.6	1930	4	US-09-270-767-24487	Sequence 24487, A
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	193	73	6.6	6798	4	US-09-949-016-12102	Sequence 12102, A
	194	73	6.6	6798	4	US-09-949-016-13819	Sequence 13819, A
c	195	73	6.6	92155	4	US-09-949-016-17484	Sequence 17484, A
c	196	73	6.6	98708	4	US-09-949-016-16392	Sequence 16392, A
	197	73	6.6	260247	4	US-09-949-016-13358	Sequence 13358, A
	198	73	6.6	818128	4	US-09-949-016-14546	Sequence 14546, A
	199	73	6.6	818128	4	US-09-949-016-14547	Sequence 14547, A
	200	73	6.6	818128	4	US-09-949-016-14548	Sequence 14548, A
	201	73	6.6	818128	4	US-09-949-016-14549	Sequence 14549, A
	202	73	6.6	818128	4	US-09-949-016-14550	Sequence 14550, A
	203	73	6.6	818128	4	US-09-949-016-14551	Sequence 14551, A
	204	73	6.6	818128	4	US-09-949-016-14552	Sequence 14552, A
	205	73	6.6	818128	4	US-09-949-016-14553	Sequence 14553, A
	206	73	6.6	818128	4	US-09-949-016-14554	Sequence 14554, A
	207	73	6.6	818128	4	US-09-949-016-14555	Sequence 14555, A
	208	73	6.6	818128	4	US-09-949-016-14556	Sequence 14556, A
	209	73	6.6	818128	4	US-09-949-016-14557	Sequence 14557, A
	210	73	6.6	818128	4	US-09-949-016-14558	Sequence 14558, A
	211	73	6.6	818128	4	US-09-949-016-14559	Sequence 14559, A
	212	73	6.6	818128	4	US-09-949-016-14560	Sequence 14560, A
	213	73	6.6	818128	4	US-09-949-016-14561	Sequence 14561, A
	214	73	6.6	818128	4	US-09-949-016-14562	Sequence 14562, A
	215	73	6.6	818128	4	US-09-949-016-14564	Sequence 14564, A
	216	73	6.6	818128	4	US-09-949-016-14565	Sequence 14565, A
	217	73	6.6	818128	4	US-09-949-016-14566	Sequence 14566, A
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	220	73	6.6	1230230	4	US-09-438-185A-1	Sequence 1, Appli
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	222	73	6.6	4411529	3	US-09-103-840A-1	Sequence 1, Appli
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c	225	72.5	6.6	601	4	US-09-949-016-85159	Sequence 85159, A
c	226	72.5	6.6	601	4	US-09-949-016-120840	Sequence 120840,
c	227	72.5	6.6	601	4	US-09-949-016-120841	Sequence 120841,
	228	72.5	6.6	759	4	US-10-029-517-10	Sequence 10, Appl
	229	72.5	6.6	900	4	US-09-495-052-61	Sequence 61, Appl
c	230	72.5	6.6	1723	4	US-09-949-016-113	Sequence 113, App
c	231	72.5	6.6	1725	4	US-09-949-016-2886	Sequence 2886, Ap

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	233	72.5	6.6	46603	4	US-09-949-016-15636	Sequence 15636, A
	234	72.5	6.6	76610	4	US-09-949-016-15521	Sequence 15521, A
c	235	72.5	6.6	93510	4	US-09-949-016-15095	Sequence 15095, A
c	236	72.5	6.6	218940	4	US-09-949-016-17539	Sequence 17539, A
c	237	72.5	6.6	222691	4	US-09-949-016-11762	Sequence 11762, A
c	238	72.5	6.6	222697	4	US-09-949-016-15842	Sequence 15842, A
	239	72	6.5	577	4	US-10-029-517-14	Sequence 14, Appl
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	241	72	6.5	591	2	US-09-213-392-2	Sequence 2, Appli
	242	72	6.5	591	2	US-09-083-661-2	Sequence 2, Appli
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	244	72	6.5	1162	2	US-08-332-562A-135	Sequence 135, App
	245	72	6.5	1245	4	US-09-755-665-13	Sequence 13, Appl
	246	72	6.5	1445	4	US-09-461-325-13	Sequence 13, Appl
	247	72	6.5	1445	4	US-10-012-542-13	Sequence 13, Appl
	248	72	6.5	1445	4	US-10-115-123-13	Sequence 13, Appl
	249	72	6.5	1533	4	US-09-540-236-228	Sequence 228, App
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c	251	72	6.5	1599	2	US-08-284-391B-3	Sequence 3, Appli
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c	255	72	6.5	1599	5	PCT-US95-00454-3	Sequence 3, Appli
	256	72	6.5	1977	4	US-09-614-891-5	Sequence 5, Appli
c	257	72	6.5	15016	4	US-09-601-198-60	Sequence 60, Appl
	258	72	6.5	183202	4	US-09-949-016-13614	Sequence 13614, A
c	259	71.5	6.5	1419	4	US-09-543-681A-2388	Sequence 2388, Ap
	260	71.5	6.5	1788	1	US-09-041-075A-9	Sequence 9, Appli
	261	71.5	6.5	6470	4	US-09-620-312D-255	Sequence 255, App
c	262	71.5	6.5	7680	4	US-09-953-318-3	Sequence 3, Appli
	263	71.5	6.5	51927	4	US-09-949-016-17347	Sequence 17347, A
	264	71.5	6.5	51927	4	US-09-949-016-17348	Sequence 17348, A
	265	71.5	6.5	73853	4	US-09-949-016-12029	Sequence 12029, A
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	267	71.5	6.5	174259	4	US-09-949-016-11968	Sequence 11968, A
	268	71.5	6.5	174262	4	US-09-949-016-14259	Sequence 14259, A
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	270	71	6.4	1042	4	US-09-799-451-745	Sequence 745, App
	271	71	6.4	1117	4	US-09-949-016-3274	Sequence 3274, Ap
	272	71	6.4	1297	4	US-09-023-655-876	Sequence 876, App
	273	71	6.4	1629	4	US-09-543-681A-2692	Sequence 2692, Ap
	274	71	6.4	1683	4	US-09-943-075A-8	Sequence 8, Appli
	275	71	6.4	1794	3	US-09-213-719-1	Sequence 1, Appli
	276	71	6.4	1794	4	US-09-949-016-97	Sequence 97, Appl
	277	71	6.4	2669	1	US-09-985-799-91	Sequence 91, Appl
	278	71	6.4	2669	1	US-09-985-799-101	Sequence 101, App
	279	71	6.4	2669	1	US-09-977-371-91	Sequence 91, Appl
	280	71	6.4	2669	1	US-09-977-371-101	Sequence 101, App
	281	71	6.4	2669	1	US-08-594-031-91	Sequence 91, Appl
	282	71	6.4	2669	1	US-08-594-031-101	Sequence 101, App
	283	71	6.4	2855	4	US-09-949-016-4102	Sequence 4102, Ap
	284	71	6.4	4078	4	US-09-016-434-1132	Sequence 1132, Ap
	285	71	6.4	4675	4	US-09-566-921-97	Sequence 97, Appl
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c	287	71	6.4	5207	4	US-09-774-528-20	Sequence 20, Appl
	288	71	6.4	5632	4	US-09-358-055B-141	Sequence 141, App
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	290	71	6.4	5690	2	US-08-716-679-2	Sequence 2, Appli
	291	71	6.4	6000	1	US-08-348-006B-6	Sequence 6, Appli
	292	71	6.4	6000	2	US-08-800-825A-6	Sequence 6, Appli
	293	71	6.4	6000	3	US-09-158-657-6	Sequence 6, Appli
	294	71	6.4	6000	5	PCT-US94-10166-6	Sequence 6, Appli
	295	71	6.4	6363	4	US-09-023-655-879	Sequence 879, App
	296	71	6.4	6370	3	US-09-245-041-12	Sequence 12, Appl
	297	71	6.4	6370	4	US-09-358-055B-12	Sequence 12, Appl
	298	71	6.4	6370	4	US-09-893-238-12	Sequence 12, Appl
	299	71	6.4	8589	3	US-09-245-041-14	Sequence 14, Appl
	300	71	6.4	8589	4	US-09-358-055B-14	Sequence 14, Appl
	301	71	6.4	8589	4	US-09-893-238-14	Sequence 14, Appl
c	302	71	6.4	36618	4	US-09-949-016-16935	Sequence 16935, A
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c	304	71	6.4	148567	4	US-10-254-869-3	Sequence 3, Appli
c	305	71	6.4	148567	4	US-10-667-442-3	Sequence 3, Appli
	306	71	6.4	198942	4	US-09-949-016-13209	Sequence 13209, A
	307	70.5	6.4	1657	3	US-08-948-564-11	Sequence 11, Appl
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c	309	70.5	6.4	1659	1	US-08-440-179-1	Sequence 1, Appli
c	310	70.5	6.4	1659	3	US-09-039-657-1	Sequence 1, Appli
c	311	70.5	6.4	1659	5	PCT-US91-02339-2	Sequence 2, Appli
	312	70.5	6.4	1910	3	US-09-149-476-297	Sequence 297, App
	313	70.5	6.4	1945	3	US-09-149-476-164	Sequence 164, App
c	314	70.5	6.4	2047	3	US-08-836-261A-1	Sequence 1, Appli
	315	70.5	6.4	2430	4	US-09-620-312D-176	Sequence 176, App
	316	70.5	6.4	2768	4	US-09-949-016-5686	Sequence 5686, Ap
	317	70.5	6.4	2923	3	US-09-619-353-9	Sequence 9, Appli
	318	70.5	6.4	3017	4	US-09-799-451-153	Sequence 153, App
	319	70.5	6.4	3158	4	US-09-710-279-4054	Sequence 4054, Ap
	320	70.5	6.4	4079	4	US-09-016-434-1208	Sequence 1208, Ap
	321	70.5	6.4	4132	4	US-09-300-958A-10	Sequence 10, Appl
	322	70.5	6.4	4204	4	US-09-023-655-1292	Sequence 1292, Ap
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	324	70.5	6.4	7475	3	US-09-096-570-1	Sequence 1, Appli
	325	70.5	6.4	7475	3	US-09-265-617B-1	Sequence 1, Appli
	326	70.5	6.4	33155	4	US-09-949-016-16421	Sequence 16421, A
	327	70.5	6.4	34001	4	US-09-596-002-18	Sequence 18, Appl
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c	330	70.5	6.4	100551	4	US-09-949-016-16207	Sequence 16207, A
	331	70.5	6.4	251769	4	US-09-949-016-13185	Sequence 13185, A
	332	70.5	6.4	251769	4	US-09-949-016-13186	Sequence 13186, A
c	333	70.5	6.4	260247	4	US-09-949-016-13358	Sequence 13358, A
	334	70.5	6.4	266748	4	US-09-949-016-13187	Sequence 13187, A
	335	70.5	6.4	266748	4	US-09-949-016-13188	Sequence 13188, A
	336	70	6.4	703	4	US-09-023-655-1097	Sequence 1097, Ap
	337	70	6.4	1016	4	US-09-270-767-976	Sequence 976, App
	338	70	6.4	1016	4	US-09-270-767-16258	Sequence 16258, A
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	340	70	6.4	1223	4	US-09-949-016-2283	Sequence 2283, Ap
	341	70	6.4	1278	4	US-09-489-039A-2274	Sequence 2274, Ap
	342	70	6.4	1317	4	US-09-248-796A-9956	Sequence 9956, Ap
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	344	70	6.4	3172	6	5196511-1	Patent No. 5196511
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	346	70	6.4	3303	3	US-09-409-648-6	Sequence 6, Appli
	347	70	6.4	3303	4	US-09-054-272-9	Sequence 9, Appli
	348	70	6.4	13508	4	US-08-956-171E-120	Sequence 120, App
	349	70	6.4	13508	4	US-08-781-986A-120	Sequence 120, App
	350	70	6.4	42931	4	US-08-311-731A-129	Sequence 129, App
	351	70	6.4	211049	4	US-09-949-016-15770	Sequence 15770, A
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c	354	69.5	6.3	359	4	US-09-620-405B-294	Sequence 294, App
c	355	69.5	6.3	359	4	US-09-339-338-294	Sequence 294, App
c	356	69.5	6.3	359	4	US-09-433-826B-294	Sequence 294, App
c	357	69.5	6.3	359	4	US-09-604-287A-294	Sequence 294, App
c	358	69.5	6.3	359	4	US-09-834-759-294	Sequence 294, App
c	359	69.5	6.3	359	4	US-09-590-751A-294	Sequence 294, App
c	360	69.5	6.3	359	4	US-09-551-621-294	Sequence 294, App
c	361	69.5	6.3	371	3	US-09-643-597-145	Sequence 145, App
c	362	69.5	6.3	371	4	US-09-480-884A-145	Sequence 145, App
c	363	69.5	6.3	371	4	US-09-542-615A-145	Sequence 145, App
c	364	69.5	6.3	371	4	US-09-606-421B-145	Sequence 145, App
c	365	69.5	6.3	371	4	US-09-221-107-145	Sequence 145, App
c	366	69.5	6.3	371	4	US-09-466-396A-145	Sequence 145, App
c	367	69.5	6.3	371	4	US-09-476-496A-145	Sequence 145, App
c	368	69.5	6.3	371	4	US-09-630-940B-145	Sequence 145, App
c	369	69.5	6.3	371	4	US-09-285-479-145	Sequence 145, App
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	371	69.5	6.3	601	4	US-09-949-016-166302	Sequence 166302,
	372	69.5	6.3	601	4	US-09-949-016-177703	Sequence 177703,
	373	69.5	6.3	842	4	US-09-270-767-12313	Sequence 12313, A
	374	69.5	6.3	873	4	US-09-451-291-4	Sequence 4, Appli
	375	69.5	6.3	1173	4	US-09-620-312D-1022	Sequence 1022, Ap
	376	69.5	6.3	1617	4	US-09-328-352-2944	Sequence 2944, Ap
	377	69.5	6.3	1892	4	US-09-949-016-4236	Sequence 4236, Ap

	378	69.5	6.3	1894	4	US-09-949-016-947	Sequence 947, App
c	379	69.5	6.3	1902	4	US-09-824-551-1	Sequence 1, Appli
c	380	69.5	6.3	1931	1	US-08-530-492-2	Sequence 2, Appli
c	381	69.5	6.3	1931	3	US-08-906-517-2	Sequence 2, Appli
c	382	69.5	6.3	1934	4	US-09-186-002-1	Sequence 1, Appli
	383	69.5	6.3	2349	4	US-09-489-847-41	Sequence 41, Appl
c	384	69.5	6.3	2567	3	US-08-993-260-4	Sequence 4, Appli
	385	69.5	6.3	2603	5	PCT-US91-01726-1	Sequence 1, Appli
	386	69.5	6.3	3593	4	US-09-645-069-22	Sequence 22, Appl
	387	69.5	6.3	7902	3	US-08-961-527-112	Sequence 112, App
c	388	69.5	6.3	8349	4	US-09-186-002-16	Sequence 16, Appl
c	389	69.5	6.3	10249	4	US-09-186-002-14	Sequence 14, Appl
c	390	69.5	6.3	10252	4	US-09-186-002-15	Sequence 15, Appl
c	391	69.5	6.3	10339	4	US-09-186-002-13	Sequence 13, Appl
c	392	69.5	6.3	65966	4	US-09-949-016-17152	Sequence 17152, A
c	393	69.5	6.3	73818	4	US-09-949-016-16822	Sequence 16822, A
	394	69.5	6.3	87323	4	US-09-949-016-13828	Sequence 13828, A
	395	69.5	6.3	219964	4	US-09-949-016-15086	Sequence 15086, A
c	396	69.5	6.3	232547	4	US-09-949-016-16603	Sequence 16603, A
	397	69.5	6.3	298336	4	US-09-949-016-16600	Sequence 16600, A
	398	69	6.3	601	4	US-09-949-016-191417	Sequence 191417,
c	399	69	6.3	843	3	US-08-829-525-22	Sequence 22, Appl
c	400	69	6.3	843	3	US-08-609-583A-22	Sequence 22, Appl
c	401	69	6.3	843	3	US-08-937-399-22	Sequence 22, Appl
c	402	69	6.3	843	3	US-09-310-367-22	Sequence 22, Appl
c	403	69	6.3	843	3	US-09-032-337-22	Sequence 22, Appl
c	404	69	6.3	843	4	US-09-464-231-22	Sequence 22, Appl
c	405	69	6.3	1608	2	US-08-622-166A-1	Sequence 1, Appli
	406	69	6.3	2028	2	US-08-933-750C-85	Sequence 85, Appl
	407	69	6.3	2028	3	US-09-234-613-85	Sequence 85, Appl
	408	69	6.3	2242	4	US-09-482-273-35	Sequence 35, Appl
	409	69	6.3	2337	4	US-09-328-352-3781	Sequence 3781, Ap
	410	69	6.3	2381	4	US-09-482-273-97	Sequence 97, Appl
	411	69	6.3	2502	4	US-09-418-963-1	Sequence 1, Appli
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c	413	69	6.3	2710	3	US-08-480-070C-8	Sequence 8, Appli
c	414	69	6.3	2710	3	US-08-829-525-8	Sequence 8, Appli
c	415	69	6.3	2710	3	US-08-609-583A-8	Sequence 8, Appli
c	416	69	6.3	2710	3	US-08-937-399-8	Sequence 8, Appli
c	417	69	6.3	2710	3	US-09-310-367-8	Sequence 8, Appli
c	418	69	6.3	2710	3	US-09-032-337-8	Sequence 8, Appli
c	419	69	6.3	2710	4	US-09-464-231-8	Sequence 8, Appli
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	421	69	6.3	3227	4	US-09-919-497-2	Sequence 2, Appli
	422	69	6.3	3662	4	US-09-907-794A-289	Sequence 289, App
	423	69	6.3	3662	4	US-09-905-125A-289	Sequence 289, App
	424	69	6.3	3662	4	US-09-902-775A-289	Sequence 289, App
	425	69	6.3	3662	4	US-09-906-700-289	Sequence 289, App
	426	69	6.3	3662	4	US-09-903-603A-289	Sequence 289, App
	427	69	6.3	3662	4	US-09-904-920A-289	Sequence 289, App
	428	69	6.3	3662	4	US-09-909-064-289	Sequence 289, App
	429	69	6.3	3662	4	US-09-905-381A-289	Sequence 289, App
	430	69	6.3	3662	4	US-09-906-618-289	Sequence 289, App
	431	69	6.3	4053	4	US-09-907-794A-293	Sequence 293, App
	432	69	6.3	4053	4	US-09-905-125A-293	Sequence 293, App
	433	69	6.3	4053	4	US-09-902-775A-293	Sequence 293, App
	434	69	6.3	4053	4	US-09-906-700-293	Sequence 293, App
	435	69	6.3	4053	4	US-09-903-603A-293	Sequence 293, App
	436	69	6.3	4053	4	US-09-904-920A-293	Sequence 293, App
	437	69	6.3	4053	4	US-09-909-064-293	Sequence 293, App
	438	69	6.3	4053	4	US-09-905-381A-293	Sequence 293, App
	439	69	6.3	4053	4	US-09-906-618-293	Sequence 293, App
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c	441	69	6.3	5655	3	US-08-996-685-1	Sequence 1, Appli
c	442	69	6.3	5655	3	US-08-880-179-2	Sequence 2, Appli
	443	69	6.3	9919	3	US-08-880-179-1	Sequence 1, Appli
c	444	69	6.3	14621	4	US-09-949-016-16547	Sequence 16547, A
	445	69	6.3	15615	4	US-09-949-016-17221	Sequence 17221, A
c	446	69	6.3	51259	3	US-08-781-891-209	Sequence 209, App
c	447	69	6.3	51259	4	US-09-618-166-209	Sequence 209, App
c	448	69	6.3	112132	3	US-09-741-150-3	Sequence 3, Appli
c	449	69	6.3	112132	4	US-10-160-187-3	Sequence 3, Appli
c	450	69	6.3	116652	4	US-09-949-016-13413	Sequence 13413, A
c	451	69	6.3	314798	4	US-09-949-016-13539	Sequence 13539, A
c	452	69	6.3	524032	4	US-09-949-016-16928	Sequence 16928, A
c	453	69	6.3	524032	4	US-09-949-016-16929	Sequence 16929, A
c	454	69	6.3	524032	4	US-09-949-016-16930	Sequence 16930, A
c	455	69	6.3	524032	4	US-09-949-016-16931	Sequence 16931, A
c	456	69	6.3	529885	4	US-09-949-016-14340	Sequence 14340, A
c	457	69	6.3	529885	4	US-09-949-016-14341	Sequence 14341, A
c	458	69	6.3	529885	4	US-09-949-016-14342	Sequence 14342, A
c	459	69	6.3	529885	4	US-09-949-016-14343	Sequence 14343, A
c	460	69	6.3	529885	4	US-09-949-016-14344	Sequence 14344, A
c	461	69	6.3	529885	4	US-09-949-016-14345	Sequence 14345, A
c	462	69	6.3	529885	4	US-09-949-016-14346	Sequence 14346, A
c	463	69	6.3	529885	4	US-09-949-016-14347	Sequence 14347, A
c	464	69	6.3	636591	4	US-09-949-016-11808	Sequence 11808, A
c	465	69	6.3	636591	4	US-09-949-016-13388	Sequence 13388, A
	466	68.5	6.2	537	4	US-09-621-976-3109	Sequence 3109, Ap
c	467	68.5	6.2	601	4	US-09-949-016-189182	Sequence 189182,
c	468	68.5	6.2	800	5	PCT-US95-04801-4	Sequence 4, Appli
c	469	68.5	6.2	802	4	US-09-634-238-60	Sequence 60, Appl
	470	68.5	6.2	879	4	US-09-583-110-1869	Sequence 1869, Ap
c	471	68.5	6.2	1443	4	US-09-724-623-15	Sequence 15, Appl
c	472	68.5	6.2	1467	4	US-09-248-796A-4717	Sequence 4717, Ap
	473	68.5	6.2	1469	4	US-09-634-238-42	Sequence 42, Appl
	474	68.5	6.2	1569	1	US-08-680-726A-57	Sequence 57, Appl
	475	68.5	6.2	1569	3	US-09-092-409-57	Sequence 57, Appl
	476	68.5	6.2	2172	4	US-09-328-352-2802	Sequence 2802, Ap
	477	68.5	6.2	2454	1	US-08-359-696-3	Sequence 3, Appli
	478	68.5	6.2	3927	3	US-09-293-238B-1	Sequence 1, Appli
	479	68.5	6.2	3933	1	US-08-199-776-1	Sequence 1, Appli
	480	68.5	6.2	3933	3	US-08-663-731-1	Sequence 1, Appli
	481	68.5	6.2	3933	3	US-08-879-338-1	Sequence 1, Appli
	482	68.5	6.2	3933	5	PCT-US95-02044-1	Sequence 1, Appli
	483	68.5	6.2	4972	3	US-09-035-648-17	Sequence 17, Appl
	484	68.5	6.2	4972	3	US-09-001-951-17	Sequence 17, Appl
	485	68.5	6.2	4972	3	US-08-818-829-17	Sequence 17, Appl
	486	68.5	6.2	10592	1	US-08-680-726A-51	Sequence 51, Appl
c	487	68.5	6.2	10592	1	US-08-680-726A-52	Sequence 52, Appl
	488	68.5	6.2	10592	3	US-09-092-409-51	Sequence 51, Appl
c	489	68.5	6.2	10592	3	US-09-092-409-52	Sequence 52, Appl
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c	491	68.5	6.2	10862	4	US-09-705-949-1	Sequence 1, Appli
c	492	68.5	6.2	10892	4	US-09-452-638-52	Sequence 52, Appl
	493	68.5	6.2	37710	4	US-09-949-016-15761	Sequence 15761, A
	494	68.5	6.2	37712	4	US-09-949-016-12692	Sequence 12692, A
c	495	68.5	6.2	46347	4	US-09-949-016-13469	Sequence 13469, A
c	496	68.5	6.2	46492	4	US-09-949-016-12953	Sequence 12953, A
c	497	68.5	6.2	46492	4	US-09-949-016-12954	Sequence 12954, A
	498	68.5	6.2	75378	4	US-09-949-016-17140	Sequence 17140, A
	499	68.5	6.2	93493	4	US-09-949-016-12063	Sequence 12063, A
	500	68.5	6.2	94987	4	US-09-949-016-12510	Sequence 12510, A
	501	68.5	6.2	95020	4	US-09-949-016-13272	Sequence 13272, A
	502	68.5	6.2	96987	4	US-09-949-016-14429	Sequence 14429, A
c	503	68.5	6.2	119762	4	US-09-949-016-17313	Sequence 17313, A
c	504	68.5	6.2	131978	4	US-09-949-016-13117	Sequence 13117, A
c	505	68.5	6.2	177251	4	US-09-949-016-15841	Sequence 15841, A
	506	68.5	6.2	218940	4	US-09-949-016-17539	Sequence 17539, A
c	507	68.5	6.2	254964	4	US-09-949-016-12583	Sequence 12583, A
c	508	68.5	6.2	254964	4	US-09-949-016-17392	Sequence 17392, A
	509	68	6.2	601	4	US-09-949-016-82201	Sequence 82201, A
	510	68	6.2	601	4	US-09-949-016-189793	Sequence 189793,
	511	68	6.2	788	4	US-09-424-378A-11	Sequence 11, Appl
	512	68	6.2	793	4	US-09-322-409-42	Sequence 42, Appl
	513	68	6.2	793	4	US-09-451-527-42	Sequence 42, Appl
	514	68	6.2	795	4	US-09-322-409-48	Sequence 48, Appl
c	515	68	6.2	795	4	US-09-322-409-50	Sequence 50, Appl
	516	68	6.2	795	4	US-09-451-527-48	Sequence 48, Appl
c	517	68	6.2	795	4	US-09-451-527-50	Sequence 50, Appl
	518	68	6.2	873	4	US-09-322-409-46	Sequence 46, Appl
c	519	68	6.2	873	4	US-09-322-409-47	Sequence 47, Appl
	520	68	6.2	873	4	US-09-451-527-46	Sequence 46, Appl
c	521	68	6.2	873	4	US-09-451-527-47	Sequence 47, Appl
	522	68	6.2	882	4	US-09-540-236-480	Sequence 480, App
	523	68	6.2	942	4	US-09-322-409-43	Sequence 43, Appl

c 524	68	6.2	942	4	US-09-322-409-45	Sequence 45, Appl
525	68	6.2	942	4	US-09-451-527-43	Sequence 43, Appl
c 526	68	6.2	942	4	US-09-451-527-45	Sequence 45, Appl
527	68	6.2	1623	4	US-09-248-796A-4215	Sequence 4215, Ap
c 528	68	6.2	2198	4	US-09-620-312D-852	Sequence 852, App
c 529	68	6.2	3450	4	US-09-902-540-9001	Sequence 9001, Ap
530	68	6.2	4994	4	US-09-814-915A-52	Sequence 52, Appl
c 531	68	6.2	6563	3	US-09-453-702B-192	Sequence 192, App
532	68	6.2	7305	4	US-09-902-540-961	Sequence 961, App
533	68	6.2	8091	4	US-09-230-652-1	Sequence 1, Appli
534	68	6.2	8257	3	US-09-484-970B-65	Sequence 65, Appl
535	68	6.2	16365	4	US-09-949-016-16970	Sequence 16970, A
536	68	6.2	19167	4	US-09-949-016-17174	Sequence 17174, A
c 537	68	6.2	20441	4	US-09-949-016-14476	Sequence 14476, A
538	68	6.2	29037	4	US-09-949-016-14131	Sequence 14131, A
c 539	68	6.2	29769	4	US-09-949-016-16422	Sequence 16422, A
c 540	68	6.2	35707	4	US-09-949-016-17120	Sequence 17120, A
c 541	68	6.2	38983	4	US-09-949-016-15700	Sequence 15700, A
c 542	68	6.2	51807	4	US-09-949-016-15333	Sequence 15333, A
543	68	6.2	70947	4	US-09-949-016-15165	Sequence 15165, A
544	68	6.2	157822	4	US-09-949-016-16723	Sequence 16723, A
545	68	6.2	254964	4	US-09-949-016-12583	Sequence 12583, A
546	68	6.2	254964	4	US-09-949-016-17392	Sequence 17392, A
547	68	6.2	325791	4	US-09-768-185A-1	Sequence 1, Appli
548	68	6.2	1664976	4	US-08-916-421B-1	Sequence 1, Appli
549	68	6.2	1664976	4	US-09-692-570-1	Sequence 1, Appli
c 550	67.5	6.1	601	4	US-09-949-016-22627	Sequence 22627, A
c 551	67.5	6.1	601	4	US-09-949-016-58699	Sequence 58699, A
c 552	67.5	6.1	601	4	US-09-949-016-82617	Sequence 82617, A
c 553	67.5	6.1	601	4	US-09-949-016-88746	Sequence 88746, A
554	67.5	6.1	601	4	US-09-949-016-103774	Sequence 103774,
555	67.5	6.1	834	3	US-08-339-214-15	Sequence 15, Appl
556	67.5	6.1	925	3	US-08-339-214-46	Sequence 46, Appl
557	67.5	6.1	1143	4	US-09-540-236-1067	Sequence 1067, Ap
558	67.5	6.1	1623	3	US-08-339-214-25	Sequence 25, Appl
559	67.5	6.1	1696	4	US-09-774-528-151	Sequence 151, App
560	67.5	6.1	2440	4	US-09-949-016-1036	Sequence 1036, Ap
561	67.5	6.1	2440	4	US-09-949-016-1454	Sequence 1454, Ap
562	67.5	6.1	6263	4	US-09-023-655-1473	Sequence 1473, Ap
c 563	67.5	6.1	7672	4	US-09-220-132-24	Sequence 24, Appl
564	67.5	6.1	9074	4	US-09-949-016-13467	Sequence 13467, A
c 565	67.5	6.1	9901	4	US-09-949-016-15184	Sequence 15184, A
566	67.5	6.1	12122	4	US-09-949-016-16902	Sequence 16902, A
c 567	67.5	6.1	16287	4	US-09-949-016-17203	Sequence 17203, A
568	67.5	6.1	27600	4	US-09-949-016-15290	Sequence 15290, A
c 569	67.5	6.1	32616	4	US-09-949-016-13407	Sequence 13407, A
570	67.5	6.1	42376	4	US-09-949-016-16276	Sequence 16276, A
571	67.5	6.1	44499	4	US-09-949-016-12711	Sequence 12711, A
c 572	67.5	6.1	65792	4	US-09-596-002-31	Sequence 31, Appl
573	67.5	6.1	121068	4	US-09-949-016-14138	Sequence 14138, A
c 574	67.5	6.1	172677	4	US-09-949-016-13444	Sequence 13444, A
575	67.5	6.1	198632	4	US-09-949-016-12781	Sequence 12781, A
576	67.5	6.1	198637	4	US-09-949-016-17393	Sequence 17393, A
577	67.5	6.1	229354	4	US-09-705-400-64	Sequence 64, Appl
c 578	67.5	6.1	264358	4	US-09-949-016-15725	Sequence 15725, A
c 579	67.5	6.1	269223	4	US-09-596-002-41	Sequence 41, Appl
580	67	6.1	510	4	US-09-248-796A-8443	Sequence 8443, Ap
c 581	67	6.1	601	4	US-09-949-016-95253	Sequence 95253, A
c 582	67	6.1	601	4	US-09-949-016-95431	Sequence 95431, A
c 583	67	6.1	601	4	US-09-949-016-95609	Sequence 95609, A
c 584	67	6.1	601	4	US-09-949-016-95787	Sequence 95787, A
c 585	67	6.1	601	4	US-09-949-016-112543	Sequence 112543,
c 586	67	6.1	601	4	US-09-949-016-191546	Sequence 191546,
c 587	67	6.1	601	4	US-09-949-016-191724	Sequence 191724,
c 588	67	6.1	601	4	US-09-949-016-191902	Sequence 191902,
c 589	67	6.1	601	4	US-09-949-016-192080	Sequence 192080,
c 590	67	6.1	601	4	US-09-949-016-202687	Sequence 202687,
591	67	6.1	660	3	US-08-812-946A-1	Sequence 1, Appli
592	67	6.1	708	4	US-09-543-681A-2848	Sequence 2848, Ap
593	67	6.1	795	4	US-09-248-796A-1027	Sequence 1027, Ap
c 594	67	6.1	815	4	US-09-369-247-15	Sequence 15, Appl
595	67	6.1	1053	4	US-09-107-433-555	Sequence 555, App
c 596	67	6.1	1060	4	US-09-270-767-13544	Sequence 13544, A
597	67	6.1	1064	2	US-08-529-878B-40	Sequence 40, Appl
598	67	6.1	1152	4	US-09-583-110-616	Sequence 616, App
599	67	6.1	1302	4	US-09-328-352-2377	Sequence 2377, Ap
600	67	6.1	1479	4	US-09-252-991A-3960	Sequence 3960, Ap
601	67	6.1	1482	4	US-09-710-279-1831	Sequence 1831, Ap
602	67	6.1	1514	4	US-09-023-655-1316	Sequence 1316, Ap
603	67	6.1	1782	3	US-09-134-001C-1154	Sequence 1154, Ap
604	67	6.1	1815	4	US-10-329-668-3	Sequence 3, Appli
c 605	67	6.1	2060	4	US-09-270-767-12193	Sequence 12193, A
606	67	6.1	2431	3	US-09-221-017B-351	Sequence 351, App
607	67	6.1	2523	4	US-09-715-962-1	Sequence 1, Appli
608	67	6.1	2763	4	US-09-949-016-3798	Sequence 3798, Ap
609	67	6.1	3097	2	US-08-849-480A-2	Sequence 2, Appli
c 610	67	6.1	3301	4	US-09-710-279-4209	Sequence 4209, Ap
611	67	6.1	3794	4	US-09-710-279-3705	Sequence 3705, Ap
612	67	6.1	4086	4	US-09-614-221A-478	Sequence 478, App
613	67	6.1	5322	4	US-09-949-016-14845	Sequence 14845, A
614	67	6.1	7053	4	US-09-949-016-17436	Sequence 17436, A
c 615	67	6.1	7179	4	US-09-949-016-12365	Sequence 12365, A
c 616	67	6.1	10544	4	US-09-949-001-28	Sequence 28, Appl
c 617	67	6.1	10544	4	US-09-949-001-33	Sequence 33, Appl
618	67	6.1	19269	4	US-09-902-540-1175	Sequence 1175, Ap
619	67	6.1	22871	4	US-09-949-016-15688	Sequence 15688, A
620	67	6.1	22871	4	US-09-949-016-15689	Sequence 15689, A
621	67	6.1	27684	4	US-09-949-016-12504	Sequence 12504, A
622	67	6.1	29614	4	US-09-949-016-12390	Sequence 12390, A
c 623	67	6.1	41318	4	US-09-949-016-16225	Sequence 16225, A
c 624	67	6.1	41737	4	US-09-949-016-12204	Sequence 12204, A
c 625	67	6.1	41741	4	US-09-949-016-16983	Sequence 16983, A
626	67	6.1	51835	4	US-09-949-016-17101	Sequence 17101, A
627	67	6.1	52032	4	US-09-949-016-11789	Sequence 11789, A
c 628	67	6.1	119211	4	US-09-596-002-40	Sequence 40, Appl
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c 630	67	6.1	151295	4	US-09-949-016-14568	Sequence 14568, A
c 631	67	6.1	151295	4	US-09-949-016-14569	Sequence 14569, A
c 632	67	6.1	151295	4	US-09-949-016-14570	Sequence 14570, A
c 633	67	6.1	151295	4	US-09-949-016-14571	Sequence 14571, A
c 634	67	6.1	151295	4	US-09-949-016-14572	Sequence 14572, A
c 635	67	6.1	156942	4	US-09-949-016-12227	Sequence 12227, A
c 636	67	6.1	156950	4	US-09-949-016-15946	Sequence 15946, A
c 637	67	6.1	198632	4	US-09-949-016-12781	Sequence 12781, A
c 638	67	6.1	198637	4	US-09-949-016-17393	Sequence 17393, A
c 639	67	6.1	199471	4	US-09-949-016-14083	Sequence 14083, A
c 640	67	6.1	203475	4	US-09-949-016-14516	Sequence 14516, A
c 641	67	6.1	203475	4	US-09-949-016-14517	Sequence 14517, A
c 642	67	6.1	203475	4	US-09-949-016-14518	Sequence 14518, A
c 643	67	6.1	203475	4	US-09-949-016-14519	Sequence 14519, A
c 644	67	6.1	203475	4	US-09-949-016-17226	Sequence 17226, A
c 645	67	6.1	203475	4	US-09-949-016-17227	Sequence 17227, A
c 646	67	6.1	203475	4	US-09-949-016-17228	Sequence 17228, A
c 647	67	6.1	203475	4	US-09-949-016-17229	Sequence 17229, A
c 648	67	6.1	248968	4	US-09-949-016-12614	Sequence 12614, A
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c 651	67	6.1	393753	4	US-09-949-016-14574	Sequence 14574, A
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c 653	67	6.1	818128	4	US-09-949-016-14546	Sequence 14546, A
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c 655	67	6.1	818128	4	US-09-949-016-14548	Sequence 14548, A
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c 659	67	6.1	818128	4	US-09-949-016-14552	Sequence 14552, A
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c 663	67	6.1	818128	4	US-09-949-016-14556	Sequence 14556, A
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c 666	67	6.1	818128	4	US-09-949-016-14559	Sequence 14559, A
c 667	67	6.1	818128	4	US-09-949-016-14560	Sequence 14560, A
c 668	67	6.1	818128	4	US-09-949-016-14561	Sequence 14561, A
c 669	67	6.1	818128	4	US-09-949-016-14562	Sequence 14562, A

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c 671	67	6.1	818128	4	US-09-949-016-14565	Sequence 14565, A
c 672	67	6.1	818128	4	US-09-949-016-14566	Sequence 14566, A
c 673	67	6.1	818128	4	US-09-949-016-14567	Sequence 14567, A
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c 678	66.5	6.0	601	4	US-09-949-016-58697	Sequence 58697, A
c 679	66.5	6.0	601	4	US-09-949-016-58698	Sequence 58698, A
c 680	66.5	6.0	601	4	US-09-949-016-91216	Sequence 91216, A
c 681	66.5	6.0	601	4	US-09-949-016-91217	Sequence 91217, A
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c 683	66.5	6.0	601	4	US-09-949-016-197807	Sequence 197807,
c 684	66.5	6.0	601	4	US-09-949-016-197854	Sequence 197854,
c 685	66.5	6.0	897	4	US-09-248-796A-3257	Sequence 3257, Ap
686	66.5	6.0	1095	4	US-08-914-372C-6	Sequence 6, Appli
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688	66.5	6.0	1335	4	US-09-826-509-550	Sequence 550, App
689	66.5	6.0	1384	1	US-08-414-625-3	Sequence 3, Appli
690	66.5	6.0	1411	4	US-09-949-016-3794	Sequence 3794, Ap
691	66.5	6.0	1413	4	US-09-866-028-60	Sequence 60, Appl
692	66.5	6.0	1413	4	US-09-944-457-60	Sequence 60, Appl
693	66.5	6.0	1512	2	US-08-270-581-1	Sequence 1, Appli
694	66.5	6.0	1512	3	US-09-146-893-1	Sequence 1, Appli
c 695	66.5	6.0	1569	4	US-09-949-016-3898	Sequence 3898, Ap
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697	66.5	6.0	1633	3	US-09-119-788-1	Sequence 1, Appli
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706	66.5	6.0	1804	4	US-09-795-847B-1	Sequence 1, Appli
707	66.5	6.0	1804	4	US-09-869-414-1	Sequence 1, Appli
708	66.5	6.0	1804	4	US-09-548-366F-1	Sequence 1, Appli
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710	66.5	6.0	1804	4	US-09-794-925A-1	Sequence 1, Appli
711	66.5	6.0	1804	4	US-09-806-194A-1	Sequence 1, Appli
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713	66.5	6.0	1862	3	US-09-434-427-1	Sequence 1, Appli
714	66.5	6.0	1863	4	US-09-886-143-1	Sequence 1, Appli
715	66.5	6.0	1868	4	US-09-949-016-5204	Sequence 5204, Ap
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c 717	66.5	6.0	1894	4	US-09-949-016-69	Sequence 69, Appl
c 718	66.5	6.0	1897	4	US-09-949-016-5146	Sequence 5146, Ap
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723	66.5	6.0	2513	4	US-10-101-464A-13	Sequence 13, Appl
724	66.5	6.0	2962	4	US-09-902-540-6991	Sequence 6991, Ap
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c 726	66.5	6.0	3448	2	US-08-596-405-3	Sequence 3, Appli
c 727	66.5	6.0	3448	2	US-08-877-620-3	Sequence 3, Appli
c 728	66.5	6.0	3448	4	US-09-287-368-3	Sequence 3, Appli
c 729	66.5	6.0	3448	4	US-09-626-795-3	Sequence 3, Appli
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731	66.5	6.0	5078	4	US-09-620-312D-565	Sequence 565, App
732	66.5	6.0	6422	4	US-09-976-594-715	Sequence 715, App
733	66.5	6.0	8297	4	US-09-949-016-14843	Sequence 14843, A
734	66.5	6.0	12739	4	US-09-902-540-1011	Sequence 1011, Ap
735	66.5	6.0	13773	4	US-09-949-016-15536	Sequence 15536, A
c 736	66.5	6.0	18613	4	US-08-956-171E-112	Sequence 112, App
c 737	66.5	6.0	18613	4	US-08-781-986A-112	Sequence 112, App
c 738	66.5	6.0	31754	4	US-09-949-016-16451	Sequence 16451, A
c 739	66.5	6.0	34047	4	US-09-949-016-13503	Sequence 13503, A
740	66.5	6.0	36437	4	US-09-949-016-13415	Sequence 13415, A
741	66.5	6.0	38506	3	US-09-320-878-19	Sequence 19, Appl
742	66.5	6.0	38506	4	US-09-141-908-1	Sequence 1, Appli
743	66.5	6.0	38506	4	US-09-657-440-19	Sequence 19, Appl
744	66.5	6.0	44166	4	US-09-949-016-15829	Sequence 15829, A
745	66.5	6.0	44439	4	US-09-949-016-17102	Sequence 17102, A
c 746	66.5	6.0	47683	4	US-09-949-016-16460	Sequence 16460, A
747	66.5	6.0	47968	4	US-09-949-016-15240	Sequence 15240, A
748	66.5	6.0	54180	4	US-09-949-016-14894	Sequence 14894, A
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754	66.5	6.0	107421	4	US-09-949-016-15532	Sequence 15532, A
c 755	66.5	6.0	154600	4	US-09-949-016-14757	Sequence 14757, A
c 756	66.5	6.0	175236	4	US-09-949-016-14353	Sequence 14353, A
757	66.5	6.0	187580	4	US-09-949-016-13266	Sequence 13266, A
c 758	66.5	6.0	212139	4	US-09-949-016-16065	Sequence 16065, A
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c 761	66.5	6.0	263694	4	US-09-949-016-16915	Sequence 16915, A
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763	66	6.0	246	4	US-09-016-434-751	Sequence 751, App
764	66	6.0	366	4	US-09-489-039A-5836	Sequence 5836, Ap
765	66	6.0	585	4	US-09-248-796A-8824	Sequence 8824, Ap
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c 767	66	6.0	601	4	US-09-949-016-50484	Sequence 50484, A
c 768	66	6.0	601	4	US-09-949-016-112542	Sequence 112542,
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c 771	66	6.0	1023	3	US-09-641-807A-3	Sequence 3, Appli
c 772	66	6.0	1023	3	US-09-723-096-3	Sequence 3, Appli
773	66	6.0	1135	4	US-09-203-958A-3	Sequence 3, Appli
774	66	6.0	1146	4	US-09-540-236-1695	Sequence 1695, Ap
775	66	6.0	1359	4	US-09-248-796A-819	Sequence 819, App
776	66	6.0	1434	4	US-09-583-110-894	Sequence 894, App
777	66	6.0	1449	4	US-09-107-532A-1214	Sequence 1214, Ap
778	66	6.0	1616	4	US-09-270-767-2247	Sequence 2247, Ap
779	66	6.0	1616	4	US-09-270-767-17529	Sequence 17529, A
c 780	66	6.0	1755	4	US-09-248-796A-1126	Sequence 1126, Ap
781	66	6.0	1874	4	US-09-270-767-12369	Sequence 12369, A
c 782	66	6.0	1977	4	US-09-614-891-5	Sequence 5, Appli
783	66	6.0	2114	4	US-09-949-016-1960	Sequence 1960, Ap
784	66	6.0	2198	4	US-09-949-016-5582	Sequence 5582, Ap
785	66	6.0	2203	4	US-09-917-254-29	Sequence 29, Appl
786	66	6.0	2203	4	US-09-949-016-596	Sequence 596, App
787	66	6.0	2269	3	US-09-394-645-1	Sequence 1, Appli
788	66	6.0	2269	3	US-09-243-560B-1	Sequence 1, Appli
789	66	6.0	2433	4	US-09-300-958A-24	Sequence 24, Appl
790	66	6.0	2498	4	US-09-620-312D-90	Sequence 90, Appl
791	66	6.0	2574	4	US-09-270-767-10955	Sequence 10955, A
c 792	66	6.0	2818	1	US-08-366-276-1	Sequence 1, Appli
793	66	6.0	2939	2	US-08-560-398-11	Sequence 11, Appl
794	66	6.0	3361	4	US-09-710-279-4125	Sequence 4125, Ap
795	66	6.0	3461	3	US-08-468-856B-6	Sequence 6, Appli
796	66	6.0	3461	3	US-08-468-859A-6	Sequence 6, Appli
797	66	6.0	3708	1	US-08-185-232A-1	Sequence 1, Appli
798	66	6.0	3708	1	US-08-416-523-1	Sequence 1, Appli
799	66	6.0	3708	3	US-08-789-478-1	Sequence 1, Appli
c 800	66	6.0	3837	3	US-09-724-517-1	Sequence 1, Appli
c 801	66	6.0	3837	3	US-09-641-807A-1	Sequence 1, Appli
c 802	66	6.0	3837	3	US-09-723-096-1	Sequence 1, Appli
803	66	6.0	4052	2	US-08-833-226-1	Sequence 1, Appli
804	66	6.0	7620	4	US-08-956-171E-36	Sequence 36, Appl
805	66	6.0	7620	4	US-08-781-986A-36	Sequence 36, Appl
806	66	6.0	9350	4	US-09-949-016-16640	Sequence 16640, A
807	66	6.0	9365	3	US-09-608-285A-8	Sequence 8, Appli
808	66	6.0	9365	3	US-09-350-836B-8	Sequence 8, Appli
809	66	6.0	9365	3	US-09-370-265-8	Sequence 8, Appli
810	66	6.0	9365	4	US-09-557-800C-8	Sequence 8, Appli
811	66	6.0	9365	4	US-09-370-625A-8	Sequence 8, Appli
812	66	6.0	11758	4	US-09-949-016-11859	Sequence 11859, A
813	66	6.0	12232	4	US-09-949-016-12570	Sequence 12570, A
814	66	6.0	12240	4	US-09-949-016-16209	Sequence 16209, A
c 815	66	6.0	13206	3	US-08-961-527-33	Sequence 33, Appl

	816	66	6.0	16236	4	US-09-949-016-16298	Sequence 16298, A
	817	66	6.0	19167	4	US-09-949-016-12432	Sequence 12432, A
	818	66	6.0	22407	4	US-09-596-002-16	Sequence 16, Appl
	819	66	6.0	25603	4	US-09-819-607-3	Sequence 3, Appli
	820	66	6.0	26103	4	US-09-949-016-15685	Sequence 15685, A
	821	66	6.0	26105	4	US-09-949-016-11879	Sequence 11879, A
c	822	66	6.0	28555	4	US-09-949-016-13046	Sequence 13046, A
	823	66	6.0	33753	4	US-09-949-016-15741	Sequence 15741, A
	824	66	6.0	33756	4	US-09-949-016-12006	Sequence 12006, A
	825	66	6.0	56678	4	US-09-949-016-17453	Sequence 17453, A
c	826	66	6.0	69813	4	US-09-949-016-12455	Sequence 12455, A
c	827	66	6.0	69813	4	US-09-949-016-13905	Sequence 13905, A
c	828	66	6.0	69813	4	US-09-949-016-13906	Sequence 13906, A
c	829	66	6.0	69833	4	US-09-949-016-12861	Sequence 12861, A
c	830	66	6.0	76848	4	US-09-949-016-14201	Sequence 14201, A
	831	66	6.0	85869	4	US-09-949-016-12017	Sequence 12017, A
	832	66	6.0	85878	4	US-09-949-016-16321	Sequence 16321, A
	833	66	6.0	101981	4	US-09-949-016-13995	Sequence 13995, A
	834	66	6.0	101982	4	US-09-949-016-12590	Sequence 12590, A
c	835	66	6.0	103377	4	US-09-949-016-14089	Sequence 14089, A
	836	66	6.0	107140	4	US-09-949-016-14834	Sequence 14834, A
c	837	66	6.0	110585	4	US-09-949-016-13427	Sequence 13427, A
c	838	66	6.0	121049	4	US-09-949-016-17513	Sequence 17513, A
	839	66	6.0	126176	4	US-09-949-016-16137	Sequence 16137, A
	840	66	6.0	126176	4	US-09-949-016-16138	Sequence 16138, A
	841	66	6.0	300598	4	US-09-949-016-11868	Sequence 11868, A
	842	66	6.0	302604	4	US-09-949-016-14588	Sequence 14588, A
	843	66	6.0	302604	4	US-09-949-016-14589	Sequence 14589, A
	844	66	6.0	308362	4	US-09-949-016-17119	Sequence 17119, A
	845	65.5	5.9	425	4	US-09-541-094-10	Sequence 10, Appl
	846	65.5	5.9	489	4	US-09-540-236-639	Sequence 639, App
c	847	65.5	5.9	601	4	US-09-949-016-74178	Sequence 74178, A
	848	65.5	5.9	601	4	US-09-949-016-77181	Sequence 77181, A
	849	65.5	5.9	601	4	US-09-949-016-103775	Sequence 103775,
c	850	65.5	5.9	601	4	US-09-949-016-145574	Sequence 145574,
	851	65.5	5.9	635	4	US-10-029-517-107	Sequence 107, App
	852	65.5	5.9	645	4	US-09-583-110-1974	Sequence 1974, Ap
	853	65.5	5.9	804	4	US-09-322-409-22	Sequence 22, Appl
c	854	65.5	5.9	804	4	US-09-322-409-24	Sequence 24, Appl
	855	65.5	5.9	804	4	US-09-451-527-22	Sequence 22, Appl
c	856	65.5	5.9	804	4	US-09-451-527-24	Sequence 24, Appl
	857	65.5	5.9	882	4	US-09-322-409-9	Sequence 9, Appli
c	858	65.5	5.9	882	4	US-09-322-409-10	Sequence 10, Appl
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	862	65.5	5.9	983	4	US-09-176-200-1	Sequence 1, Appli
	863	65.5	5.9	983	4	US-09-915-593-1	Sequence 1, Appli
	864	65.5	5.9	1013	4	US-09-322-409-6	Sequence 6, Appli
c	865	65.5	5.9	1013	4	US-09-322-409-8	Sequence 8, Appli
	866	65.5	5.9	1013	4	US-09-451-527-6	Sequence 6, Appli
c	867	65.5	5.9	1013	4	US-09-451-527-8	Sequence 8, Appli
	868	65.5	5.9	1058	3	US-08-818-112-45	Sequence 45, Appl
	869	65.5	5.9	1058	3	US-08-818-111-45	Sequence 45, Appl
	870	65.5	5.9	1058	3	US-09-056-556-45	Sequence 45, Appl
	871	65.5	5.9	1058	3	US-09-072-596-45	Sequence 45, Appl
	872	65.5	5.9	1058	4	US-09-072-967-45	Sequence 45, Appl
	873	65.5	5.9	1068	4	US-09-270-767-12721	Sequence 12721, A
	874	65.5	5.9	1095	1	US-08-680-726A-55	Sequence 55, Appl
	875	65.5	5.9	1095	3	US-09-092-409-55	Sequence 55, Appl
	876	65.5	5.9	1095	4	US-08-914-372C-5	Sequence 5, Appli
	877	65.5	5.9	1095	4	US-08-914-372C-36	Sequence 36, Appl
	878	65.5	5.9	1104	4	US-09-489-039A-5309	Sequence 5309, Ap
	879	65.5	5.9	1121	4	US-09-949-016-5103	Sequence 5103, Ap
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	881	65.5	5.9	1151	3	US-09-430-503-3	Sequence 3, Appli
	882	65.5	5.9	1151	3	US-09-430-503-5	Sequence 5, Appli
	883	65.5	5.9	1151	3	US-09-430-503-7	Sequence 7, Appli
	884	65.5	5.9	1152	1	US-08-221-750A-10	Sequence 10, Appl
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	886	65.5	5.9	1266	4	US-09-270-767-6939	Sequence 6939, Ap
	887	65.5	5.9	1266	4	US-09-270-767-22221	Sequence 22221, A
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	894	65.5	5.9	2308	4	US-09-949-016-65	Sequence 65, Appl
	895	65.5	5.9	2335	4	US-09-023-655-1312	Sequence 1312, Ap
	896	65.5	5.9	2387	4	US-09-949-016-2268	Sequence 2268, Ap
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	898	65.5	5.9	2722	3	US-08-720-229-10	Sequence 10, Appl
	899	65.5	5.9	2839	5	PCT-US94-07297-38	Sequence 38, Appl
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	902	65.5	5.9	3321	4	US-09-866-510-13	Sequence 13, Appl
	903	65.5	5.9	3321	4	US-09-866-510-15	Sequence 15, Appl
	904	65.5	5.9	3321	4	US-09-866-510-17	Sequence 17, Appl
	905	65.5	5.9	3321	4	US-09-866-510-19	Sequence 19, Appl
	906	65.5	5.9	3321	4	US-09-866-510-21	Sequence 21, Appl
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	908	65.5	5.9	3478	1	US-08-396-479B-1	Sequence 1, Appli
	909	65.5	5.9	3478	1	US-08-818-823-1	Sequence 1, Appli
	910	65.5	5.9	3516	4	US-09-417-197-130	Sequence 130, App
	911	65.5	5.9	3546	4	US-09-417-197-132	Sequence 132, App
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	917	65.5	5.9	4465	1	US-08-180-195-1	Sequence 1, Appli
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	922	65.5	5.9	4465	3	US-09-583-210-1	Sequence 1, Appli
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	930	65.5	5.9	5427	3	US-08-461-917-3	Sequence 3, Appli
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	932	65.5	5.9	5427	4	US-08-464-436-3	Sequence 3, Appli
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	935	65.5	5.9	5570	4	US-09-023-655-1193	Sequence 1193, Ap
	936	65.5	5.9	5727	4	US-09-628-188A-1	Sequence 1, Appli
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	944	65.5	5.9	68490	4	US-09-949-016-15849	Sequence 15849, A
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	946	65.5	5.9	99797	4	US-09-949-016-15255	Sequence 15255, A
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	952	65	5.9	566	4	US-09-270-767-2534	Sequence 2534, Ap
	953	65	5.9	566	4	US-09-270-767-17816	Sequence 17816, A
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c	955	65	5.9	570	4	US-09-792-568-4	Sequence 4, Appli
c	956	65	5.9	594	4	US-09-252-991A-1754	Sequence 1754, Ap
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	959	65	5.9	601	4	US-09-949-016-116427	Sequence 116427,
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c	961	65	5.9	601	4	US-09-949-016-202688	Sequence 202688,

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c 964	65	5.9	666	4	US-09-248-796A-985	Sequence 985, App
965	65	5.9	668	4	US-09-270-767-1567	Sequence 1567, Ap
966	65	5.9	668	4	US-09-270-767-16849	Sequence 16849, A
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c 968	65	5.9	969	4	US-10-101-464A-297	Sequence 297, App
c 969	65	5.9	1145	4	US-08-956-171E-777	Sequence 777, App
c 970	65	5.9	1145	4	US-08-781-986A-777	Sequence 777, App
971	65	5.9	1149	4	US-09-248-796A-191	Sequence 191, App
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974	65	5.9	1328	3	US-09-370-838-24	Sequence 24, Appl
975	65	5.9	1328	4	US-09-854-133-24	Sequence 24, Appl
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c 983	65	5.9	1764	2	US-09-237-507-2	Sequence 2, Appli
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985	65	5.9	2160	3	US-09-382-256-15	Sequence 15, Appl
986	65	5.9	2160	3	US-09-395-115-15	Sequence 15, Appl
987	65	5.9	2160	3	US-08-436-265-15	Sequence 15, Appl
988	65	5.9	2160	3	US-09-679-187-15	Sequence 15, Appl
989	65	5.9	2160	4	US-09-267-963D-15	Sequence 15, Appl
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993	65	5.9	2724	3	US-09-171-699-1	Sequence 1, Appli
994	65	5.9	2724	5	PCT-US94-04180-1	Sequence 1, Appli
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996	65	5.9	2728	1	US-08-753-985-7	Sequence 7, Appli
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998	65	5.9	2934	4	US-09-949-016-5255	Sequence 5255, Ap
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c1004	65	5.9	4114	4	US-09-710-279-3572	Sequence 3572, Ap
c1005	65	5.9	4260	2	US-08-658-665-38	Sequence 38, Appl
c1006	65	5.9	4260	3	US-08-796-101-2	Sequence 2, Appli
c1007	65	5.9	4260	3	US-09-085-273-38	Sequence 38, Appl
c1008	65	5.9	4260	4	US-09-916-963-38	Sequence 38, Appl
c1009	65	5.9	4768	2	US-08-658-665-41	Sequence 41, Appl
c1010	65	5.9	4768	3	US-08-796-101-5	Sequence 5, Appli
c1011	65	5.9	4768	3	US-09-085-273-41	Sequence 41, Appl
c1012	65	5.9	4768	4	US-09-916-963-41	Sequence 41, Appl
c1013	65	5.9	5234	2	US-08-658-665-73	Sequence 73, Appl
c1014	65	5.9	5234	3	US-08-796-101-37	Sequence 37, Appl
c1015	65	5.9	5234	3	US-09-085-273-73	Sequence 73, Appl
c1016	65	5.9	5234	4	US-09-916-963-73	Sequence 73, Appl
c1017	65	5.9	7091	2	US-08-658-665-40	Sequence 40, Appl
c1018	65	5.9	7091	3	US-08-796-101-4	Sequence 4, Appli
c1019	65	5.9	7091	3	US-09-085-273-40	Sequence 40, Appl
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c1026	65	5.9	51671	4	US-09-949-016-15962	Sequence 15962, A
c1027	65	5.9	56551	4	US-09-949-016-12030	Sequence 12030, A
c1028	65	5.9	71879	4	US-09-949-016-17465	Sequence 17465, A
c1029	65	5.9	80632	4	US-09-949-016-12951	Sequence 12951, A
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c1031	65	5.9	86440	4	US-09-949-016-16990	Sequence 16990, A
c1032	65	5.9	100567	4	US-09-949-016-16934	Sequence 16934, A
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c1039	65	5.9	253345	4	US-09-949-016-12656	Sequence 12656, A
c1040	65	5.9	253364	4	US-09-949-016-13639	Sequence 13639, A
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1044	64.5	5.9	513	4	US-09-134-000C-906	Sequence 906, App
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c1048	64.5	5.9	940	4	US-09-023-655-537	Sequence 537, App
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1055	64.5	5.9	1217	4	US-09-016-434-1164	Sequence 1164, Ap
1056	64.5	5.9	1230	4	US-09-252-991A-2136	Sequence 2136, Ap
1057	64.5	5.9	1245	4	US-09-902-540-2561	Sequence 2561, Ap
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c1059	64.5	5.9	1461	4	US-09-543-681A-2028	Sequence 2028, Ap
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1065	64.5	5.9	1630	3	US-08-468-859A-2	Sequence 2, Appli
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1069	64.5	5.9	1996	3	US-09-265-315-44	Sequence 44, Appl
1070	64.5	5.9	1996	3	US-09-265-315-44	Sequence 44, Appl
1071	64.5	5.9	1996	3	US-09-266-417-44	Sequence 44, Appl
1072	64.5	5.9	1996	4	US-09-528-709-44	Sequence 44, Appl
1073	64.5	5.9	1996	4	US-09-527-745-44	Sequence 44, Appl
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c1077	64.5	5.9	2525	3	US-09-265-315-84	Sequence 84, Appl
c1078	64.5	5.9	2525	3	US-09-265-315-84	Sequence 84, Appl
c1079	64.5	5.9	2525	3	US-09-266-417-84	Sequence 84, Appl
c1080	64.5	5.9	2525	4	US-09-528-709-84	Sequence 84, Appl
c1081	64.5	5.9	2525	4	US-09-527-745-84	Sequence 84, Appl
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c1087	64.5	5.9	6555	4	US-09-949-016-5295	Sequence 5295, Ap
c1088	64.5	5.9	6567	4	US-09-902-540-732	Sequence 732, App
c1089	64.5	5.9	6943	3	US-09-453-702B-213	Sequence 213, App
c1090	64.5	5.9	7350	4	US-09-949-016-364	Sequence 364, App
1091	64.5	5.9	10088	4	US-08-956-171E-32	Sequence 32, Appl
1092	64.5	5.9	10088	4	US-08-781-986A-32	Sequence 32, Appl
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1094	64.5	5.9	11496	4	US-09-949-016-15558	Sequence 15558, A
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c1102	64.5	5.9	35059	4	US-09-949-016-13831	Sequence 13831, A
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c1105	64.5	5.9	37622	4	US-09-949-016-15726	Sequence 15726, A
1106	64.5	5.9	44377	4	US-09-949-016-11840	Sequence 11840, A
1107	64.5	5.9	44378	4	US-09-949-016-15969	Sequence 15969, A

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1205	64	5.8	12658	4	US-08-781-986A-127	Sequence 127, App
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c1257	63.5	5.8	601	4	US-09-949-016-205786	Sequence 205786,
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1264	63.5	5.8	1086	4	US-08-914-372C-3	Sequence 3, Appli
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1272	63.5	5.8	1565	4	US-09-657-440-24	Sequence 24, Appl
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1279	63.5	5.8	2082	4	US-09-248-796A-345	Sequence 345, App
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1288	63.5	5.8	3695	1	US-08-203-676-1	Sequence 1, Appli
1289	63.5	5.8	3695	2	US-08-822-238-1	Sequence 1, Appli
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c1339	63.5	5.8	304533	4	US-09-949-016-15372	Sequence 15372, A
c1340	63.5	5.8	305491	4	US-09-949-016-17550	Sequence 17550, A
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c1342	63.5	5.8	421883	4	US-09-949-016-12557	Sequence 12557, A
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c1345	63	5.7	345	3	US-09-218-950-36	Sequence 36, Appl
c1346	63	5.7	345	4	US-08-394-388A-36	Sequence 36, Appl
1347	63	5.7	400	4	US-08-956-171E-4125	Sequence 4125, Ap
1348	63	5.7	400	4	US-08-781-986A-4125	Sequence 4125, Ap
1349	63	5.7	414	4	US-09-647-468-63	Sequence 63, Appl
c1350	63	5.7	461	4	US-09-702-705-792	Sequence 792, App
c1351	63	5.7	461	4	US-09-736-457-792	Sequence 792, App
c1352	63	5.7	461	4	US-09-614-124B-792	Sequence 792, App
c1353	63	5.7	461	4	US-09-671-325-792	Sequence 792, App
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c1356	63	5.7	479	4	US-09-702-705-70	Sequence 70, Appl
c1357	63	5.7	479	4	US-09-736-457-70	Sequence 70, Appl
c1358	63	5.7	479	4	US-09-614-124B-70	Sequence 70, Appl
c1359	63	5.7	479	4	US-09-671-325-70	Sequence 70, Appl
c1360	63	5.7	479	4	US-09-589-184-70	Sequence 70, Appl
c1361	63	5.7	479	4	US-09-658-824-70	Sequence 70, Appl
1362	63	5.7	508	4	US-09-524-101D-7	Sequence 7, Appli
c1363	63	5.7	513	4	US-09-248-796A-3508	Sequence 3508, Ap
1364	63	5.7	514	4	US-09-495-050A-203	Sequence 203, App
1365	63	5.7	549	4	US-09-328-352-90	Sequence 90, Appl
c1366	63	5.7	601	4	US-09-949-016-33303	Sequence 33303, A
1367	63	5.7	601	4	US-09-949-016-36755	Sequence 36755, A
1368	63	5.7	601	4	US-09-949-016-50153	Sequence 50153, A
1369	63	5.7	601	4	US-09-949-016-50156	Sequence 50156, A
1370	63	5.7	601	4	US-09-949-016-50157	Sequence 50157, A
1371	63	5.7	601	4	US-09-949-016-154814	Sequence 154814,
1372	63	5.7	684	4	US-09-134-000C-3083	Sequence 3083, Ap
1373	63	5.7	791	4	US-09-702-705-1805	Sequence 1805, Ap
1374	63	5.7	791	4	US-09-736-457-1805	Sequence 1805, Ap
1375	63	5.7	791	4	US-09-671-325-1805	Sequence 1805, Ap
1376	63	5.7	791	4	US-09-949-016-1743	Sequence 1743, Ap
c1377	63	5.7	849	4	US-09-134-000C-421	Sequence 421, App
1378	63	5.7	906	4	US-09-489-039A-1893	Sequence 1893, Ap
1379	63	5.7	909	4	US-09-107-532A-1981	Sequence 1981, Ap
1380	63	5.7	933	4	US-09-543-681A-2686	Sequence 2686, Ap
1381	63	5.7	1044	4	US-09-415-277C-13	Sequence 13, Appl
1382	63	5.7	1044	4	US-09-415-277C-15	Sequence 15, Appl
1383	63	5.7	1087	4	US-09-919-039-69	Sequence 69, Appl
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c1385	63	5.7	1275	4	US-09-023-655-317	Sequence 317, App
1386	63	5.7	1359	4	US-09-711-164-195	Sequence 195, App
c1387	63	5.7	1368	1	US-08-290-448A-79	Sequence 79, Appl
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1396	63	5.7	1452	4	US-09-949-016-5250	Sequence 5250, Ap
1397	63	5.7	1452	4	US-09-949-016-5251	Sequence 5251, Ap
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1401	63	5.7	1566	4	US-09-489-039A-947	Sequence 947, App
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1403	63	5.7	1596	4	US-09-270-767-1002	Sequence 1002, Ap
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1408	63	5.7	1900	4	US-09-949-016-4515	Sequence 4515, Ap
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1412	63	5.7	2022	4	US-09-583-110-199	Sequence 199, App
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c1414	63	5.7	2107	3	US-08-235-836C-73	Sequence 73, Appl
1415	63	5.7	2146	4	US-09-620-312D-443	Sequence 443, App
1416	63	5.7	2200	4	US-09-774-528-309	Sequence 309, App
1417	63	5.7	2229	4	US-09-910-174B-1	Sequence 1, Appli
1418	63	5.7	2229	4	US-09-620-461-1	Sequence 1, Appli
1419	63	5.7	2381	3	US-09-221-017B-812	Sequence 812, App
1420	63	5.7	3046	1	US-08-726-725-1	Sequence 1, Appli
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1428	63	5.7	5976	3	US-08-621-944A-2	Sequence 2, Appli
1429	63	5.7	5976	3	US-08-945-567D-2	Sequence 2, Appli
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1441	63	5.7	16321	4	US-09-949-016-12490	Sequence 12490, A
1442	63	5.7	18469	4	US-09-902-540-1205	Sequence 1205, Ap
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1461	63	5.7	63544	4	US-09-949-016-14025	Sequence 14025, A
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c1472	63	5.7	119981	4	US-09-949-016-11844	Sequence 11844, A
1473	63	5.7	119982	4	US-09-949-016-13606	Sequence 13606, A
c1474	63	5.7	119982	4	US-09-949-016-13606	Sequence 13606, A
c1475	63	5.7	137046	4	US-09-949-016-12427	Sequence 12427, A
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1478	63	5.7	147840	4	US-09-949-016-15236	Sequence 15236, A
1479	63	5.7	161900	4	US-09-949-016-12685	Sequence 12685, A
1480	63	5.7	161914	4	US-09-949-016-12906	Sequence 12906, A
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c1482	63	5.7	205163	4	US-09-949-016-17009	Sequence 17009, A
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1484	63	5.7	227979	4	US-09-949-016-11842	Sequence 11842, A
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c1487	63	5.7	254778	4	US-09-949-016-12417	Sequence 12417, A
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c1489	63	5.7	275110	4	US-09-949-016-16070	Sequence 16070, A
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ALIGNMENTS

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RESULT 1
US-08-905-223-27
; Sequence 27, Application US/08905223
; Patent No. 6222029
;  GENERAL INFORMATION:
;    APPLICANT:  Edwards, Jean-Baptiste D.
;    APPLICANT:  Duelert, Aymeric
;    APPLICANT:  Lacroix, Bruno
;    TITLE OF INVENTION:  5' ESTs FOR SECRETED PROTEINS
;    NUMBER OF SEQUENCES:  503
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson & Bear
;      STREET:  501 West Broadway
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92101-3505
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Win95
;      SOFTWARE:  Word
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/905,223
;      FILING DATE:
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Israelsen, Ned A.
;      REGISTRATION NUMBER:  29,655
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 235-8550
;      TELEFAX:  (619) 235-0176
;  INFORMATION FOR SEQ ID NO:  27:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  848 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  DOUBLE
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  CDNA
;    ORIGINAL SOURCE:
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;      ORGANISM:  Homo Sapiens
;      DEVELOPMENTAL STAGE:  Fetal
;      TISSUE TYPE:  kidney
;    FEATURE:
;      NAME/KEY:  sig_peptide
;      LOCATION:  32..73
;      IDENTIFICATION METHOD:  Von Heijne matrix
;      OTHER INFORMATION:  score 10.7
;      OTHER INFORMATION:  seq LWLLPFLVTAIHA/EL
US-08-905-223-27

Alignment Scores:
Pred. No.:              3.7e-131      Length:         848
Score:                  1064.00       Matches:        208
Percent Similarity:     97.65%        Conservative:   0
Best Local Similarity:  97.65%        Mismatches:     4
Query Match:            96.55%        Indels:         1
DB:                     3             Gaps:           0

US-09-989-724-387 (1-212) x US-08-905-223-27 (1-848)

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Qy         21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
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Db        632 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCA 668

RESULT 2
US-09-247-155-27
; Sequence 27, Application US/09247155A
; Patent No. 6312922
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, Jean-Baptiste
;  APPLICANT: Duclert, Aymeric
;  APPLICANT: Bougueleret, Lydie
;  TITLE OF INVENTION: Complementary DNAs
;  FILE REFERENCE: GENSET.021A
;  CURRENT APPLICATION NUMBER: US/09/247,155A
;  CURRENT FILING DATE: 1999-02-09
;  EARLIER APPLICATION NUMBER: 60/074,121
;  EARLIER FILING DATE: 1998-02-09
;  EARLIER APPLICATION NUMBER: 60/081,563
;  EARLIER FILING DATE: 1998-04-13
;  EARLIER APPLICATION NUMBER: 60/096,116
;  EARLIER FILING DATE: 1998-08-10
;  EARLIER APPLICATION NUMBER: 60/099,273
;  EARLIER FILING DATE: 1998-10-04
;  NUMBER OF SEQ ID NOS: 182
;  SOFTWARE: Patent.pm
; SEQ ID NO 27
;   LENGTH: 848
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: sig_peptide
;   LOCATION: 32..73
;   OTHER INFORMATION: Von Heijne matrix
US-09-247-155-27

Alignment Scores:
Pred. No.:              3.7e-131      Length:         848
Score:                  1064.00       Matches:        208
Percent Similarity:     97.65%        Conservative:   0
Best Local Similarity:  97.65%        Mismatches:     4
Query Match:            96.55%        Indels:         1
DB:                     3             Gaps:           0

US-09-989-724-387 (1-212) x US-09-247-155-27 (1-848)

Qy          1 MetLeuTrpLeuLeuPhePheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20
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Qy         41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
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Qy        101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120
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Db        332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy        121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 451

Qy        141 ProIleTrpIleIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy        161 LeuIleLeuSerGlyIleTrpGlnArgArgArgLysAsnLysGluProSerGluValAsp 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        512 CTGATTTTATCAGGGATCTGGCAACGTADAARAAAGAACAAAGAACCATCTGAAGTGGAT 571

Qy        181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        572 GACGCTGAARATAAKTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 631
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Qy        201 LeuAspMetLysGly-GlyIleLeuMetMetProSer 212
              ||||||||||||||| ||||||||||||||||||||||
Db        632 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCA 668

RESULT 3
US-09-663-600A-27
; Sequence 27, Application US/09663600A
; Patent No. 6573068
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, Jean-Baptiste
;  APPLICANT:  Duclert, Aymeric
;  APPLICANT:  Bougueleret, Lydie
;  TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
;  FILE REFERENCE: 31.US3.CIP
;  CURRENT APPLICATION NUMBER: US/09/663,600A
;  CURRENT FILING DATE:  2000-09-15
;  PRIOR APPLICATION NUMBER: 09/191,997
;  PRIOR FILING DATE: 1998-11-13
;  PRIOR APPLICATION NUMBER: 60/066,677
;  PRIOR FILING DATE: 1997-11-13
;  PRIOR APPLICATION NUMBER: 60/069,957
;  PRIOR FILING DATE: 1997-12-17
;  PRIOR APPLICATION NUMBER: 60/074,121
;  PRIOR FILING DATE: 1998-02-09
;  PRIOR APPLICATION NUMBER: 60/081,563
;  PRIOR FILING DATE: 1998-04-13
;  PRIOR APPLICATION NUMBER: 60/096,116
;  PRIOR FILING DATE: 1998-08-10
;  PRIOR APPLICATION NUMBER: 60/099,273
;  PRIOR FILING DATE: 1998-09-04
;  NUMBER OF SEQ ID NOS: 229
;  SOFTWARE: Patent.pm
; SEQ ID NO 27
;   LENGTH: 848
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: sig_peptide
;   LOCATION: 32..73
;   OTHER INFORMATION: Von Heijne matrix
US-09-663-600A-27

Alignment Scores:
Pred. No.:              3.7e-131      Length:          848
Score:                  1064.00       Matches:         208
Percent Similarity:     97.65%        Conservative:    0
Best Local Similarity:  97.65%        Mismatches:      4
Query Match:            96.55%        Indels:          1
DB:                     4             Gaps:            0

US-09-989-724-387 (1-212) x US-09-663-600A-27 (1-848)

Qy          1 MetLeuTrpLeuLeuPhePheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91

Qy         21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy         41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy         61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 271

Qy         81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 331

Qy        101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy        121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 451

Qy        141 ProIleTrpIleIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy        161 LeuIleLeuSerGlyIleTrpGlnArgArgArgLysAsnLysGluProSerGluValAsp 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        512 CTGATTTTATCAGGGATCTGGCAACGTADAARAAAGAACAAAGAACCATCTGAAGTGGAT 571

Qy        181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        572 GACGCTGAARATAAKTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 631

Qy        201 LeuAspMetLysGly-GlyIleLeuMetMetProSer 212
              ||||||||||||||| ||||||||||||||||||||||
Db        632 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCA 668

RESULT 4
US-09-621-976-5
; Sequence 5, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Jobert, S.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;  FILE REFERENCE: GENSET.054PR2
;  CURRENT APPLICATION NUMBER: US/09/621,976
;  CURRENT FILING DATE:  2000-07-21
;  NUMBER OF SEQ ID NOS: 19335
;  SOFTWARE: Patent.pm
; SEQ ID NO 5
;   LENGTH: 848
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 32..697
;   NAME/KEY: sig_peptide
;   LOCATION: 32..73
;   OTHER INFORMATION: Von Heijne matrix
US-09-621-976-5

Alignment Scores:
Pred. No.:              3.7e-131      Length:          848
Score:                  1064.00       Matches:         208
Percent Similarity:     97.65%        Conservative:    0
Best Local Similarity:  97.65%        Mismatches:      4
Query Match:            96.55%        Indels:          1
DB:                     4             Gaps:            0

US-09-989-724-387 (1-212) x US-09-621-976-5 (1-848)

Qy          1 MetLeuTrpLeuLeuPhePheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91

Qy         21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy         41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy         61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 271

Qy         81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 331

Qy        101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy        121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 451

Qy        141 ProIleTrpIleIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy        161 LeuIleLeuSerGlyIleTrpGlnArgArgArgLysAsnLysGluProSerGluValAsp 180
                ||||||||||||||||||||||||      ||||||||||||||||||||||||||||||||
Db        512 CTGATTTTATCAGGGATCTGGCAACGTADAARAAAGAACAAAGAACCATCTGAAGTGGAT 571

Qy        181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200
                |||||||||      ||||||||||||||||||||||||||||||||||||||||||||||||
Db        572 GACGCTGAARATAAKTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 631

Qy        201 LeuAspMetLysGly-GlyIleLeuMetMetProSer 212
                |||||||||||||| ||||||||||||||||||||
Db        632 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCA 668

RESULT 5
US-09-513-999C-5
; Sequence 5, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Duclert, A.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
;  FILE REFERENCE: 59.US2.REG
;  CURRENT APPLICATION NUMBER: US/09/513,999C
;  CURRENT FILING DATE:  2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/122,487
;  PRIOR FILING DATE: 1999-02-26
;  NUMBER OF SEQ ID NOS: 36681
;  SOFTWARE: Patent.pm
; SEQ ID NO 5
;   LENGTH: 848
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 32..697
;   FEATURE:
;   NAME/KEY: sig_peptide
;   LOCATION: 32..73
;   OTHER INFORMATION: Von Heijne matrix
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 540
;   OTHER INFORMATION: d=a or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 543
;   OTHER INFORMATION: r=a or g
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 581
;   OTHER INFORMATION: r=a or g
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 586
;   OTHER INFORMATION: k=g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 725
;   OTHER INFORMATION: r=a or g
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 788
;   OTHER INFORMATION: w=a or t
;   FEATURE:
;   NAME/KEY: UNSURE
;   LOCATION: 156
;   OTHER INFORMATION: Xaa=Ile or Lys or Arg
;   FEATURE:
;   NAME/KEY: UNSURE
;   LOCATION: 157
;   OTHER INFORMATION: Xaa=Lys or Arg
;   FEATURE:
;   NAME/KEY: UNSURE
;   LOCATION: 170
;   OTHER INFORMATION: Xaa=Asp or Asn
;   FEATURE:
;   NAME/KEY: UNSURE
;   LOCATION: 171
;   OTHER INFORMATION: Xaa=Lys or Asn
US-09-513-999C-5

Alignment Scores:
Pred. No.:              3.7e-131        Length:         848
Score:                  1064.00         Matches:        208
Percent Similarity:     97.65%          Conservative:   0
Best Local Similarity:  97.65%          Mismatches:     4
Query Match:            96.55%          Indels:         1
DB:                     4               Gaps:           0

US-09-989-724-387 (1-212) x US-09-513-999C-5 (1-848)

Qy          1 MetLeuTrpLeuLeuPhePheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91

Qy         21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy         41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy         61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 271

Qy         81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 331

Qy        101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy        121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 451

Qy        141 ProIleTrpIleIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy        161 LeuIleLeuSerGlyIleTrpGlnArgArgArgLysAsnLysGluProSerGluValAsp 180
                ||||||||||||||||||||||||      ||||||||||||||||||||||||||||||||
Db        512 CTGATTTTATCAGGGATCTGGCAACGTADAARAAAGAACAAAGAACCATCTGAAGTGGAT 571
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Qy        181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200
              ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        572 GACGCTGAAARATAAKTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 631

Qy        201 LeuAspMetLysGly-GlyIleLeuMetMetProSer 212
              ||||||||||||||| ||||||||||||||||||||
Db        632 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCA 668

RESULT 6
US-09-471-276-5
; Sequence 5, Application US/09471276
; Patent No. 6822072
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT: Duclert A.
;  APPLICANT: Giordano, J.Y.
;  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6822072
;  FILE REFERENCE: GENSET.025CP1
;  CURRENT APPLICATION NUMBER: US/09/471,276
;  CURRENT FILING DATE: 1999-12-21
;  EARLIER APPLICATION NUMBER: 09/057,719
;  EARLIER FILING DATE: 1998-04-09
;  EARLIER APPLICATION NUMBER: 09/069,047
;  EARLIER FILING DATE: 1998-04-28
;  EARLIER APPLICATION NUMBER: PCT/IB99/00712
;  EARLIER FILING DATE: 1999-04-09
;  NUMBER OF SEQ ID NOS: 1622
;  SOFTWARE: Patent.pm
; SEQ ID NO 5
;   LENGTH: 848
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 32..697
;   NAME/KEY: sig_peptide
;   LOCATION: 32..73
;   OTHER INFORMATION: Von Heijne matrix
US-09-471-276-5

Alignment Scores:
Pred. No.:              3.7e-131      Length:          848
Score:                  1064.00       Matches:         208
Percent Similarity:     97.65%        Conservative:    0
Best Local Similarity:  97.65%        Mismatches:      4
Query Match:            96.55%        Indels:          1
DB:                     4             Gaps:            0

US-09-989-724-387 (1-212) x US-09-471-276-5 (1-848)

Qy          1 MetLeuTrpLeuLeuPhePheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 ATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACCAGGT 91

Qy         21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151

Qy         41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA 211

Qy         61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGG 271

Qy         81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 GTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAG 331

Qy        101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 GTGCAATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGAC 391

Qy        121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 CAAACTCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTG 451

Qy        141 ProIleTrpIleIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        452 CCCATCTGGATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511

Qy        161 LeuIleLeuSerGlyIleTrpGlnArgArgArgLysAsnLysGluProSerGluValAsp 180
              |||||||||||||||||||||||||||      ||||||||||||||||||||||||||
Db        512 CTGATTTTATCAGGGATCTGGCAACGTADAARAAAGAACAAAGAACCATCTGAAGTGGAT 571

Qy        181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200
              ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        572 GACGCTGAARATAAKTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCC 631

Qy        201 LeuAspMetLysGly-GlyIleLeuMetMetProSer 212
              ||||||||||||||| ||||||||||||||||||||
Db        632 CTGGACATGAAGGGAGGGCATATTAATGATGCCTTCA 668

RESULT 7
US-08-989-299-3
; Sequence 3, Application US/08989299
; Patent No. 6194556
;  GENERAL INFORMATION:
;    APPLICANT:  Acton, Susan L.
;    APPLICANT:  Robinson, Keith E.
;    TITLE OF INVENTION:  ANGIOTENSIN CONVERTING ENZYME HOMOLOG
;    TITLE OF INVENTION:  AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FOLEY, HOAG & ELIOT LLP
;      STREET:  One Post Office Square
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109-2170
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/989,299
;      FILING DATE:  11-DEC-1997
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Arnold E., Beth
;      REGISTRATION NUMBER:  35,430
;      REFERENCE/DOCKET NUMBER:  MIA-025.01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-832-1000
;      TELEFAX:  617-832-7000
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2415 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-989-299-3

Alignment Scores:
Pred. No.:              3.45e-39      Length:          2415
Score:                  376.00        Matches:         79
Percent Similarity:     67.27%        Conservative:    32
Best Local Similarity:  47.88%        Mismatches:      48
Query Match:            34.12%        Indels:          6
DB:                     3             Gaps:            3
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US-09-989-724-387 (1-212) x US-08-989-299-3 (1-2415)

Qy         19 ProGlyAlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLys 38
              |||   |||:::   :::   |||||||||:::|||:::::::::|||||||||||||||
Db       1834 CCATATGCAGACCAAAGCATCAAAGTGAGGATAAGCCTAAAATCAGCTCTTGGAGATAAA 1893

Qy         39 AlaTyrAlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMet 58
              ||||||   |||:::   ||||||   |||||||||::::::   ||||||::::::|||
Db       1894 GCATATGAATGGAACGACAATGAAATGTACCTGTTCCGATCATCTGTTGCATATGCTATG 1953

Qy         59 Arg-----------LysValProAsnArgGluAlaThr---GluIleSerHisValLeu 73
              |||           ||||||   |||:::                           |||
Db       1954 AGGCAGTACTTTTTAAAAGTAAAAAATCAGATGATTCTTTTTGGGGAGGAGGATGTGCGA 2013

Qy         74 LeuCysAsnValThrGlnArgValSerPheTrpPheValValThrAspProSerLys--- 92
              :::   |||:::      |||:::||||||   |||   ||||||   |||
Db       2014 GTGGCTAATTTGAAACCAAGAATCTCCTTTAATTTCTTTGTCACTGCACCTAAAAATGTG 2073

Qy         93 AsnHisThrLeuProAlaValGluValGlnSerAlaIleArgMetAsnLysAsnArgIle 112
              :::      :::|||       ||||||:::   ||||||||||:::::::::||||||
Db       2074 TCTGATATCATTCCTAGAACTGAAGTTGAAAAGGCCATCAGGATGTCCCGGAGCCGTATC 2133

Qy        113 AsnAsnAlaPhePheLeuAsnAspGlnThrLeuGluPheLeuLysIleProSerThrLeu 132
              |||:::||||||   ||||||||   :::||||||||||||   |||      ||||||
Db       2134 AATGATGCTTTCCGTCTGAATGACAACAGCCTAGAGTTTCTGGGGATACAGCCAACACTT 2193

Qy        133 AlaProProMetAspProSerValProIleTrpIleIleIlePheGlyValIlePheCys 152
              ||||||       |||   |||   ||||||:::|||:::||||||||:::
Db       2194 GGACCTCCTAACCAGCCCCCTGTTTCCATATGGCTGATTGTTTTTGGAGTTGTGATGGGA 2253

Qy        153 IleIleIleValAlaIleAlaLeuLeuIleLeuSerGlyIleTrpGlnArgArgArgLys 172
              :::|||:::|||   |||   :::||||||   :::||||||   |||::::::|||
Db       2254 GTGATAGTGGTTGGCATTGTCATCCTGATCTTCACTGGGATCAGAGATCGGAAGAAGAAA 2313

Qy        173 AsnLysGluProSer 177
              ||||||      |||
Db       2314 AATAAAGCAAGAAGT 2328

RESULT 8
US-09-407-427-3
; Sequence 3, Application US/09407427
; Patent No. 6610497
; GENERAL INFORMATION:
;  APPLICANT:  Acton, Susan L.
;  APPLICANT:  Robison, Keith E.
;  TITLE OF INVENTION:  ANGIOTENSIN CONVERTING ENZYME HOMOLOG  AND THERAPEUTIC
;  TITLE OF INVENTION:  AND DIAGNOSTIC USES THEREFOR
;  FILE REFERENCE:  MNI-132CP2
;  CURRENT APPLICATION NUMBER: US/09/407,427
;  CURRENT FILING DATE:  1999-09-29
;  PRIOR APPLICATION NUMBER:  09/163,648
;  PRIOR FILING DATE:  1998-09-30
;  PRIOR APPLICATION NUMBER:  08/989,299
;  PRIOR FILING DATE:  1997-12-11
;  NUMBER OF SEQ ID NOS:  14
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 2415
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-407-427-3

Alignment Scores:
Pred. No.:              3.45e-39       Length:          2415
Score:                  376.00         Matches:         79
Percent Similarity:     67.27%         Conservative:    32
Best Local Similarity:  47.88%         Mismatches:      48
Query Match:            34.12%         Indels:          6
DB:                     4              Gaps:            3

US-09-989-724-387 (1-212) x US-09-407-427-3 (1-2415)

Qy         19 ProGlyAlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLys 38
              |||   |||:::   :::   |||||||||:::|||:::::::::|||||||||||||||
Db       1834 CCATATGCAGACCAAAGCATCAAAGTGAGGATAAGCCTAAAATCAGCTCTTGGAGATAAA 1893

Qy         39 AlaTyrAlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMet 58
              ||||||   |||:::   ||||||   |||||||||::::::   ||||||::::::|||
Db       1894 GCATATGAATGGAACGACAATGAAATGTACCTGTTCCGATCATCTGTTGCATATGCTATG 1953

Qy         59 Arg-----------LysValProAsnArgGluAlaThr---GluIleSerHisValLeu 73
              |||           ||||||   |||:::                           |||
Db       1954 AGGCAGTACTTTTTAAAAGTAAAAAATCAGATGATTCTTTTTGGGGAGGAGGATGTGCGA 2013

Qy         74 LeuCysAsnValThrGlnArgValSerPheTrpPheValValThrAspProSerLys--- 92
              :::   |||:::      |||:::||||||   |||   ||||||   |||
Db       2014 GTGGCTAATTTGAAACCAAGAATCTCCTTTAATTTCTTTGTCACTGCACCTAAAAATGTG 2073

Qy         93 AsnHisThrLeuProAlaValGluValGlnSerAlaIleArgMetAsnLysAsnArgIle 112
              :::      :::|||       ||||||:::   ||||||||||:::::::::||||||
Db       2074 TCTGATATCATTCCTAGAACTGAAGTTGAAAAGGCCATCAGGATGTCCCGGAGCCGTATC 2133

Qy        113 AsnAsnAlaPhePheLeuAsnAspGlnThrLeuGluPheLeuLysIleProSerThrLeu 132
              |||:::||||||   ||||||||   :::||||||||||||   |||      ||||||
Db       2134 AATGATGCTTTCCGTCTGAATGACAACAGCCTAGAGTTTCTGGGGATACAGCCAACACTT 2193

Qy        133 AlaProProMetAspProSerValProIleTrpIleIleIlePheGlyValIlePheCys 152
              ||||||       |||   |||   ||||||:::|||:::||||||||:::
Db       2194 GGACCTCCTAACCAGCCCCCTGTTTCCATATGGCTGATTGTTTTTGGAGTTGTGATGGGA 2253

Qy        153 IleIleIleValAlaIleAlaLeuLeuIleLeuSerGlyIleTrpGlnArgArgArgLys 172
              :::|||:::|||   |||   :::||||||   :::||||||   |||::::::|||
Db       2254 GTGATAGTGGTTGGCATTGTCATCCTGATCTTCACTGGGATCAGAGATCGGAAGAAGAAA 2313

Qy        173 AsnLysGluProSer 177
              ||||||      |||
Db       2314 AATAAAGCAAGAAGT 2328

RESULT 9
US-09-949-016-5413
; Sequence 5413, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5413
;   LENGTH: 3388
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-5413

Alignment Scores:
Pred. No.:              5.89e-39       Length:          3388
Score:                  376.00         Matches:         79
Percent Similarity:     67.27%         Conservative:    32
Best Local Similarity:  47.88%         Mismatches:      48
Query Match:            34.12%         Indels:          6
DB:                     4              Gaps:            3

US-09-989-724-387 (1-212) x US-09-949-016-5413 (1-3388)

Qy         19 ProGlyAlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLys 38
              |||   |||:::   :::   |||||||||:::|||:::::::::|||||||||||||||
Db       1937 CCATATGCAGACCAAAGCATCAAAGTGAGGATAAGCCTAAAATCAGCTCTTGGAGATAAA 1996
```

```
Qy         39 AlaTyrAlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMet 58
              ||||||   |||:::   ||||||   ||||||||:::::::   |||||:::::::|||
Db       1997 GCATATGAATGGAACGACAATGAAATGTACCTGTTCCGATCATCTGTTGCATATGCTATG 2056

Qy         59 Arg------------LysValProAsnArgGluAlaThr---GluIleSerHisValLeu 73
              |||            ||||||   |||:::                          |||
Db       2057 AGGCAGTACTTTTTAAAAGTAAAAAATCAGATGATTCTTTTTGGGGAGGAGGATGTGCGA 2116

Qy         74 LeuCysAsnValThrGlnArgValSerPheTrpPheValValThrAspProSerLys--- 92
              :::   |||:::      |||:::||||||   |||   ||||||   |||
Db       2117 GTGGCTAATTTGAAACCAAGAATCTCCTTTAATTTCTTTGTCACTGCACCTAAAAATGTG 2176

Qy         93 AsnHisThrLeuProAlaValGluValGlnSerAlaIleArgMetAsnLysAsnArgIle 112
              :::      :::|||      ||||||:::   ||||||||||||:::::::::||||||
Db       2177 TCTGATATCATTCCTAGAACTGAAGTTGAAAAGGCCATCAGGATGTCCCGGAGCCGTATC 2236

Qy        113 AsnAsnAlaPhePheLeuAsnAspGlnThrLeuGluPheLeuLysIleProSerThrLeu 132
              |||:::||||||   ||||||||   :::||||||||||||   |||      ||||||
Db       2237 AATGATGCTTTCCGTCTGAATGACAACAGCCTAGAGTTTCTGGGGATACAGCCAACACTT 2296

Qy        133 AlaProProMetAspProSerValProIleTrpIleIleIlePheGlyValIlePheCys 152
                 ||||||      |||   |||   ||||||:::|||:::|||||||||:::
Db       2297 GGACCTCCTAACCAGCCCCCTGTTTCCATATGGCTGATTGTTTTTGGAGTTGTGATGGGA 2356

Qy        153 IleIleIleValAlaIleAlaLeuLeuIleLeuSerGlyIleTrpGlnArgArgArgLys 172
              :::|||:::|||   |||   :::||||||   :::||||||      |||:::::|||
Db       2357 GTGATAGTGGTTGGCATTGTCATCCTGATCTTCACTGGGATCAGAGATCGGAAGAAGAAA 2416

Qy        173 AsnLysGluProSer 177
              ||||||      |||
Db       2417 AATAAAGCAAGAAGT 2431

RESULT 10
US-08-989-299-1
; Sequence 1, Application US/08989299
; Patent No. 6194556
;  GENERAL INFORMATION:
;    APPLICANT:  Acton, Susan L.
;    APPLICANT:  Robinson, Keith E.
;    TITLE OF INVENTION:  ANGIOTENSIN CONVERTING ENZYME HOMOLOG
;    TITLE OF INVENTION:  AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FOLEY, HOAG & ELIOT LLP
;      STREET:  One Post Office Square
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109-2170
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/989,299
;      FILING DATE:  11-DEC-1997
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Arnold E., Beth
;      REGISTRATION NUMBER:  35,430
;      REFERENCE/DOCKET NUMBER:  MIA-025.01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-832-1000
;      TELEFAX:  617-832-7000
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3396 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  82..2496
US-08-989-299-1

Alignment Scores:
Pred. No.:                5.91e-39      Length:          3396
Score:                    376.00        Matches:         79
Percent Similarity:       67.27%        Conservative:    32
Best Local Similarity:    47.88%        Mismatches:      48
Query Match:              34.12%        Indels:          6
DB:                       3             Gaps:            3

US-09-989-724-387 (1-212) x US-08-989-299-1 (1-3396)

Qy         19 ProGlyAlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLys 38
              |||   |||:::   :::   |||||||||:::|||:::::::::|||||||||||||||
Db       1915 CCATATGCAGACCAAAGCATCAAAGTGAGGATAAGCCTAAAATCAGCTCTTGGAGATAAA 1974

Qy         39 AlaTyrAlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMet 58
              ||||||   |||:::   ||||||   |||||||||:::::   ||||||:::::|||
Db       1975 GCATATGAATGGAACGACAATGAAATGTACCTGTTCCGATCATCTGTTGCATATGCTATG 2034

Qy         59 Arg------------LysValProAsnArgGluAlaThr---GluIleSerHisValLeu 73
              |||            ||||||   |||:::                          |||
Db       2035 AGGCAGTACTTTTTAAAAGTAAAAAATCAGATGATTCTTTTTGGGGAGGAGGATGTGCGA 2094

Qy         74 LeuCysAsnValThrGlnArgValSerPheTrpPheValValThrAspProSerLys--- 92
              :::   |||:::      |||:::||||||   |||   ||||||   |||
Db       2095 GTGGCTAATTTGAAACCAAGAATCTCCTTTAATTTCTTTGTCACTGCACCTAAAAATGTG 2154

Qy         93 AsnHisThrLeuProAlaValGluValGlnSerAlaIleArgMetAsnLysAsnArgIle 112
              :::      :::|||      ||||||:::   ||||||||||||:::::::::||||||
Db       2155 TCTGATATCATTCCTAGAACTGAAGTTGAAAAGGCCATCAGGATGTCCCGGAGCCGTATC 2214

Qy        113 AsnAsnAlaPhePheLeuAsnAspGlnThrLeuGluPheLeuLysIleProSerThrLeu 132
              |||:::||||||   ||||||||   :::||||||||||||   |||      ||||||
Db       2215 AATGATGCTTTCCGTCTGAATGACAACAGCCTAGAGTTTCTGGGGATACAGCCAACACTT 2274

Qy        133 AlaProProMetAspProSerValProIleTrpIleIleIlePheGlyValIlePheCys 152
                 ||||||      |||   |||   ||||||:::|||:::|||||||||:::
Db       2275 GGACCTCCTAACCAGCCCCCTGTTTCCATATGGCTGATTGTTTTTGGAGTTGTGATGGGA 2334

Qy        153 IleIleIleValAlaIleAlaLeuLeuIleLeuSerGlyIleTrpGlnArgArgArgLys 172
              :::|||:::|||   |||   :::||||||   :::||||||      |||:::::|||
Db       2335 GTGATAGTGGTTGGCATTGTCATCCTGATCTTCACTGGGATCAGAGATCGGAAGAAGAAA 2394

Qy        173 AsnLysGluProSer 177
              ||||||      |||
Db       2395 AATAAAGCAAGAAGT 2409

RESULT 11
US-10-158-847-141
; Sequence 141, Application US/10158847
; Patent No. 6592865
; GENERAL INFORMATION:
;  APPLICANT: Tom Parry et al.
;  TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
;  FILE REFERENCE: PF557
;  CURRENT APPLICATION NUMBER: US/10/158,847
;  CURRENT FILING DATE:  2002-06-03
;  PRIOR APPLICATION NUMBER: 60/295,004
;  PRIOR FILING DATE: 2001-06-04
;  NUMBER OF SEQ ID NOS: 158
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 141
;   LENGTH: 3396
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-158-847-141

Alignment Scores:
Pred. No.:                5.91e-39      Length:          3396
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Score:	376.00	Matches:	79
Percent Similarity:	67.27%	Conservative:	32
Best Local Similarity:	47.88%	Mismatches:	48
Query Match:	34.12%	Indels:	6
DB:	4	Gaps:	3

US-09-989-724-387 (1-212) x US-10-158-847-141 (1-3396)

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Qy         19 ProGlyAlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLys 38
Db       1915 CCATATGCAGACCAAAGCATCAAAGTGAGGATAAGCCTAAAATCAGCTCTTGGAGATAAA 1974

Qy         39 AlaTyrAlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMet 58
Db       1975 GCATATGAATGGAACGACAATGAAATGTACCTGTTCCGATCATCTGTTGCATATGCTATG 2034

Qy         59 Arg----------LysValProAsnArgGluAlaThr---GluIleSerHisValLeu 73
Db       2035 AGGCAGTACTTTTTAAAAGTAAAAAATCAGATGATTCTTTTTGGGGAGGAGGATGTGCGA 2094

Qy         74 LeuCysAsnValThrGlnArgValSerPheTrpPheValValThrAspProSerLys--- 92
Db       2095 GTGGCTAATTTGAAACCAAGAATCTCCTTTAATTTCTTTGTCACTGCACCTAAAAATGTG 2154

Qy         93 AsnHisThrLeuProAlaValGluValGlnSerAlaIleArgMetAsnLysAsnArgIle 112
Db       2155 TCTGATATCATTCCTAGAACTGAAGTTGAAAAGGCCATCAGGATGTCCCGGAGCCGTATC 2214

Qy        113 AsnAsnAlaPhePheLeuAsnAspGlnThrLeuGluPheLeuLysIleProSerThrLeu 132
Db       2215 AATGATGCTTTCCGTCTGAATGACAACAGCCTAGAGTTTCTGGGGATACAGCCAACACTT 2274

Qy        133 AlaProProMetAspProSerValProIleTrpIleIleIlePheGlyValIlePheCys 152
Db       2275 GGACCTCCTAACCAGCCCCCTGTTTCCATATGGCTGATTGTTTTTGGAGTTGTGATGGGA 2334

Qy        153 IleIleIleValAlaIleAlaLeuLeuIleLeuSerGlyIleTrpGlnArgArgArgLys 172
Db       2335 GTGATAGTGGTTGGCATTGTCATCCTGATCTTCACTGGGATCAGAGATCGGAAGAAGAAA 2394

Qy        173 AsnLysGluProSer 177
Db       2395 AATAAAGCAAGAAGT 2409
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RESULT 12
US-09-407-427-1
; Sequence 1, Application US/09407427
; Patent No. 6610497
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG AND THERAPEUTIC
; TITLE OF INVENTION: AND DIAGNOSTIC USES THEREFOR
; FILE REFERENCE: MNI-132CP2
; CURRENT APPLICATION NUMBER: US/09/407,427
; CURRENT FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 09/163,648
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 08/989,299
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3396
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (82)..(2496)
US-09-407-427-1

Alignment Scores:
Pred. No.: 5.91e-39 Length: 3396

Score:	376.00	Matches:	79
Percent Similarity:	67.27%	Conservative:	32
Best Local Similarity:	47.88%	Mismatches:	48
Query Match:	34.12%	Indels:	6
DB:	4	Gaps:	3

US-09-989-724-387 (1-212) x US-09-407-427-1 (1-3396)

```
Qy         19 ProGlyAlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLys 38
Db       1915 CCATATGCAGACCAAAGCATCAAAGTGAGGATAAGCCTAAAATCAGCTCTTGGAGATAAA 1974

Qy         39 AlaTyrAlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMet 58
Db       1975 GCATATGAATGGAACGACAATGAAATGTACCTGTTCCGATCATCTGTTGCATATGCTATG 2034

Qy         59 Arg----------LysValProAsnArgGluAlaThr---GluIleSerHisValLeu 73
Db       2035 AGGCAGTACTTTTTAAAAGTAAAAAATCAGATGATTCTTTTTGGGGAGGAGGATGTGCGA 2094

Qy         74 LeuCysAsnValThrGlnArgValSerPheTrpPheValValThrAspProSerLys--- 92
Db       2095 GTGGCTAATTTGAAACCAAGAATCTCCTTTAATTTCTTTGTCACTGCACCTAAAAATGTG 2154

Qy         93 AsnHisThrLeuProAlaValGluValGlnSerAlaIleArgMetAsnLysAsnArgIle 112
Db       2155 TCTGATATCATTCCTAGAACTGAAGTTGAAAAGGCCATCAGGATGTCCCGGAGCCGTATC 2214

Qy        113 AsnAsnAlaPhePheLeuAsnAspGlnThrLeuGluPheLeuLysIleProSerThrLeu 132
Db       2215 AATGATGCTTTCCGTCTGAATGACAACAGCCTAGAGTTTCTGGGGATACAGCCAACACTT 2274

Qy        133 AlaProProMetAspProSerValProIleTrpIleIleIlePheGlyValIlePheCys 152
Db       2275 GGACCTCCTAACCAGCCCCCTGTTTCCATATGGCTGATTGTTTTTGGAGTTGTGATGGGA 2334

Qy        153 IleIleIleValAlaIleAlaLeuLeuIleLeuSerGlyIleTrpGlnArgArgArgLys 172
Db       2335 GTGATAGTGGTTGGCATTGTCATCCTGATCTTCACTGGGATCAGAGATCGGAAGAAGAAA 2394

Qy        173 AsnLysGluProSer 177
Db       2395 AATAAAGCAAGAAGT 2409
```

RESULT 13
US-10-158-847-137
; Sequence 137, Application US/10158847
; Patent No. 6592865
; GENERAL INFORMATION:
; APPLICANT: Tom Parry et al.
; TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
; FILE REFERENCE: PF557
; CURRENT APPLICATION NUMBER: US/10/158,847
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/295,004
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 137
; LENGTH: 2920
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1707)..(1707)
; OTHER INFORMATION: n equals any amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2702)..(2702)
; OTHER INFORMATION: n equals any amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2749)..(2749)

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;   OTHER INFORMATION: n equals any amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (2757)..(2757)
;   OTHER INFORMATION: n equals any amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (2788)..(2789)
;   OTHER INFORMATION: n equals any amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (2819)..(2819)
;   OTHER INFORMATION: n equals any amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (2835)..(2835)
;   OTHER INFORMATION: n equals any amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (2856)..(2856)
;   OTHER INFORMATION: n equals any amino acid
US-10-158-847-137

Alignment Scores:
Pred. No.:              8.37e-37        Length:         2920
Score:                  359.00          Matches:        75
Percent Similarity:     67.30%          Conservative:   32
Best Local Similarity:  47.17%          Mismatches:     46
Query Match:            32.58%          Indels:         6
DB:                     4               Gaps:           3

US-09-989-724-387 (1-212) x US-10-158-847-137 (1-2920)

Qy         19 ProGlyAlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLys 38
              |||   |||:::   :::   |||||||||:::|||::::::::|||||||||||||||
Db       1863 CCATATGCAGACCAAAGCATCAAAGTGAGGATAAGCCTAAAATCAGCTCTTGGAGATAAA 1922

Qy         39 AlaTyrAlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMet 58
              ||||||   |||:::   ||||||   |||||||||::::::   ||||||:::::|||
Db       1923 GCATATGAATGGAACGACAATGAAATGTACCTGTTCCGATCATCTGTTGCATATGCTATG 1982

Qy         59 Arg------------LysValProAsnArgGluAlaThr---GluIleSerHisValLeu 73
              |||             ||||||   |||:::              |||
Db       1983 AGGCAGTACTTTTTAAAAGTAAAAAATCAGATGATTCTTTTTGGGGAGGAGGATGTGCGA 2042

Qy         74 LeuCysAsnValThrGlnArgValSerPheTrpPheValValThrAspProSerLys--- 92
              :::   |||:::      |||:::||||||   |||   ||||||   |||
Db       2043 GTGGCTAATTTGAAACCAAGAATCTCCTTTAATTTCTTTGTCACTGCACCTAAAAATGTG 2102

Qy         93 AsnHisThrLeuProAlaValGluValGlnSerAlaIleArgMetAsnLysAsnArgIle 112
              :::      :::|||      |||||:::   |||||||||||:::::::::||||||
Db       2103 TCTGATATCATTCCTAGAACTGAAGTTGAAAAGGCCATCAGGATGTCCCGGAGCCGTATC 2162

Qy        113 AsnAsnAlaPhePheLeuAsnAspGlnThrLeuGluPheLeuLysIleProSerThrLeu 132
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Db       2163 AATGATGCTTTCCGTCTGAATGACGACAGCCTAGAGTTTCTGGGGATACAGCCAACACTT 2222

Qy        133 AlaProProMetAspProSerValProIleTrpIleIleIlePheGlyValIlePheCys 152
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Db       2223 GGACCTCCTAACCAGCCCCCTGTTTCCATATGGCTGATTGTTTTTGGAGTTGTGATGGGA 2282

Qy        153 IleIleIleValAlaIleAlaLeuLeuIleLeuSerGlyIleTrpGlnArgArgArg 171
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Db       2283 GTGATAGTGGTTGGCATTGTCATCCTGATCTTCACTGGGATCAGAGATCGGAAGAAG 2339

RESULT 14
US-09-289-349-6
; Sequence 6, Application US/09289349
; Patent No. 6277574
; GENERAL INFORMATION:
;  APPLICANT: Walker, Michael, G.
;  APPLICANT: Volkmuth, Wayne
;  APPLICANT: Klinger, Tod, M.
;  APPLICANT: Azimzai, Yalda
;  APPLICANT: Yue, Henry
;  TITLE OF INVENTION: GENES ASSOCIATED WITH DISEASES OF THE KIDNEY
;  FILE REFERENCE: PB-0010 US
;  CURRENT APPLICATION NUMBER: US/09/289,349
;  CURRENT FILING DATE: 1999-04-09
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PERL Program
; SEQ ID NO 6
;   LENGTH: 862
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE: -
;   OTHER INFORMATION: 2580580CT1
US-09-289-349-6

Alignment Scores:
Pred. No.:              2.71e-27        Length:         862
Score:                  281.00          Matches:        57
Percent Similarity:     98.28%          Conservative:   0
Best Local Similarity:  98.28%          Mismatches:     0
Query Match:            25.50%          Indels:         1
DB:                     3               Gaps:           0

US-09-989-724-387 (1-212) x US-09-289-349-6 (1-862)

Qy        156 ValAlaIleAlaLeuLeuIleLeuSerGlyIleTrpGlnArgArgArgLysAsnLysGlu 175
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Db          1 GTTGCAATTGCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAA 60

Qy        176 ProSerGluValAspAspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGly 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCATCTGAAGTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATTGAAAATGGC 120

Qy        196 IleProSerAspProLeuAspMetLysGly-GlyIleLeuMetMetProSer 212
              |||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        121 ATCCCCTCTGATCCCCTGGACATGAAGGGAGGGCATATTAATGATGCCTTCA 172

RESULT 15
US-09-280-116-40/c
; Sequence 40, Application US/09280116A
; Patent No. 6331427
; GENERAL INFORMATION:
;  APPLICANT: Robison, Keith E.
;  TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
;  FILE REFERENCE: 5800-24, 035800/176965
;  CURRENT APPLICATION NUMBER: US/09/280,116A
;  CURRENT FILING DATE: 1999-03-26
;  NUMBER OF SEQ ID NOS: 268
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
;   LENGTH: 2350
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: angiotensin-converting enzyme
US-09-280-116-40

Alignment Scores:
Pred. No.:              2.63e-20        Length:         2350
Score:                  233.50          Matches:        61
Percent Similarity:     62.86%          Conservative:   27
Best Local Similarity:  43.57%          Mismatches:     37
Query Match:            21.19%          Indels:         16
DB:                     3               Gaps:           4

US-09-989-724-387 (1-212) x US-09-280-116-40 (1-2350)

Qy         10 ThrAlaIleHisAlaGluLeuCysGlnProGlyAlaGluAsnAlaPheLysValArgLeu 29
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Db        435 ACTGGAGTCCATATGCAG----------------ACCAAAAGCATCAAAGTGAGGATA 394

Qy         30 -SerIleArgThrAlaLeuGlyAspLysAlaTyrAlaTrpAspThrAsnGluGluTyrLe 49
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Db        393 AAGCCTAAAATCAGCTCTTGGAGATAAAGCATATGAATGGAACGACAATGAAATGTACCT 334

Qy         49 uPheLysAlaMetValAlaPheSerMetArg-----------LysValProAsnArgGl 65

Db        333 GTTCCGATCATCTGTTGCATATGCTATGAGGCAGTACTTTTTAAAAGTAAAAAATCAGCA 274

Qy         65 uAlaThrGluIleSerHis------ValLeuLeuCysAsnValThrGlnArgValSerPh 83

Db        273 TGATTCTTT-TTGGGGAGGAAGGATGTGCGAGTGGCTAATTTGAAACCAAGAATCTCCTT 215

Qy         83 eTrpPhe-ValValThrAspProSerLys---AsnHisThrLeuProAlaValGluValG 102

Db        214 TAATTTCTTTGGTCACTGCCCCTAAAAATGTGTCTGATATCATTCCTAGAACTGAAGTTG 155

Qy        102 lnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAspGlnT 122

Db        154 AAAAGGCCATCAGGATGTCCCGGAGCCGTATCAATGATGCTTTCCGTCTGAATGACAACA 95

Qy        122 hrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140

Db         94 GCCTAGAGTTTCTGGGGATACAGCCAACACTTGGACCTCCTAACCAGCCCCCTGTT 39
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 24, 2005, 20:39:36 ; Search time 494 Seconds
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2536.488 Million cell updates/sec

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Searched: 5384158 seqs, 2955248155 residues

Total number of hits satisfying chosen parameters: 10768316

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SUMMARIES

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520	1089	98.8	1432	14	US-10-097-065-17	Sequence 17, Appl
521	1089	98.8	1432	17	US-10-372-876-17	Sequence 17, Appl
522	1082	98.2	1447	10	US-09-892-877-22	Sequence 22, Appl
523	1082	98.2	1447	10	US-09-948-783-22	Sequence 22, Appl
524	1064	96.6	848	10	US-09-903-190-27	Sequence 27, Appl
525	1064	96.6	848	15	US-10-319-763-27	Sequence 27, Appl
526	1062	96.4	1356	14	US-10-097-065-122	Sequence 122, App
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532	376	34.1	3325	13	US-10-114-893-85	Sequence 85, Appl
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535	376	34.1	3396	14	US-10-158-847-141	Sequence 141, App
536	376	34.1	3396	15	US-10-158-825-141	Sequence 141, App
537	376	34.1	3396	18	US-10-158-825-141	Sequence 141, App
538	376	34.1	3405	15	US-10-005-956-569	Sequence 569, App
539	376	34.1	3405	15	US-10-005-956-842	Sequence 842, App
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989	359	32.6	2911	9	US-09-969-384-12	Sequence 12, Appl
990	359	32.6	2920	9	US-09-969-384-2	Sequence 2, Appli
991	359	32.6	2920	14	US-10-158-847-137	Sequence 137, App
992	359	32.6	2920	15	US-10-158-825-137	Sequence 137, App
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1008	91.5	8.3	3134	14	US-10-152-661-478	Sequence 478, App
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1097	80.5	7.3	1636	19	US-10-860-790-467	Sequence 467, App
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1103	80	7.3	390	18	US-10-425-115-78618	Sequence 78618, A
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1105	79.5	7.2	906	15	US-10-032-214-113	Sequence 113, App
1106	79.5	7.2	1065	17	US-10-369-493-24032	Sequence 24032, A
1107	79.5	7.2	1506	15	US-10-156-761-4244	Sequence 4244, Ap
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1116	79	7.2	5205	15	US-10-288-252-29	Sequence 29, Appl
1117	79	7.2	5205	18	US-10-398-038-29	Sequence 29, Appl
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1126	78.5	7.1	1060	10	US-09-907-969-568	Sequence 568, App
1127	78.5	7.1	1060	15	US-10-198-053-568	Sequence 568, App
1128	78.5	7.1	1060	19	US-10-860-790-568	Sequence 568, App
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1131	78.5	7.1	1761	10	US-09-907-969-387	Sequence 387, App
1132	78.5	7.1	1761	10	US-09-827-271-387	Sequence 387, App
1133	78.5	7.1	1761	15	US-10-198-053-387	Sequence 387, App
1134	78.5	7.1	1761	19	US-10-860-790-387	Sequence 387, App
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1137	78.5	7.1	2100	14	US-10-152-661-479	Sequence 479, App
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1154	78.5	7.1	2996	18	US-10-717-296-205	Sequence 205, App
1155	78.5	7.1	2996	19	US-10-860-790-311	Sequence 311, App
1156	78.5	7.1	2996	19	US-10-860-790-462	Sequence 462, App
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c1167	78.5	7.1	15056	15	US-10-226-820-10	Sequence 10, Appl
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1177	78	7.1	134481	13	US-10-087-192-295	Sequence 295, App
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1183	77.5	7.0	2313	9	US-09-789-919-19	Sequence 19, Appl
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1185	77.5	7.0	36462	18	US-10-739-096-1	Sequence 1, Appli
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1197	76.5	6.9	1650	10	US-09-972-268-5	Sequence 5, Appli
1198	76.5	6.9	1650	14	US-10-161-572-4	Sequence 4, Appli
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1208	76	6.9	928	16	US-10-021-660-14	Sequence 14, Appl
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1225	75.5	6.9	909	15	US-10-032-214-124	Sequence 124, App
1226	75.5	6.9	909	15	US-10-032-214-134	Sequence 134, App
1227	75.5	6.9	910	15	US-10-032-214-116	Sequence 116, App
1228	75.5	6.9	910	15	US-10-032-214-140	Sequence 140, App
1229	75.5	6.9	912	15	US-10-032-214-125	Sequence 125, App
1230	75.5	6.9	912	15	US-10-032-214-132	Sequence 132, App
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1240	75.5	6.9	1721	14	US-10-097-340-211	Sequence 211, App
1241	75.5	6.9	1721	14	US-10-171-311-155	Sequence 155, App
1242	75.5	6.9	1721	15	US-10-007-926A-58	Sequence 58, Appl
1243	75.5	6.9	1721	15	US-10-029-517-3	Sequence 3, Appli
1244	75.5	6.9	1721	17	US-10-172-118-775	Sequence 775, App
1245	75.5	6.9	1721	17	US-10-342-887-775	Sequence 775, App
1246	75.5	6.9	1721	18	US-10-775-920-88	Sequence 88, Appl
1247	75.5	6.9	1799	17	US-10-447-839A-19	Sequence 19, Appl
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1249	75.5	6.9	1804	15	US-10-029-517-17	Sequence 17, Appl
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1251	75.5	6.9	1804	18	US-10-775-920-84	Sequence 84, Appl
1252	75.5	6.9	1823	15	US-10-101-510-339	Sequence 339, App
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1260	75.5	6.9	4139	9	US-09-964-824A-578	Sequence 578, App
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1262	75.5	6.9	4139	9	US-09-880-107-2121	Sequence 2121, Ap
1263	75.5	6.9	4139	11	US-09-968-007A-751	Sequence 751, App
1264	75.5	6.9	4139	14	US-10-171-311-157	Sequence 157, App
1265	75.5	6.9	4139	15	US-10-177-293-310	Sequence 310, App
1266	75.5	6.9	4139	17	US-10-440-464-155	Sequence 155, App
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1269	75.5	6.9	4139	18	US-10-775-920-85	Sequence 85, Appl
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c1273	75.5	6.9	7646	17	US-10-329-624-121	Sequence 121, App
c1274	75.5	6.9	9461	13	US-10-194-163-513	Sequence 513, App
1275	75.5	6.9	96594	11	US-09-997-722-22	Sequence 22, Appl
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c1280	75	6.8	667	17	US-10-027-632-239890	Sequence 239890,
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1295	75	6.8	5361	18	US-10-783-528-19	Sequence 19, Appl
1296	75	6.8	5373	17	US-10-641-643-1318	Sequence 1318, Ap
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1298	75	6.8	8827	9	US-09-893-238-1	Sequence 1, Appli
1299	75	6.8	12571	9	US-09-965-553-20	Sequence 20, Appl
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1301	75	6.8	12571	17	US-10-395-607-20	Sequence 20, Appl
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1304	75	6.8	153740	18	US-10-322-696-85	Sequence 85, Appl
1305	74.5	6.8	924	9	US-09-825-882-17	Sequence 17, Appl
1306	74.5	6.8	924	17	US-10-343-650A-679	Sequence 679, App
1307	74.5	6.8	924	18	US-10-724-208-17	Sequence 17, Appl
1308	74.5	6.8	924	18	US-10-770-127-188	Sequence 188, App
1309	74.5	6.8	924	18	US-10-724-209-17	Sequence 17, Appl
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c1312	74.5	6.8	1286	17	US-10-027-632-122566	Sequence 122566,
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1314	74.5	6.8	1711	17	US-10-152-319A-1765	Sequence 1765, Ap
1315	74.5	6.8	1725	18	US-10-363-829-117	Sequence 117, App
1316	74.5	6.8	1727	9	US-09-822-830A-41	Sequence 41, Appl
1317	74.5	6.8	2149	17	US-10-641-643-765	Sequence 765, App
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1328	74	6.7	1861	18	US-10-739-930-476	Sequence 476, App
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1330	74	6.7	1919	17	US-10-333-227-15	Sequence 15, Appl
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1333	74	6.7	2163	18	US-10-425-115-66386	Sequence 66386, A
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c1337	74	6.7	2862	14	US-10-267-718-35	Sequence 35, Appl
c1338	74	6.7	2954	9	US-09-354-453-34	Sequence 34, Appl
c1339	74	6.7	2954	14	US-10-267-718-34	Sequence 34, Appl
1340	74	6.7	4398	18	US-10-425-115-119186	Sequence 119186,
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c1342	74	6.7	6760	14	US-10-267-718-33	Sequence 33, Appl
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1344	74	6.7	45152	13	US-10-087-192-1387	Sequence 1387, Ap
1345	74	6.7	113486	18	US-10-417-375-18	Sequence 18, Appl
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1353	73.5	6.7	912	15	US-10-032-214-109	Sequence 109, App
1354	73.5	6.7	912	15	US-10-032-214-122	Sequence 122, App
1355	73.5	6.7	913	15	US-10-032-214-121	Sequence 121, App
1356	73.5	6.7	934	18	US-10-494-672-327	Sequence 327, App
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